

STIC-Biotech/ChemLib

100839

sm

From: Spector, Lorraine  
Sent: Monday, August 11, 2003 1:39 PM  
To: STIC-Biotech/ChemLib  
Subject: SEARCH request for Serial No. 09/938418

CRSE

STIC,

Please search SEQ ID NO: 2 (nucleic acid) and 7 (protein). For the protein, please ALSO do a word search with word size of 6 amino acids.

-pending  
-issued  
-commercial

Thanks.

Lorraine Spector  
703-308-1793  
U.S. Patent and Trademark Office  
Art Unit 1647  
lorraine.spector@uspto.gov  
CM1-10B11  
Mailbox 10-B19

RECEIVED  
AUG 11 2003  
(SIC)

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 8/13  
Date Completed: 8/21  
Searcher Prep/Review: SS  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 100839**

**TO: Lorraine Spector**  
**Location: cm-1/10b19**  
**Art Unit: 1647**  
**Thursday, August 21, 2003**  
**Case Serial Number: 09938418**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**CM1-6B06**  
**Phone: 305-1954**

**paul.schulwitz@uspto.gov**

### **Search Notes**

Examiner Spector,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(703)305-1954



**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using SW model

Run on: August 13, 2003, 13:25:12 ; Search time 373 Seconds

(without alignments)  
567,016 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 1301  
Sequence: 1 MRRGPRASPRRLRLGLLL.....GDASTGMSVSRRIIEELPR 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

```

1: /cgn2_6/ptodata/1/paa/PCTUS.COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06.COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07.COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08.COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081.COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082.COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083.COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084.COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085.COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086.COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087.COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088.COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089.COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090.COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091.COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092.COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093.COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094.COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095.COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096.COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097.COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US098.COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US099.COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099B.COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B.COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100.COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101.COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102.COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103.COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104.COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US104.COMB.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1301	100.0	243	1 PCT-US02-02781-4559
2	1301	100.0	243	1 PCT-US02-12378-514

Result No.	Score	Query Match Length	ID	Description
3	1301	100.0	243	23 US-09-834-759-514
4	1301	100.0	243	24 US-09-938-418-7
5	1301	100.0	243	24 US-09-946-374-352
6	1301	100.0	243	24 US-09-946-374-431
7	1301	100.0	243	26 US-10-006-041A-352
8	1301	100.0	243	26 US-10-006-041A-431
9	1301	100.0	243	26 US-10-006-063A-352
10	1301	100.0	243	26 US-10-006-063A-431
11	1301	100.0	243	26 US-10-006-116A-352
12	1301	100.0	243	26 US-10-006-116A-431
13	1301	100.0	243	26 US-10-006-117A-352
14	1301	100.0	243	26 US-10-006-117A-431
15	1301	100.0	243	26 US-10-006-130A-352
16	1301	100.0	243	26 US-10-006-130A-431
17	1301	100.0	243	26 US-10-006-172A-352
18	1301	100.0	243	26 US-10-006-172A-431
19	1301	100.0	243	26 US-10-006-185A-352
20	1301	100.0	243	26 US-10-006-185A-431
21	1301	100.0	243	26 US-10-006-746A-352
22	1301	100.0	243	26 US-10-006-746A-431
23	1301	100.0	243	26 US-10-006-768A-352
24	1301	100.0	243	26 US-10-006-768A-431
25	1301	100.0	243	26 US-10-006-818A-352
26	1301	100.0	243	26 US-10-006-818A-431
27	1301	100.0	243	26 US-10-006-856A-352
28	1301	100.0	243	26 US-10-006-856A-431
29	1301	100.0	243	26 US-10-006-867-122
30	1301	100.0	243	26 US-10-007-194A-352
31	1301	100.0	243	26 US-10-007-194A-431
32	1301	100.0	243	26 US-10-007-236A-352
33	1301	100.0	243	26 US-10-007-236A-431
34	1301	100.0	243	26 US-10-007-785A-352
35	1301	100.0	243	26 US-10-007-785A-431
36	1301	100.0	243	26 US-10-011-671A-352
37	1301	100.0	243	26 US-10-011-671A-431
38	1301	100.0	243	26 US-10-011-692A-352
39	1301	100.0	243	26 US-10-011-692A-431
40	1301	100.0	243	26 US-10-011-795A-352
41	1301	100.0	243	26 US-10-011-795A-431
42	1301	100.0	243	26 US-10-011-795B-352
43	1301	100.0	243	26 US-10-011-795B-431
44	1301	100.0	243	26 US-10-011-833A-352
45	1301	100.0	243	26 US-10-011-833A-431

## ALIGNMENTS

```

RESULT 1
PCT-US02-02781-4559
; Sequence 4559, Application PC/PUS0202781
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Benson, Darin R.
; APPLICANT: Katos, Michael J.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566PC
; CURRENT APPLICATION NUMBER: PCT/US02/02781
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4559
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-02781-4559

```

Query Match 100.0%; Score 1301; DB 1; Length 243;

Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORTLRGLLLLLLLQLPAPSSASEIPKQKAOLOREVVLDYNGMCLQSPA 60  
DB 1 MRPOGPASPORTLRGLLLLLLLQLPAPSSASEIPKQKAOLOREVVLDYNGMCLQSPA 60

QY 61 GVPGRDGSFGANVITGTGIPGRDGFKEGKGECLRESEESWTPTYKQCSMSLNYGIDL 120  
DB 61 GVPGRDGSFGANVITGTGIPGRDGFKEGKGECLRESEESWTPTYKQCSMSLNYGIDL 120

QY 121 GRIACCTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFNGACSGPLPEAITIYIDQ 180  
DB 121 GRIACCTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFNGACSGPLPEAITIYIDQ 180

QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240

QY 241 LPK 243  
DB 241 LPK 243

## RESULT 2

PCT-US02-12378-514  
Sequence 514, Application PC/TUS0212378  
GENERAL INFORMATION:  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Persing, David H.  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Devin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedicik, Thomas S.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Durham, Margarita  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.47003BC  
CURRENT APPLICATION NUMBER: PCT/US02/12378  
CURRENT FILING DATE: 2002-04-15  
NUMBER OF SEQ ID NOS: 627  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 514  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-12378-514

Query Match 100.0%; Score 1301; DB 1; Length 243;

Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORTLRGLLLLLLLQLPAPSSASEIPKQKAOLOREVVLDYNGMCLQSPA 60  
DB 1 MRPOGPASPORTLRGLLLLLLLQLPAPSSASEIPKQKAOLOREVVLDYNGMCLQSPA 60

QY 61 GVPGRDGSFGANVITGTGIPGRDGFKEGKGECLRESEESWTPTYKQCSMSLNYGIDL 120  
DB 61 GVPGRDGSFGANVITGTGIPGRDGFKEGKGECLRESEESWTPTYKQCSMSLNYGIDL 120

QY 121 GRIACCTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFNGACSGPLPEAITIYIDQ 180  
DB 121 GRIACCTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFNGACSGPLPEAITIYIDQ 180

QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240

DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

## RESULT 3

US-09-834-759-514  
Sequence 514, Application US/09834759  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Devin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C9  
CURRENT APPLICATION NUMBER: US/09/834,759  
CURRENT FILING DATE: 2001-04-13  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 514  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-834-759-514

Query Match 100.0%; Score 1301; DB 23; Length 243;

Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORTLRGLLLLLLLQLPAPSSASEIPKQKAOLOREVVLDYNGMCLQSPA 60  
DB 1 MRPOGPASPORTLRGLLLLLLLQLPAPSSASEIPKQKAOLOREVVLDYNGMCLQSPA 60

QY 61 GVPGRDGSFGANVITGTGIPGRDGFKEGKGECLRESEESWTPTYKQCSMSLNYGIDL 120  
DB 61 GVPGRDGSFGANVITGTGIPGRDGFKEGKGECLRESEESWTPTYKQCSMSLNYGIDL 120

QY 121 GRIACCTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFNGACSGPLPEAITIYIDQ 180  
DB 121 GRIACCTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFNGACSGPLPEAITIYIDQ 180

QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDPYKGDASTGMNSVSRITIEE 240

QY 241 LPK 243  
DB 241 LPK 243

## RESULT 4

US-09-938-418-7  
Sequence 7, Application US/09938418  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Gurney, Austin L.  
APPLICANT: Polakis, Paul  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Wu, Thomas D.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TITLE OF INVENTION: TREATMENT OF TUMOR  
FILE REFERENCE: P5009R1  
CURRENT APPLICATION NUMBER: US/09/938,418





DB 121 GKAEFTKMRNSALRVLFSGSLKRCNACCQWYTFNAGCECSGPLPIEAIITYLDQ 180  
QY 181 GSEPMNSTINHRTSSVEGICGEGIGALVDVAIWGTCDSDYPRGDASTGNNVSRIIEE 240  
DB 181 GSEPMNSTINHRTSSVEGICGEGIGALVDVAIWGTCDSDYPRGDASTGNNVSRIIEE 240  
QY 241 LPR 243  
DB 241 LPR 243

RESULT 6  
US-09-946-374-431  
Sequence 431, Application US/09946374  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Olang  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830PICI  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/102207

PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/10178  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807  
PRIOR FILING DATE: 1998-10-27

Query Match 100.0%; Score 1301; DB 24; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1,6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRPGPASPQRRLGLLLLLLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQCPA 60

|||||  
Db 1 MRPGPASPQRRLGLLLLLLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQCPA 60  
OY 61 GVPGRDGPANVIGTPIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
|||||  
Db 61 GVPGRDGPANVIGTPIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
OY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGAECGSLPTEAITIYLDQ 180  
|||||  
Db 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGAECGSLPTEAITIYLDQ 180  
OY 181 GSPEMNSTINIHRTSSVBEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMSVSRITIEE 240  
|||||  
Db 181 GSPEMNSTINIHRTSSVBEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMSVSRITIEE 240  
OY 241 LPK 243  
|||||  
Db 241 LPK 243

RESULT 7  
US-10-006-041A-352  
; Sequence 352, Application US/10006041A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geo, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C8  
; CURRENT APPLICATION NUMBER: US/10/006,041A  
; PRIOR FILING DATE: 2001-12-06  
; Prior Application removed - See file wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 352  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-041A-352

Query Match 100.0%; Score 1301; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1,6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRPGPASPQRRLGLLLLLLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQCPA 60  
|||||  
Db 1 MRPGPASPQRRLGLLLLLLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQCPA 60  
OY 61 GVPGRDGPANVIGTPIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
|||||  
Db 61 GVPGRDGPANVIGTPIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
OY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGAECGSLPTEAITIYLDQ 180  
|||||  
Db 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGAECGSLPTEAITIYLDQ 180  
OY 181 GSPEMNSTINIHRTSSVBEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMSVSRITIEE 240  
|||||  
Db 181 GSPEMNSTINIHRTSSVBEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMSVSRITIEE 240  
OY 241 LPK 243  
|||||

Db 241 LPK 243

## RESULT 8

US-10-006-041A-431

Sequence 431, Application US/10006041A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PIC8  
CURRENT APPLICATION NUMBER: US/10/006,041A  
CURRENT FILING DATE: 2001-12-06  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 431  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-10-006-041A-431

Query Match 100.0%; Score 1301; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKGRKQAKLRQREVVDLYNMCLOGPA 60  
Db 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKGRKQAKLRQREVVDLYNMCLOGPA 60

QY 61 GVPGRGSPGANVITPGTPIGRDGFKEGECLEARSFEESWTPNTKQCSWSLNTGIDL 120  
Db 61 GVPGRGSPGANVITPGTPIGRDGFKEGECLEARSFEESWTPNTKQCSWSLNTGIDL 120

QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRMWTFENGAECSGPIPIAIIYLDQ 180  
Db 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRMWTFENGAECSGPIPIAIIYLDQ 180

QY 181 GSPENSTINIHRTSSVEGICBEGIGAGLVDAIWTGTSYPRGDASTGNSVSRITIEE 240  
Db 181 GSPENSTINIHRTSSVEGICBEGIGAGLVDAIWTGTSYPRGDASTGNSVSRITIEE 240

QY 241 LPK 243  
Db 241 LPK 243

## RESULT 9

US-10-006-063A-352

Sequence 352, Application US/10006063A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PIC3

CURRENT APPLICATION NUMBER: US/10/006,063A

CURRENT FILING DATE: 2002-03-15

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 477

SEQ ID NO 352

LENGTH: 243

TYPE: PRT

ORGANISM: Homo saplens

US-10-006-063A-352

Query Match 100.0%; Score 1301; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKGRKQAKLRQREVVDLYNMCLOGPA 60  
Db 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKGRKQAKLRQREVVDLYNMCLOGPA 60

QY 61 GVPGRGSPGANVITPGTPIGRDGFKEGECLEARSFEESWTPNTKQCSWSLNTGIDL 120  
Db 61 GVPGRGSPGANVITPGTPIGRDGFKEGECLEARSFEESWTPNTKQCSWSLNTGIDL 120

QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRMWTFENGAECSGPIPIAIIYLDQ 180  
Db 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRMWTFENGAECSGPIPIAIIYLDQ 180

QY 181 GSPENSTINIHRTSSVEGICBEGIGAGLVDAIWTGTSYPRGDASTGNSVSRITIEE 240  
Db 181 GSPENSTINIHRTSSVEGICBEGIGAGLVDAIWTGTSYPRGDASTGNSVSRITIEE 240

QY 241 LPK 243  
Db 241 LPK 243

## RESULT 10

US-10-006-063A-431

Sequence 431, Application US/10006063A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PIC3  
CURRENT APPLICATION NUMBER: US/10/006,063A  
CURRENT FILING DATE: 2002-03-15  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 431  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-10-006-063A-431





;; PRIOR APPLICATION NUMBER: 60/101743  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101915  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101916  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/102207  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102240  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102307  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102330  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103338  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28  
;; PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 1301; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1,6e-118;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGLLLLLLPAPSSASEIPKGRKQOLRQREVVLDLYNMCLOGPA 60  
DQ 1 MRPGPASPQRRLGLLLLLLPAPSSASEIPKGRKQOLRQREVVLDLYNMCLOGPA 60  
QY 61 GVPGRDGGPGANVYIPGTGIPGRDGFKEGCECLRESFEESWTPNNYKQCSWSSILNIGIDL 120  
DQ 61 GVPGRDGGPGANVYIPGTGIPGRDGFKEGCECLRESFEESWTPNNYKQCSWSSILNIGIDL 120  
QY 121 GKTAECTFTKRSNSALRYLFGSLRLKCNACCQRYFTFNAGCSGPLIEALITYLDQ 180  
DQ 121 GKTAECTFTKRSNSALRYLFGSLRLKCNACCQRYFTFNAGCSGPLIEALITYLDQ 180  
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVAVAIWGTCSDPYKGDASTGNNVSRIITIEE 240  
DQ 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVAVAIWGTCSDPYKGDASTGNNVSRIITIEE 240  
QY 241 LPK 243  
DQ 241 LPK 243

RESULT 12  
US-10-006-116A-431  
; Sequence 431, Application US/10006116A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC15  
; CURRENT APPLICATION NUMBER: US/10/006,116A  
; PRIOR FILING DATE: 2001-12-16  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09

1	PRIOR APPLICATION NUMBER: 60/0935956
2	PRIOR FILING DATE: 1998-09-09
3	PRIOR APPLICATION NUMBER: 60/0935988
4	PRIOR FILING DATE: 1998-09-09
5	PRIOR APPLICATION NUMBER: 60/0936020
6	PRIOR FILING DATE: 1998-09-09
7	PRIOR APPLICATION NUMBER: 60/0936422
8	PRIOR FILING DATE: 1998-09-09
9	PRIOR APPLICATION NUMBER: 60/0937411
10	PRIOR FILING DATE: 1998-09-10
11	PRIOR APPLICATION NUMBER: 60/0937544
12	PRIOR FILING DATE: 1998-09-10
13	PRIOR APPLICATION NUMBER: 60/0937633
14	PRIOR FILING DATE: 1998-09-10
15	PRIOR APPLICATION NUMBER: 60/0937922
16	PRIOR FILING DATE: 1998-09-10
17	PRIOR APPLICATION NUMBER: 60/0938088
18	PRIOR FILING DATE: 1998-09-10
19	PRIOR APPLICATION NUMBER: 60/0938122
20	PRIOR FILING DATE: 1998-09-10
21	PRIOR APPLICATION NUMBER: 60/0938155
22	PRIOR FILING DATE: 1998-09-10
23	PRIOR APPLICATION NUMBER: 60/0938166
24	PRIOR FILING DATE: 1998-09-10
25	PRIOR APPLICATION NUMBER: 60/1003855
26	PRIOR FILING DATE: 1998-09-15
27	PRIOR APPLICATION NUMBER: 60/1003888
28	PRIOR FILING DATE: 1998-09-15
29	PRIOR APPLICATION NUMBER: 60/1003960
30	PRIOR FILING DATE: 1998-09-15
31	PRIOR APPLICATION NUMBER: 60/1005544
32	PRIOR FILING DATE: 1998-09-16
33	PRIOR APPLICATION NUMBER: 60/1006277
34	PRIOR FILING DATE: 1998-09-16
35	PRIOR APPLICATION NUMBER: 60/1006611
36	PRIOR FILING DATE: 1998-09-16
37	PRIOR APPLICATION NUMBER: 60/1006622
38	PRIOR FILING DATE: 1998-09-16
39	PRIOR APPLICATION NUMBER: 60/1006644
40	PRIOR FILING DATE: 1998-09-16
41	PRIOR APPLICATION NUMBER: 60/1006833
42	PRIOR FILING DATE: 1998-09-17
43	PRIOR APPLICATION NUMBER: 60/1006848
44	PRIOR FILING DATE: 1998-09-18
45	PRIOR APPLICATION NUMBER: 60/1008449
46	PRIOR FILING DATE: 1998-09-18
47	PRIOR APPLICATION NUMBER: 60/100919
48	PRIOR FILING DATE: 1998-09-17
49	PRIOR APPLICATION NUMBER: 60/1009300
50	PRIOR FILING DATE: 1998-09-17
51	PRIOR APPLICATION NUMBER: 60/1010144
52	PRIOR FILING DATE: 1998-09-18
53	PRIOR APPLICATION NUMBER: 60/101068
54	PRIOR FILING DATE: 1998-09-18
55	PRIOR APPLICATION NUMBER: 60/1010711
56	PRIOR FILING DATE: 1998-09-18
57	PRIOR APPLICATION NUMBER: 60/101279
58	PRIOR FILING DATE: 1998-09-22
59	PRIOR APPLICATION NUMBER: 60/101471
60	PRIOR FILING DATE: 1998-09-23
61	PRIOR APPLICATION NUMBER: 60/101472
62	PRIOR FILING DATE: 1998-09-23
63	PRIOR APPLICATION NUMBER: 60/101474
64	PRIOR FILING DATE: 1998-09-23
65	PRIOR APPLICATION NUMBER: 60/101475
66	PRIOR FILING DATE: 1998-09-23
67	PRIOR APPLICATION NUMBER: 60/101476

PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101477
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101477
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101733
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101744
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101744
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/102207
PRIOR FILING DATE:	1998-09-25
PRIOR APPLICATION NUMBER:	60/102240
PRIOR FILING DATE:	1998-09-25
PRIOR APPLICATION NUMBER:	60/102307
PRIOR FILING DATE:	1998-09-25
PRIOR APPLICATION NUMBER:	60/102333
PRIOR FILING DATE:	1998-09-25
PRIOR APPLICATION NUMBER:	60/102488
PRIOR FILING DATE:	1998-09-30
PRIOR APPLICATION NUMBER:	60/102488
PRIOR FILING DATE:	1998-09-30
PRIOR APPLICATION NUMBER:	60/102571
PRIOR FILING DATE:	1998-09-30
PRIOR APPLICATION NUMBER:	60/102688
PRIOR FILING DATE:	1998-10-01
PRIOR APPLICATION NUMBER:	60/102688
PRIOR FILING DATE:	1998-10-01
PRIOR APPLICATION NUMBER:	60/103315
PRIOR FILING DATE:	1998-10-07
PRIOR APPLICATION NUMBER:	60/103328
PRIOR FILING DATE:	1998-10-07
PRIOR APPLICATION NUMBER:	60/103355
PRIOR FILING DATE:	1998-10-07
PRIOR APPLICATION NUMBER:	60/103366
PRIOR FILING DATE:	1998-10-07
PRIOR APPLICATION NUMBER:	60/103401
PRIOR FILING DATE:	1998-10-06
PRIOR APPLICATION NUMBER:	60/103449
PRIOR FILING DATE:	1998-10-06
PRIOR APPLICATION NUMBER:	60/103633
PRIOR FILING DATE:	1998-10-08
PRIOR APPLICATION NUMBER:	60/103678
PRIOR FILING DATE:	1998-10-08
PRIOR APPLICATION NUMBER:	60/103679
PRIOR FILING DATE:	1998-10-08
PRIOR APPLICATION NUMBER:	60/103711
PRIOR FILING DATE:	1998-10-08
PRIOR APPLICATION NUMBER:	60/104257
PRIOR FILING DATE:	1998-10-14
PRIOR APPLICATION NUMBER:	60/104987
PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/105000
PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/105002
PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/105104
PRIOR FILING DATE:	1998-10-21

```

; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106029

Query Match      100.0%; Score 1301; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 1,6e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60
      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60
Db      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60

QY      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120
      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120
Db      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120

QY      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
Db      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180

QY      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGWNVSRIITIEE 240
      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGWNVSRIITIEE 240
Db      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGWNVSRIITIEE 240

QY      241 LPK 243
      241 LPK 243
Db      241 LPK 243

RESULT 13
US-10-006-117A-352
; Sequence 352, Application US/10006117A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

US-10-006-117A-352

Query Match      100.0%; Score 1301; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 1,6e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60
      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60
Db      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60

QY      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120
      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120
Db      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120

QY      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
Db      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180

QY      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGWNVSRIITIEE 240
      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGWNVSRIITIEE 240
Db      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGWNVSRIITIEE 240

QY      241 LPK 243
      241 LPK 243
Db      241 LPK 243

RESULT 14
US-10-006-117A-431
; Sequence 431, Application US/10006117A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-006-117A-431

Query Match      100.0%; Score 1301; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 1,6e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60
      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60
Db      1 MRPGPASPQRRLGILLILLILLOLPAPSSASEIPKQKQKQRLRQREVVDLYNGMCILOGPA 60

QY      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120
      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120
Db      61 GVPGRDSSPGANVYIPGTGIPGRDGFKEGECLERESFESWTPNYKQCSWSSLYNTGIDL 120

QY      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
Db      121 GKIAECTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNAGCSGPLPIEAIITYLDQ 180
```

Db 121 GKIACTFTKMRNSALRYLFGSLRLKCRNACCQWYFTFNGAECSGPLIEATITVLDQ 180  
QY 181 GSPENKSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDYPRKGDASTGWSVSRIITIEE 240  
Db 181 GSPENKSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDYPRKGDASTGWSVSRIITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

## RESULT 15

US-10-006-130A-352  
; Sequence 352, Application US/10006130A

## ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C7  
; CURRENT APPLICATION NUMBER: US/10/006,130A  
; CURRENT FILING DATE: 2002-03-19  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 352  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-130A-352

Query Match 100.0%; Score 1301; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.6e-118;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRLGLILLILLQLLPAPSSASEIPKQKQALRQREVVDLYNGMCIQGPA 60  
Db 1 MRPGPAASPORLRLGLILLILLQLLPAPSSASEIPKQKQALRQREVVDLYNGMCIQGPA 60  
QY 61 GVPGRDGSPPGANVITGTPGIGRQDFKGEKGECLRESFEESWTPNYKQCSMSLNYGIDL 120  
Db 61 GVPGRDGSPPGANVITGTPGIGRQDFKGEKGECLRESFEESWTPNYKQCSMSLNYGIDL 120  
QY 121 GKIACTFTKMRNSALRYLFGSLRLKCRNACCQWYFTFNGAECSGPLIEATITVLDQ 180  
Db 121 GKIACTFTKMRNSALRYLFGSLRLKCRNACCQWYFTFNGAECSGPLIEATITVLDQ 180  
QY 181 GSPENKSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDYPRKGDASTGWSVSRIITIEE 240  
Db 181 GSPENKSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDYPRKGDASTGWSVSRIITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

Search completed: August 13, 2003, 13:35:04  
Job time : 375 secs



DB 241 LPR 243

RESULT 2  
US-60-487-610-1777  
; Sequence 1777, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; FILE REFERENCE: C1001469  
; CURRENT APPLICATION NUMBER: US/60/487, 610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1777  
; LENGTH: 1737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-487-610-1777

Query Match  
Best Local Similarity 9.4%; Score 122.5; DB 7; Length 1737;  
Best Local Similarity 35.0%; Pred. No. 0.00057;  
Matches 35; Conservative 8; Mismatches 28; Indels 29; Gaps 4;

OY 20 LILQIPAPSSASEIPKGRKQAKLRQREVVDLYNGMCLGPGAGVPGRDSPGA---NVIPG 76  
DB 1638 ILNQIPSHSSIR-----TVGGPPEPGRPGSPGAPGSGPPG 1675

OY 77 TPGIPGRDGFKEGGE--CLRESF--EESWTPNYKQCSMS 112  
DB 1676 TPGFPGNAGVPGTPEGRKLGPTFGESESAMQPMAPWLSMT 1715

RESULT 3  
US-60-485-450-1149  
; Sequence 1149, Application US/60485450  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: CHANG, Sheng-Yung  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
; FILE REFERENCE: C1001470  
; CURRENT APPLICATION NUMBER: US/60/485, 450  
; CURRENT FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 47859  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1149  
; LENGTH: 1737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-485-450-1149

Query Match  
Best Local Similarity 9.4%; Score 122.5; DB 7; Length 1737;  
Best Local Similarity 35.0%; Pred. No. 0.00057;  
Matches 35; Conservative 8; Mismatches 28; Indels 29; Gaps 4;

OY 20 LILQIPAPSSASEIPKGRKQAKLRQREVVDLYNGMCLGPGAGVPGRDSPGA---NVIPG 76  
DB 1638 ILNQIPSHSSIR-----TVGGPPEPGRPGSPGAPGSGPPG 1675

OY 77 TPGIPGRDGFKEGGE--CLRESF--EESWTPNYKQCSMS 112  
DB 1676 TPGFPGNAGVPGTPEGRKLGPTFGESESAMQPMAPWLSMT 1715

RESULT 4  
US-10-450-186-26  
; Sequence 26, Application US/10450186

; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION; GRIFFIN, Jennifer A.;  
; APPLICANT: YAO, Monique G.; DUGGAN, Brendan M.;  
; APPLICANT: YUE, Henry; DING, Li;  
; APPLICANT: LAL, Preeti G.; LEE, Ernestine A.;  
; APPLICANT: RAMKUMAR, Jayalakmi; THANGAVELU, Kavitha;  
; APPLICANT: XU, Yumlung; LEE, Sally;  
; APPLICANT: TANG, Y. Tom; NGUYEN, Daniel B.;  
; APPLICANT: WARREN, Bridget A.; HONCHELL, Cynthia D.;  
; APPLICANT: GIETZEN, Kimberly J.; BAUGHN, Mariah R.;  
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.;  
; APPLICANT: CHANLA, Narinder K.; LU, Yan;  
; APPLICANT: ELIOTY, Vicki S.; LU, Dyung Alina M.;  
; APPLICANT: HAFALIA, April J.A.; AZIMZAI, Yalda;  
; APPLICANT: KHAN, Farrah A.; TRAN, Uyen K.  
; TITLE OF INVENTION: SECRETED PROTEINS  
; FILE REFERENCE: PI-0345 USN  
; CURRENT APPLICATION NUMBER: US/10/450, 186  
; CURRENT FILING DATE: 2003-06-09  
; PRIOR APPLICATION NUMBER: PCT/US01/48517  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255, 639  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 60/257, 852  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: US 60/260, 105  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/262, 932  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/263, 096  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/263, 090  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/265, 926  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PERL Program  
; SEQ ID NO 26  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No: 7485334CD1  
US-10-450-186-26

Query Match  
Best Local Similarity 9.2%; Score 120; DB 6; Length 287;  
Best Local Similarity 34.7%; Pred. No. 0.0001;  
Matches 42; Conservative 10; Mismatches 57; Indels 12; Gaps 4;

OY 27 PSSASEIPKGRKQAKLRQREV--DLYNG---MCILOGPAGVPGRDSPGANVIPGTPGIPG 82  
DB 44 PAGAKAPPGPSTAL---EYMDLSANPPPPFPGGDPGRGKPGPRGPPGPPG 100

OY 83 RDGFKEGGECLREFEESWTPNYKQCSWSSLNLTGIDGKTAECTFTMRNSALRVLF 142  
DB 101 PRGPPGEGDGRPL-----PGLQTLTSAAGVGVSGETGGGDDTEGEVTSLSAIFS 155

OY 143 G 143  
DB 156 G 156

RESULT 5  
US-60-487-610-2410  
; Sequence 2410, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; FILE REFERENCE: C1001469

```

; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2410
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2410

Query Match          9.1%; Score 118.5; DB 7; Length 614;
Best Local Similarity 36.3%; Pred. No. 0.00038;
Matches    33; Conservative   2; Mismatches    23; Indels    33; Gaps     4

      3 PGCPAAS--PORTKGLLILLLLQLPAPSSASEIPKQKAOLRREVVLDYNGMCLQGPA 60
      ||||| - - - : || - - - | - - - | - - - | - - - | - - - | - - - |
Db       357 PGPGGSGCGPGGVNR-----EPGPg-----PAG-----AAGPA 385

      61 GVPRDGSRGANVIFGTPIGRDGFKEKG 91
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       386 GNPGADGGPGANGANGAPGIAGAPEFPGAR 416


RESULT 6
US-60-485-450-1524
; Sequence 1524, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILT, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: C1001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1524
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1524

Query Match          9.1%; Score 118.5; DB 7; Length 614;
Best Local Similarity 36.3%; Pred. No. 0.00038;
Matches    33; Conservative   2; Mismatches    23; Indels    33; Gaps     4

      3 PGCPAAS--PORTKGLLILLLLQLPAPSSASEIPKQKAOLRREVVLDYNGMCLQGPA 60
      ||||| - - - : || - - - | - - - | - - - | - - - | - - - | - - - |
Db       357 PGPGGSGCGPGGVNR-----EPGPg-----PAG-----AAGPA 385

      61 GVPRDGSRGANVIFGTPIGRDGFKEKG 91
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       386 GNPGADGGPGANGANGAPGIAGAPEFPGAR 416


RESULT 7
US-60-487-610-2411
; Sequence 2411, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILT, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2411
; LENGTH: 1164

```

```

: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-487-610-2411

Query Match
Best Local Similarity 36.3%; Score 118.5; DB 7; Length 1164;
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4

OY 3 PGPRAAS--PTRLKLLLLLLQLPAPSSASEIPKGGKRAOLRQREYVDLYNGKCLGPA 60
DB 57 PGPGRGSGPGGVNRG-----EPGPGG---PAG-----AAGPA 85
61 GVPGRDGSPPGANVIRPTGPIGRDGFKEKG 91
DB 86 GNPGRDGPQAKGANGAPGAPGPFPGAR 116

RESULT 8
US-60-485-450-1525
: Sequence 1525, Application US/60485450
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
: TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
: FILE REFERENCE: C1001470
: CURRENT APPLICATION NUMBER: US/60/485,450
: CURRENT FILING DATE: 2003-07-09
: NUMBER OF SEQ ID NOS: 47859
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1525
: LENGTH: 1164
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-485-450-1525

Query Match
Best Local Similarity 36.3%; Score 118.5; DB 7; Length 1164;
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4

OY 3 PGPRAAS--PTRLKLLLLLLQLPAPSSASEIPKGGKRAOLRQREYVDLYNGKCLGPA 60
DB 57 PGPGRGSGPGGVNRG-----EPGPGG---PAG-----AAGPA 85
61 GVPGRDGSPPGANVIRPTGPIGRDGFKEKG 91
DB 86 GNPGRDGPQAKGANGAPGAPGPFPGAR 116

RESULT 9
US-60-487-610-2407
: Sequence 2407, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2407
: LENGTH: 1284
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-487-610-2407

Query Match
Best Local Similarity 36.3%; Score 118.5; DB 7; Length 1284;
Matches 36.3%; Pred. No. 0.00099; Pred. 0.00099;

```

Matches	33; Conservative	2; Mismatches	23; Indels	33; Gaps	4;
Oy	3	POGPAAS--PORTRGILLTLLTLLLOLPAPASASEIRKGRKQALRQREVVLDYNGMCLDSPA	60		
Db	177	POGPRGSGSPGCGVSG-----BRCPFG-----PAG-----AAQPA	205		
Oy	61	GVPRGDSFGPCANVLPGRTPGIRGRGOFKGEKG	91		
Db	206	GNPGADGQPGKANGANGAPGIAAGGCFPGAR	236		

```

RESULT 10
US-60-485-450-1521
: Sequence 1521, Application US/60485450
: GENERAL INFORMATION:
: APPLICANT: CANGIL, Michele
: APPLICANT: CANG, Sheng-yung
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
: TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CI001470
: CURRENT APPLICATION NUMBER: US/60/485,450
: CURRENT FILING DATE: 2003-07-09
: NUMBER OF SEQ ID NOS: 47859
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1521
: LENGTH: 1284
: TYPE: PR1
: ORGANISM: Homo sapiens
: US-60-485-450-1521

```

Query Match	9.1%	Score 118.5;	DB 7;	length 1284;
Best Local Similarity	36.3%	Pred. No. 0.00099;		
Matches	33;	Conservative	2;	Mismatches 23; Indels 33; Gaps 4;

  

OY	3	PGCGAAS--PGRLLPRLLLLLLLQLPAPSSASEIPKCKAKQLRQREYVDLYNGMKLOCPA	60
Db	177	PGCGRSGEGPGCGVGC-----EPGPGG-----FAG-----AAGPA	205
OY	61	GVGGRDSSPGCANVLPCTPGIRGDRGFKCEKG	91
Db	206	GNPGADGQPGKAGKANGAGPAGAGCGFPARG	236

```

RESULT 11
PCT-US02-18638A-36
; Sequence 36, Application PC/TUS0218638A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035PC
; CURRENT APPLICATION NUMBER: PCT/US02/18638A
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
; CTT-US02-18638A-36

```

Query Match	9.1%;	Score 118.5;	DB 1;	Length 1464;
Best Local Similarity	36.3%;	Pred. No. 0.0012;		
Matches	33;	Conservative	2;	Mismatches 23;
				Indels 33;
				Gaps 4;

QY	3	PGCPAAS--PQRIKGLILLILLQLPAPSASSAIPGCKQAKQIQRREVVDLYNGMCLOGPA	60
Db	357	PGCPRSEGGQGVGR-----EPGPG-----PAG-----AAGPA	386
QY	61	GVPGRDGSFGANYIIPETPGIPGRDGKGEKNG	91
Db	386	GNPGADGQPGKAKGANGAPSIAGAPGPPCARG	416

```

RESULT 12
US-10-291-265-243
Sequence 243, Application US/10291265
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 243
LENGTH: 1464
TYPE: PRNT
ORGANISM: Homo sapiens
US-10-291-265-243

```

Query Match	9.1%;	Score 118.5;	DB 6;	length 1464;
Best Local Similarity	36.3%;	Pred. NO. 0.0012;		
Matches	33;	Conservative	2;	Mismatches 23; Indels 33; Gaps 4

  

QY	3	PGGPAAS--PORTLGGLLLLLLLLQLPAPSSASBEIPKGRKAKDLRQREYVDLYNGMKLOQPA	60
Db	357	PGCRGSEGGHQGVGCG-----EPGPGG---PAG-----AAGPA	385

  

QY	61	GVPGRDSSPGCANVTPGTPGLPGRDGFKEGK	91
Db	386	GNPGADGQPGKRGANGAPGINGAGCGFPDARG	416

```

RESULT 13
US-60-487-610-2409
: Sequence 2409, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2409
: LENGTH: 1464
: TYPE: PRF
: ORGANISM: Homo sapiens
: US-60-487-610-2409

```

Query Match	9.1%;	Score 118.5;	DB 7;	Length 1464;
Best Local Similarity	36.3%;	Pred. No. 0.0012;		
Matches 33; Conservative	2;	Mismatches 23;	Indels 33;	Gaps 4;





**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:27:27 ; Search time 55 Seconds  
(without alignments)  
578.796 Million cell updates/sec

Title: US-09-938-418-7  
Perfect score: 1301  
Sequence: 1 MRQGPASPRRLGILLL.....GDASTGWSYRIIEELPK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues  
Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\*  
1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	243	10 US-09-938-418-7	Sequence 7, Appli
2	1301	100.0	243	11 US-09-946-374-352	Sequence 352, App
3	1301	100.0	243	11 US-09-946-374-431	Sequence 431, App
4	1301	100.0	243	12 US-10-015-387A-352	Sequence 352, App
5	1301	100.0	243	12 US-10-015-387A-431	Sequence 431, App
6	1301	100.0	243	12 US-10-063-735-122	Sequence 122, App
7	1301	100.0	243	12 US-10-063-130A-352	Sequence 352, App
8	1301	100.0	243	12 US-10-063-130A-431	Sequence 431, App
9	1301	100.0	243	12 US-10-063-867-122	Sequence 122, App
10	1301	100.0	243	14 US-10-052-586-366	Sequence 366, App
11	1301	100.0	243	14 US-10-052-586-366	Sequence 366, App
12	1301	100.0	243	14 US-10-063-547-122	Sequence 514, App
13	1301	100.0	243	14 US-10-063-547-122	Sequence 122, App
14	1301	100.0	243	15 US-10-174-590-366	Sequence 366, App
15	1301	100.0	243	15 US-10-176-758-366	Sequence 366, App

16	1301	100.0	243	15 US-10-175-737-366	Sequence 366, App
17	1301	100.0	243	15 US-10-063-616-122	Sequence 122, App
18	1301	100.0	243	15 US-10-173-706-366	Sequence 366, App
19	1301	100.0	243	15 US-10-175-738-366	Sequence 366, App
20	1301	100.0	243	15 US-10-175-752-366	Sequence 366, App
21	1301	100.0	243	15 US-10-176-482-366	Sequence 366, App
22	1301	100.0	243	15 US-10-176-757-366	Sequence 366, App
23	1301	100.0	243	15 US-10-176-913-366	Sequence 366, App
24	1301	100.0	243	15 US-10-180-552-366	Sequence 366, App
25	1301	100.0	243	15 US-10-180-557-366	Sequence 366, App
26	1301	100.0	243	15 US-10-076-622-514	Sequence 514, App
27	1301	100.0	243	15 US-10-063-502-122	Sequence 122, App
28	1301	100.0	243	15 US-10-173-700-366	Sequence 366, App
29	1301	100.0	243	15 US-10-174-572-366	Sequence 366, App
30	1301	100.0	243	15 US-10-174-579-366	Sequence 366, App
31	1301	100.0	243	15 US-10-174-582-366	Sequence 366, App
32	1301	100.0	243	15 US-10-174-588-366	Sequence 366, App
33	1301	100.0	243	15 US-10-175-739-366	Sequence 366, App
34	1301	100.0	243	15 US-10-175-740-366	Sequence 366, App
35	1301	100.0	243	15 US-10-175-743-366	Sequence 366, App
36	1301	100.0	243	15 US-10-176-488-366	Sequence 366, App
37	1301	100.0	243	15 US-10-176-492-366	Sequence 366, App
38	1301	100.0	243	15 US-10-176-747-366	Sequence 366, App
39	1301	100.0	243	15 US-10-176-750-366	Sequence 366, App
40	1301	100.0	243	15 US-10-176-985-366	Sequence 366, App
41	1301	100.0	243	15 US-10-176-987-366	Sequence 366, App
42	1301	100.0	243	15 US-10-176-992-366	Sequence 366, App
43	1301	100.0	243	15 US-10-176-993-366	Sequence 366, App
44	1301	100.0	243	15 US-10-184-658-366	Sequence 366, App
45	1301	100.0	243	15 US-10-176-991-366	Sequence 366, App

## ALIGNMENTS

RESULT 1  
US-09-938-418-7  
Sequence 7, Application US/09938418  
Patent No. US20020161199A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Gunney, Austin L.  
APPLICANT: Polakis, Paul  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Wu, Thomas D.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR  
FILE REFERENCE: P509R1  
CURRENT APPLICATION NUMBER: US/09/938, 418  
CURRENT FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: 60/081,071  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: 60/085,697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/097,022  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/101,922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/103,679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: 1999-06-02  
PRIOR APPLICATION NUMBER: PCT/US99/20111  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US00/04342

PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/08439  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 10  
SEQ ID NO 7  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-938-418-7

Query Match 100.0%; Score 1301; DB 10; Length 243;  
Best Local Similarity 100.0%; Pred. No. 8.7e-121;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLRLILLLILQLPAPSSASEIPKQKQAKQREVVLDYNGMCLQGRA 60  
DB 1 MRPGPASPQRRLRLILLLILQLPAPSSASEIPKQKQAKQREVVLDYNGMCLQGRA 60  
QY 61 GYPGDGSFGANVIGTGPGEIPGRDGFKGKGECLRESEESWTPTYKCCSWSLNYGIDL 120  
DB 61 GYPGDGSFGANVIGTGPGEIPGRDGFKGKGECLRESEESWTPTYKCCSWSLNYGIDL 120  
QY 121 GRIACFTFKMRSNLSALVLFSSGLRLKRNACCORWYFTFGACSGPLTEATITTDQ 180  
DB 121 GRIACFTFKMRSNLSALVLFSSGLRLKRNACCORWYFTFGACSGPLTEATITTDQ 180  
QY 181 GSPEKNSITINIRHRSVSGLEGIGAGLVDAIIVGTCSDYKPGDASTGMNSVSRITIEE 240  
DB 181 GSPEKNSITINIRHRSVSGLEGIGAGLVDAIIVGTCSDYKPGDASTGMNSVSRITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

RESULT 2  
US-09-946-374-352  
Sequence 352, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

```

Query Matched: 100.0%; Score 1301; DB 11; Length 243;
Best Local Similarity 100.0%; Pred. No. 8,7e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 MRPQGPASPQRRLGILLLLLLLLQLPAPSSASEIPKGRQKQALRQREYVDLYNMCLOGPA 60
DB      1 MRPQGPASPQRLRGLLLLLLLLLQLPAPSSASEIPKGRQKQALRQREYVDLYNMCLOGPA 60
QY      61 GYPGRDGSFGANVIGTGTGIPGRDGFKEGKEGECLEESFEESWTPNTKQCSWSLNTGIDL 120
DB      61 GYPGRDGSFGANVIGTGTGIPGRDGFKEGKEGECLEESFEESWTPNTKQCSWSLNTGIDL 120
QY      121 GVIACETFTKMSNSALRVLFSSGLRLKCRNACQQRNYFFPNAGECGPLPIPIAIIYLDQ 180
DB      121 GVIACETFTKMSNSALRVLFSSGLRLKCRNACQQRNYFFPNAGECGPLPIPIAIIYLDQ 180
QY      181 GSPENKSTINIHRTSSVEGLCEGIGAGLVDAIVWGCSDYPKGDASTGMNSVRIITEE 240
DB      181 GSPENKSTINIHRTSSVEGLCEGIGAGLVDAIVWGCSDYPKGDASTGMNSVRIITEE 240
QY      241 LPR      241 LPR 243
DB      241 LPR 243

RESULT 3
US-09-946-374-431
; Sequence 431, Application US/09946374
; Publication No. US20030073129a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

```

APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661

PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01



APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2830P1C54  
 CURRENT APPLICATION NUMBER: US/10/015,387A  
 CURRENT FILING DATE: 2001-12-12  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 477  
 SEQ ID NO 431  
 LENGTH: 243  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-015-387A-431

Query Match 100.0%; Score 1301; DB 12; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 8,7e-121;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRPGPASPQRLKGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60  
 DB 1 MRPGPASPQRLKGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60  
 OY 61 GVPGRDSSPGANVLPPTGIPGRGFGKEGCECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
 DB 61 GVPGRDSSPGANVLPPTGIPGRGFGKEGCECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
 OY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACQRMWFTFNGAECGSPLEAIITYLDQ 180  
 DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACQRMWFTFNGAECGSPLEAIITYLDQ 180  
 OY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLYDVAIVWGTCSDPKGDASTGMNSVSRITIEE 240  
 DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLYDVAIVWGTCSDPKGDASTGMNSVSRITIEE 240  
 OY 241 LPK 243  
 DB 241 LPK 243

RESULT 6  
 US-10-063-735-122  
 Sequence 122, Application US/10063735  
 Publication No. US20030138882A1  
 GENERAL INFORMATION:  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gottisen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Matanabe, Colin K.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3230R1C1  
 CURRENT APPLICATION NUMBER: US/10/063,735  
 CURRENT FILING DATE: 2002-05-08  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 170  
 SEQ ID NO 122  
 LENGTH: 243  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-063-735-122

Query Match 100.0%; Score 1301; DB 12; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 8,7e-121;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MRPGPASPQRLKGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60

DB 1 MRPGPASPQRLKGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60  
 OY 61 GVPGRDSSPGANVLPPTGIPGRGFGKEGCECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
 DB 61 GVPGRDSSPGANVLPPTGIPGRGFGKEGCECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
 OY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACQRMWFTFNGAECGSPLEAIITYLDQ 180  
 DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACQRMWFTFNGAECGSPLEAIITYLDQ 180  
 OY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLYDVAIVWGTCSDPKGDASTGMNSVSRITIEE 240  
 DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLYDVAIVWGTCSDPKGDASTGMNSVSRITIEE 240  
 OY 241 LPK 243  
 DB 241 LPK 243

RESULT 7  
 US-10-006-130A-352  
 Sequence 352, Application US/10006130A  
 Publication No. US20030148375A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2830P1C7  
 CURRENT APPLICATION NUMBER: US/10/006,130A  
 CURRENT FILING DATE: 2002-03-19  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 477  
 SEQ ID NO 352  
 LENGTH: 243  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-006-130A-352

Query Match 100.0%; Score 1301; DB 12; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 8,7e-121;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRPGPASPQRLKGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60  
 DB 1 MRPGPASPQRLKGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60  
 OY 61 GVPGRDSSPGANVLPPTGIPGRGFGKEGCECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
 DB 61 GVPGRDSSPGANVLPPTGIPGRGFGKEGCECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
 OY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACQRMWFTFNGAECGSPLEAIITYLDQ 180  
 DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACQRMWFTFNGAECGSPLEAIITYLDQ 180  
 OY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLYDVAIVWGTCSDPKGDASTGMNSVSRITIEE 240  
 DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLYDVAIVWGTCSDPKGDASTGMNSVSRITIEE 240  
 OY 241 LPK 243





APPLICANT: Gurney, Austin L.  
APPLICANT: Matanabe, Colin K.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/006,867  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/063435  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/064215  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090688  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091628  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/096012  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096757  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096949  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/096959  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/097954  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097971  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097979  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098749

PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105881  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106030  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106856  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108807  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/112419  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112853  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113011  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/112854  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113300  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113408  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113430  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23



PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086023  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/086486  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087098  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087208  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088722  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089090  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1301; DB 14; Length 243;  
Best Local Similarity 100.0%; Pred. No. 87e-121;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLILLILLLPAPSSASIPKQKQADUOREVVDLYNGMCLQSPA 60  
DB 1 MRPGPASPORLRLILLILLLPAPSSASIPKQKQADUOREVVDLYNGMCLQSPA 60  
QY 61 GVPGRDGSFGANVIGTPIGIDGDFKGEKGECLRESEFEESWTPTNYKCCSMSSLYNGIDL 120  
DB 61 GVPGRDGSFGANVIGTPIGIDGDFKGEKGECLRESEFEESWTPTNYKCCSMSSLYNGIDL 120  
QY 121 GKIAECTFTKMSNSALNVLFSGLRLCRNACCQRMWFTFNGACSCGPLPLEATIIYIDQ 180  
DB 121 GKIAECTFTKMSNSALNVLFSGLRLCRNACCQRMWFTFNGACSCGPLPLEATIIYIDQ 180  
QY 181 GSPEMNSTINIHRRSSVGLCEGTGAGVDVAIWWGTCSDPKQKASGMSVSYIIIEE 240  
DB 181 GSPEMNSTINIHRRSSVGLCEGTGAGVDVAIWWGTCSDPKQKASGMSVSYIIIEE 240

Db 181 GSEPMNSTINIHRTSSVEGICBEGIGAGLVDAIWMGTCSDPKGDASTGNSVSRIITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

## RESULT 12

US-10-007-805-514  
Sequence 514, Application US/10007805  
Publication No. US20020150581A1

## GENERAL INFORMATION:

APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Davlin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hedler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Durham, Margareta  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.470C10  
CURRENT APPLICATION NUMBER: US/10/007,805  
CURRENT FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 593  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 514  
LENGTH: 243  
TYPE: PRN  
ORGANISM: Homo sapiens  
US-10-007-805-514

Query Match 100.0%; Score 1301; DB 14; Length 243;  
Best Local Similarity 100.0%; Pred. No. 8.7e-121;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLLLLLLPAPSSASEIPKQKQAKLRQREVVDLYNGMCIQGPA 60  
Db 1 MRPGPASPQRRLGILLLLLLLPAPSSASEIPKQKQAKLRQREVVDLYNGMCIQGPA 60  
QY 61 GVGGRDSSPGANYIPGTPGIPGRDGFKEGECLEBSFESWTPTNKQCSWSSLNTGIDL 120  
Db 61 GVGGRDSSPGANYIPGTPGIPGRDGFKEGECLEBSFESWTPTNKQCSWSSLNTGIDL 120  
QY 121 GRTAECTFTKMSNSALRYLFGSLRLKCRNACCORRYFTFNACSGPLPIAIIYLDQ 180  
Db 121 GRTAECTFTKMSNSALRYLFGSLRLKCRNACCORRYFTFNACSGPLPIAIIYLDQ 180  
QY 181 GSEPMNSTINIHRTSSVEGICBEGIGAGLVDAIWMGTCSDPKGDASTGNSVSRIITIEE 240  
Db 181 GSEPMNSTINIHRTSSVEGICBEGIGAGLVDAIWMGTCSDPKGDASTGNSVSRIITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

## RESULT 13

US-10-063-547-122  
Sequence 122, Application US/10063547  
Publication No. US20020182638A1

## GENERAL INFORMATION:

APPLICANT: Baton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerdtisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.

APPLICANT: Watanabe, Collin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 122  
LENGTH: 243  
TYPE: PRN  
ORGANISM: Homo Sapien  
US-10-063-547-122

Query Match 100.0%; Score 1301; DB 14; Length 243;  
Best Local Similarity 100.0%; Pred. No. 8.7e-121;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGILLLLLLLPAPSSASEIPKQKQAKLRQREVVDLYNGMCIQGPA 60  
Db 1 MRPGPASPQRRLGILLLLLLLPAPSSASEIPKQKQAKLRQREVVDLYNGMCIQGPA 60  
QY 61 GVGGRDSSPGANYIPGTPGIPGRDGFKEGECLEBSFESWTPTNKQCSWSSLNTGIDL 120  
Db 61 GVGGRDSSPGANYIPGTPGIPGRDGFKEGECLEBSFESWTPTNKQCSWSSLNTGIDL 120  
QY 121 GRTAECTFTKMSNSALRYLFGSLRLKCRNACCORRYFTFNACSGPLPIAIIYLDQ 180  
Db 121 GRTAECTFTKMSNSALRYLFGSLRLKCRNACCORRYFTFNACSGPLPIAIIYLDQ 180  
QY 181 GSEPMNSTINIHRTSSVEGICBEGIGAGLVDAIWMGTCSDPKGDASTGNSVSRIITIEE 240  
Db 181 GSEPMNSTINIHRTSSVEGICBEGIGAGLVDAIWMGTCSDPKGDASTGNSVSRIITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

## RESULT 14

US-10-174-590-366  
Sequence 366, Application US/10174590  
Publication No. US20030008352A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C42  
CURRENT APPLICATION NUMBER: US/10/174,590  
CURRENT FILING DATE: 2002-06-18  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 366  
LENGTH: 243  
TYPE: PRN  
ORGANISM: Homo Sapien  
US-10-174-590-366

Query Match 100.0%; Score 1301; DB 15; Length 243;  
Best Local Similarity 100.0%; Pred. No. 8.7e-121;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





0y	241	LPK	243
Db	241	LPK	243
<p>RESULT 2</p> <p>US-09-205-258-958</p> <p>; Sequence 958, Application US/09205258</p> <p>; Patent No. 6525174</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Young et al.</p> <p>TITLE OF INVENTION: 207 Human Secreted Proteins</p> <p>FILE REFERENCE: P2007p1</p> <p>CURRENT FILING DATE: 1998-12-04</p> <p>EARLIER APPLICATION NUMBER: 60/048,912</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,885</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/049,375</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,881</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,880</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,896</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/049,020</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,876</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,895</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,884</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,894</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,971</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,964</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,882</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,899</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,893</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,900</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,901</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,892</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,915</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/049,019</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/049,970</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,972</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,916</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,917</p> <p>EARLIER FILING DATE: 1997-06-06</p> <p>EARLIER APPLICATION NUMBER: 60/048,949</p> <p>EARLIER FILING DATE: 1997-06-06</p>			

```

1      EARLIER APPLICATION NUMBER: 60/048,974
2      EARLIER FILING DATE: 1997-06-06
3      EARLIER APPLICATION NUMBER: 60/048,883
4      EARLIER FILING DATE: 1997-06-06
5      EARLIER APPLICATION NUMBER: 60/048,897
6      EARLIER FILING DATE: 1997-06-06
7      EARLIER APPLICATION NUMBER: 60/048,898
8      EARLIER FILING DATE: 1997-06-06
9      EARLIER APPLICATION NUMBER: 60/048,962
10     EARLIER FILING DATE: 1997-06-06
11     EARLIER APPLICATION NUMBER: 60/048,963
12     EARLIER FILING DATE: 1997-06-06
13     EARLIER APPLICATION NUMBER: 60/048,877
14     EARLIER FILING DATE: 1997-06-06
15     EARLIER APPLICATION NUMBER: 60/048,878
16     EARLIER FILING DATE: 1997-06-06
17     EARLIER APPLICATION NUMBER: 60/070,923
18     EARLIER FILING DATE: 1997-12-18
19     EARLIER APPLICATION NUMBER: 60/092,921
20     EARLIER FILING DATE: 1998-07-15
21     EARLIER APPLICATION NUMBER: 60/094,657
22     EARLIER FILING DATE: 1998-07-30
23     NUMBER OF SEQ ID NOS: 1227
24     SOFTWARE: PatentIn Ver. 2.10
25     SEQ ID NO 958
26     LENGTH: 276
27     TYPE: PRT
28     ORGANISM: Homo sapiens
29     FEATURE:
30     NAME/KEY: SITE
31     LOCATION: (110)
32     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
92
```



EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 962  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-205-258-962  
Query Match 27.4%; Score 356; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 4.8e-30;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 128 FTKRNSALRVLFSSGSLRLKRNACQRMVTFNGAECGSLPDEAIIYLDGSPENMS 187  
Db 1 FTKRNSALRVLFSSGSLRLKRNACQRMVTFNGAECGSLPDEAIIYLDGSPENMS 60  
Oy 188 TINIR 193  
Db 61 TINIR 66  
RESULT 4  
US-09-205-258-961  
; Sequence 961, Application US/09205258  
; Patent No. 6523174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,970

```
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,972
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,916
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,373
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,875
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,374
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,917
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,949
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,883
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,897
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,898
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,962
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,963
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,877
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,878
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/070,923
;; EARLIER FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: 60/092,921
;; EARLIER FILING DATE: 1998-07-15
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1227
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 961
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-205-258-961

Query Match      22.8%; Score 296; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 6,56-24;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      77 TPGIRGDFGEGECLRESEFESWTPNYKOCSSSLNYGIDGKIACTF 128
DB      1 TPGIRGDFGEGECLRESEFESWTPNYKOCSSSLNYGIDGKIACTF 52

RESULT 5
US-09-205-258-963
Sequence 963 Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007p1
CURRENT APPLICATION NUMBER: US/09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
```

```
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,896
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,020
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,876
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,895
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,884
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,894
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,971
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,964
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,882
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,899
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,893
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,900
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,901
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,892
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,915
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,019
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,970
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,916
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,373
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,875
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,374
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,917
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,949
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,883
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,897
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,962
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,963
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,878
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/070,923
;; EARLIER FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: 60/092,921
;; EARLIER FILING DATE: 1998-07-15
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1227
;; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 963
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-963

Query Match      20.8%; Score 270; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-21;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      193 RTSSVGLCEGIGAGLVDAIVWGTCSDYKPGDASTGMSVSRITIEELPK 243
          |||.....|
Db      1 RTSSVGLCEGIGAGLVDAIVWGTCSDYKPGDASTGMSVSRITIEELPK 51

RESULT 6
US-09-205-258-960
; Sequence 960, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
```

```
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 960
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-960

Query Match      16.3%; Score 211.5; DB 4; Length 52;
Best Local Similarity 85.1%; Pred. No. 4.6e-15;
Matches 40; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY      34 PKGKQAKQLRQREVVDLYNMCLOGPAGVGRDGSFGANYPETPGI 80
          | | | | |
Db      7 PRG-SKRRIQRREVVDLYNMCLOGPAGVGRDGSFGANYPETPGI 52

RESULT 7
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
```

;; SEQ ID NO 240  
;; LENGTH: 93  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-489-847-240

Query Match 15.1%; Score 196; DB 4; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.3e-13;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGLLLLLQLPAPSSASEIPKQKA 40  
DB 1 MRPGPASPQRRLGLLLLLQLPAPSSASEIPKQKA 40

RESULT 8  
US-09-489-847-362  
; Sequence 362, Application US/09489847  
; Patent No. 6476195

;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al  
;; TITLE OF INVENTION: 98 Human Secreted Proteins  
;; FILE REFERENCE: P2031P1  
;; CURRENT APPLICATION NUMBER: US/09/489,847  
;; EARLIER APPLICATION NUMBER: PCT/US99/17130  
;; EARLIER FILING DATE: 1999-07-29  
;; EARLIER APPLICATION NUMBER: 60/094,657  
;; EARLIER FILING DATE: 1998-07-30  
;; EARLIER APPLICATION NUMBER: 60/095,486  
;; EARLIER FILING DATE: 1998-08-05  
;; EARLIER APPLICATION NUMBER: 60/096,319  
;; EARLIER FILING DATE: 1998-08-12  
;; EARLIER APPLICATION NUMBER: 60/095,454  
;; EARLIER FILING DATE: 1998-08-06  
;; EARLIER APPLICATION NUMBER: 60/095,455  
;; EARLIER FILING DATE: 1998-08-06  
;; NUMBER OF SEQ ID NOS: 376  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 362  
;; LENGTH: 93  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-489-847-362

Query Match 15.1%; Score 196; DB 4; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.3e-13;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGLLLLLQLPAPSSASEIPKQKA 40  
DB 1 MRPGPASPQRRLGLLLLLQLPAPSSASEIPKQKA 40

RESULT 9  
US-08-463-911-4  
; Sequence 4, Application US/08463911  
; Patent No. 5869330

;; GENERAL INFORMATION:  
;; APPLICANT: Scherer, Philipp E.  
;; APPLICANT: Lodish, Harvey F.  
;; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
;; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/463,911  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; REFERENCE/DOCKET NUMBER: WHI95-05  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540

;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 246 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-463-911-4

Query Match 9.4%; Score 122.5; DB 2; Length 246;  
Best Local Similarity 37.4%; Pred. No. 8.3e-05;  
Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;

QY 5 GPASPQRRLGLLLLLQLPAPSSASEIPKQKALQREVVLYGMCLOGPAGVG 64  
DB 4 GPSCPGCGCLLLLLFLALPLRSAS-----ACGCIPIPMGMPAG 47

QY 65 RDGS---PGANVIRETPEIGRDRGKGEKE 92  
DB 48 KDGHGLQGPKEGPIPAVPTGPKGCKGE 78

RESULT 10  
US-08-931-820-1

;; Sequence 1, Application US/08931820  
;; Patent No. 6010863  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: Assay for collagen degradation  
;; NUMBER OF SEQUENCES: 4  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/931,820  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 96202596.1  
;; FILING DATE:  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1057 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;; TISSUE TYPE: Collagen type I  
US-08-931-820-1

Query Match 9.1%; Score 118.5; DB 3; Length 1057;  
Best Local Similarity 36.3%; Pred. No. 0.0017;  
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;

```

;
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-289-578-9
Query Match
Best Local Similarity 36.3%; Score 118.5; DB 4; Length 1461;
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;

QY 3 POGPAAS--PQRLGILLILLQLPAPSSASEIPKQKQAKLRQREVVDLYNMGKLOGPA 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 196 PQGPRSESGPQGVRG-----EPGPPG-----PAG-----AAGPA 224

QY 61 GVPGRDGSFGANVYIPGTPGIPGRDGFKEGK 91
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 GNPAGDQPGAKGANGAPGAGAPGFGANG 255

RESULT 11
US-09-585-887-9
; Sequence 9, Application US/09585887
; Patent No. 6413742
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMillin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; APPLICANT: Chisholm, George
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/585,887
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/289,578
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/084,828
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-887-9

Query Match
Best Local Similarity 36.3%; Score 118.5; DB 4; Length 1461;
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;

QY 3 POGPAAS--PQRLGILLILLQLPAPSSASEIPKQKQAKLRQREVVDLYNMGKLOGPA 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 354 PQGPRSESGPQGVRG-----EPGPPG-----PAG-----AAGPA 382

QY 61 GVPGRDGSFGANVYIPGTPGIPGRDGFKEGK 91
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 383 GNPAGDQPGAKGANGAPGAGAPGFGANG 413

RESULT 12
US-09-289-578-9
; Sequence 9, Application US/09289578
; Patent No. 6428978
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMillin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; APPLICANT: Chisholm, George
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/289,578
; CURRENT FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: 60/084,828
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1461
```

```

;
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-289-578-9
Query Match
Best Local Similarity 36.3%; Score 118.5; DB 4; Length 1461;
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;

QY 3 POGPAAS--PQRLGILLILLQLPAPSSASEIPKQKQAKLRQREVVDLYNMGKLOGPA 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 354 PQGPRSESGPQGVRG-----EPGPPG-----PAG-----AAGPA 382

QY 61 GVPGRDGSFGANVYIPGTPGIPGRDGFKEGK 91
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 383 GNPAGDQPGAKGANGAPGAGAPGFGANG 413

RESULT 13
US-09-227-357-190
; Sequence 190, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
```

```

; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 190
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-190

Query Match
Best Local Similarity 8.9%; Score 115.5; DB 4; Length 128;
Best Local Similarity 46.3%; Pred. No. 0.00018;
Matches 31; Conservative 5; Mismatches 22; Indels 9; Gaps 3;

QY 30 ASEPDKGAKQLRQREVVDLY--NGMCLOGPAGVGRGSGPGANVTPGTGIPGRDG 85
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 14 ASGQPRGN---QLKGENSPRY--ICSTPLGPGPPGPGANGSPGPHRIGLPGHGRDG 68
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 86 FKGEKGE 92
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 RKGEKGE 75

RESULT 14
US-09-029-348-3
; Sequence 3, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: 0087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-3

Query Match
Best Local Similarity 8.8%; Score 115; DB 3; Length 623;
Best Local Similarity 36.1%; Pred. No. 0.0019;
Matches 39; Conservative 8; Mismatches 47; Indels 14; Gaps 5;
```

```

QY 22 LQLPASSASEIPGKQAKQLRQREVVDLY--NGMCLOGPAGVGRGSGPGANVTPGTG 79
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 LDCPNP---EIPGECCAVCPQPTAPTRPPNGGPGGPKGDPGPGIPGRNBDPGIGP 127
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 IPRDGFGEKGECLRESF---EESWTPNYKQCSWSSINVCIDLGKIA 124
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 QPSGSPGPPGIC--ESCPGPNQYSPQYDSYDYS---GVAVGGIA 170
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-09-029-348-2
; Sequence 2, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: 0087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-2

Query Match
Best Local Similarity 8.8%; Score 115; DB 3; Length 626;
Best Local Similarity 36.1%; Pred. No. 0.0019;
Matches 39; Conservative 8; Mismatches 47; Indels 14; Gaps 5;

QY 22 LQLPASSASEIPGKQAKQLRQREVVDLY--NGMCLOGPAGVGRGSGPGANVTPGTG 79
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 LDCPNP---EIPGECCAVCPQPTAPTRPPNGGPGGPKGDPGPGIPGRNBDPGIGP 127
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 IPRDGFGEKGECLRESF---EESWTPNYKQCSWSSINVCIDLGKIA 124
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 QPSGSPGPPGIC--ESCPGPNQYSPQYDSYDYS---GVAVGGIA 170
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: August 13, 2003, 13:28:42
Job time : 30 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:22:12 ; Search time 96 Seconds

(Without alignments)  
653.196 Million cell updates/sec

Title: us-09-938-418-7

Perfect score: 1301  
Sequence: 1 MRPGPASPQRRLGILLIL.....GDASTGWSVSRIIEELPK 243

Scoring table:

BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rv1rus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1294	99.5	243	4	096CG8	096CG8 homo sapien
2	1216	93.5	245	11	08CG08	08CG08 rattus norv
3	1201	92.3	245	11	09D1D6	09D1D6 mus musculu
4	1052	80.9	232	4	081X63	081X63 homo sapien
5	132	10.1	565	11	08K036	08K036 mus musculu
6	124.5	9.6	717	4	09NQ52	09NQ52 homo sapien
7	122.5	9.4	1472	13	09OZAO	09OZAO gallus gall
8	120	9.2	287	11	08CFR0	08CFR0 mus musculu
9	120	9.2	1752	5	007265	007265 strongyloce
10	119	9.1	289	5	018799	018799 caenorhabd1
11	118.5	9.1	1461	4	076045	076045 homo sapien
12	118.5	9.1	1464	4	08NA73	08NA73 homo sapien
13	118	9.1	291	5	09NAR3	09NAR3 caenorhabd1
14	118	9.1	832	4	096JF7	096JF7 homo sapien
15	115	9.1	1860	4	081ZC6	081ZC6 homo sapien
16	117.5	9.0	568	11	08CD80	08CD80 mus musculu

17	117.5	9.0	739	11	070575	070575 mus musculu
18	117.5	9.0	751	11	09R1N9	09R1N9 mus musculu
19	117	9.0	327	5	001799	001799 caenorhabd1
20	117	9.0	1659	11	09Q2S0	09Q2S0 mus musculu
21	116	8.9	886	4	09NB7	09NB7 mus musculu
22	116	8.9	888	13	090796	090796 gallus gall
23	115.5	8.9	1621	4	09H4R9	09H4R9 homo sapien
24	115.5	8.9	1684	6	08HYC1	08HYC1 canis fam1
25	115	8.8	957	4	09H0V3	09H0V3 homo sapien
26	115	8.8	957	4	09H0V3	09H0V3 homo sapien
27	115	8.8	1163	4	08N6U4	08N6U4 homo sapien
28	114.5	8.8	311	5	001304	001304 homo sapien
29	114.5	8.8	496	4	08NE08	08NE08 caenorhabd1
30	114	8.8	304	5	09XV3	09XV3 caenorhabd1
31	114	8.8	304	5	09U349	09U349 caenorhabd1
32	114	8.8	304	5	09U348	09U348 caenorhabd1
33	114	8.8	312	11	08CHX9	08CHX9 mus musculu
34	113.5	8.7	289	11	08BVD7	08BVD7 mus musculu
35	113.5	8.7	300	5	022183	022183 caenorhabd1
36	113.5	8.7	345	5	095WV2	095WV2 meloidogyne
37	113.5	8.7	1420	13	090W37	090W37 gallus gall
38	113.5	8.7	1549	11	060444	060444 cricetus
39	113.5	8.7	1600	4	09U5H6	09U5H6 homo sapien
40	113.5	8.7	2944	11	063870	063870 mus musculu
41	112.5	8.6	1307	13	08JEF7	08JEF7 xenopus lae
42	112	8.6	335	5	017402	017402 caenorhabd1
43	112	8.6	347	6	09XJ25	09XJ25 bos taurus
44	111.5	8.6	428	5	022369	022369 caenorhabd1
45	111.5	8.6	438	11	08K4P3	08K4P3 mus musculu

## ALIGNMENTS

### RESULT 1

ID	096CG8	PRELIMINARY:	PRT:	243 AA.
AC	096CG8;			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Similar to RIKEN CDNA 1110014B07 gene (Collagen triple helix repeat-containing protein 1).			
DE	Similar to RIKEN CDNA 1110014B07 gene (Collagen triple helix repeat-containing protein 1).			
GN	CTHRC1.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Kidney;			
RA	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Aortic smooth muscle;			
RA	Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;			
RT	"Expression of the novel collagen triple helix repeat-containing gene (cthrcl) suggests functions in multiple organ systems."			
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC014245; AAH14245.1; -			
DR	EMBL; AV136825; AAN15749.1; -			
DR	InterPro: IPR000087; Collagen.			
DR	Pfam: PF01391; Collagen.1.			
SO	SEQUENCE 243 AA; 26224 MW; A11FEBC66867F9 CRC64;			

Query Match 99.5%; Score 1294; DB 4; Length 243;  
Best Local Similarity 99.6%; Pred. No. 4.7e-119;  
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MRPGPASPQRRLGILLILQLPAPSSASEIPKQKQAOIQRREVVDLYNGKLOGPA 60  
DB 1 MRPGPASPQRRLGILLILQLPAPSSASEIPKQKQAOIQRREVVDLYNGKLOGPA 60





SN SEQUENCE FROM N.A.  
RA Sanuki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;  
RT "Novel polypeptide found in human cornea cDNA library."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF395488; AAO17919.1; -  
SQ SEQUENCE 232 AA; 25163 MW; E9D4BC30304837ED CRC64;

Query Match 80.9%; Score 1052; DB 4; Length 232;  
Best Local Similarity 83.1%; Pred. No. 2,7e-95;  
Matches 201; Conservative 8; Mismatches 19; Indels 14; Gaps 2;

QY 1 MRPGPASPQRRLGLLLLLDLPAPSSASEIPKQKQALQREVVDLYNMGCLGPA 60  
DB 1 MPPGGRSIT-VKLRKTVSRKRLNMGPSAFQGLGCR-----YNGMCLGPA 46  
QY 61 GVGGRDSSPGANYIPGPGIPGRDGFGEKGECLRESEESWTPNYKQCSWSSLYNGIDL 120  
DB 47 GVGGRDSSPGANGIPGPGIPGRDGFGEKGECLRESEESWTPNYKQCSWSSLYNGIDL 106  
QY 121 GKIAECTFTMRNSALRVLFSGSLRLKCRNACQWYFTFNGAECGPIPIEAIIYLDQ 180  
DB 107 GKIAECTFTMRNSALRVLFSGSLRLKCRNACQWYFTFNGAECGPIPIEAIIYLDQ 166  
QY 181 GSEPMSTINIHRTSYEGICGAGLVYVAIWTGCSYPRGDASTGMSYSRIIIEE 240  
DB 167 GSEPMSTINIHRTSYEGICGAGLVYVAIWTGCSYPRGDASTGMSYSRIIIEE 226  
QY 241 LP 242  
DB 227 LP 228

RESULT 5  
Q8K036 PRELIMINARY; PRT; 565 AA.

AC 08K036: 01-OCT-2002 (TREMblrel. 22, Created)  
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Similar to collagen, type XIII, alpha 1.  
GN COL13A1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Breast tumor;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC034164; AAH34164.1; -  
DR MGD: MGI:1277201; COL13a1.  
DR InterPro: IPR000087; Collagen.  
DR Pfam: PF01391; Collagen; 5.  
DR ProDom: PD000007; Collagen; 1.  
KW Collagen.  
SQ SEQUENCE 565 AA; 56726 MW; DBD3FF99D670195F CRC64;

Query Match 10.1%; Score 132; DB 11; Length 565;  
Best Local Similarity 33.9%; Pred. No. 0.00024;  
Matches 38; Conservative 13; Mismatches 35; Indels 26; Gaps 6;

QY 27 PSSASEI-----PKGKQKALQREVVDLYNMGCLGPA 71  
DB 393 PGAGAGGSPGPRG-AKGEKGEKEMVD-YNGSINEALQETRLALMGPRPLPGQTGPGR 450  
QY 72 NWTPGP-----GIRGDFGEKGECLRESEESWTPNYKQCSWSSLYNG 117  
DB 451 ---PGTPGGRGEGIGLPGPRGDDDKPRGRKPGAGAGWSSRTPRKMGASRRNG 499

RESULT 6

Q9N052 PRELIMINARY; PRT; 717 AA.  
AC Q9N052;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DE Type XIII collagen.  
GN COLXIII1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Snellman A., Tu H., Vaeisaeen T., Kvist A.P., Huhtala P.,  
RA Pihlajaniemi T.;  
RT "A short sequence in the N-terminal region is required for the  
RT trimerization of type XIII collagen and is conserved in other  
RT collagenous transmembrane proteins."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ293624; CAC00688.1; -  
DR Genew: HGNC:2190; COL13A1.  
DR InterPro: IPR000087; Collagen.  
DR Pfam: PF01391; Collagen; 9.  
DR ProDom: PD000007; Collagen; 1.  
KW Collagen.  
SQ SEQUENCE 717 AA; 69964 MW; A31E9C7D3E87577 CRC64;

Query Match 9.6%; Score 124.5; DB 4; Length 717;  
Best Local Similarity 42.1%; Pred. No. 0.0018;  
Matches 32; Conservative 8; Mismatches 17; Indels 19; Gaps 4;

QY 34 PKGKQKALQREVVDLYNMGCLGPA 76  
DB 431 PKG-SKEPGKGEKEMVD-YNGSINEALQETRLALMGPRPLPGQTGPGRGEGIRGKEIG 488  
QY 77 TPQIPGRDGFGEKGE 92  
DB 489 LPGPGRDGFGEKGRGX 504

RESULT 7

Q90ZAO PRELIMINARY; PRT; 1472 AA.  
AC Q90ZAO;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Collagen type XX alpha 1 precursor.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-21303548; Pubmed-11274142;  
RA Koch M., Foley J.E., Hahn R., Zhou P., Burgeson R.E., Gerecke D.R.,  
RA Gordon M.K.;  
RT "alpha 1(X) Collagen, a New Member of the Collagen Subfamily, Fibril-  
RT associated Collagens with Interrupted Triple Helices."  
RL J. Biol. Chem. 276:23120-23126(2001).  
DR EMBL: AF312825; AAK58847.1; -  
DR InterPro: IPR000087; Collagen.  
DR InterPro: IPR003961; FN III.  
DR InterPro: IPR003129; TSPN.  
DR InterPro: IPR002035; VWF\_A.  
DR Pfam: PF01391; Collagen; 4.  
DR Pfam: PF00041; fn3; 6.  
DR Pfam: PF02210; TSPN; 1.  
DR Pfam: PF00092; vwa; 1.  
DR PRINTS: PR00453; VWFADOMAIN.  
DR ProDom: PD000007; Collagen; 1.

```

DR SMART; SM00060; FN3; 6.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Collagen; Signal.
FT SIGNAL.
SQ SEQUENCE 1472 AA; 156903 MW; 5361611579C56ERD CRC64;

Query Match
Best Local Similarity 9.4%; Score 122.5; DB 13; Length 1472;
Matches 37; Conservative 7; Mismatches 27; Indels 39; Gaps 6;

OY 3 PGAPASPORLRGLLLLLLP-----APSSASEI-----PKGKAKQLRQREV 47
Db 1161 PGPPGSPGR-RG-----PGGEGEPKGEKPGPKGVPKPGSPGSGPSGQ--- 1207
OY 48 VDLVNGMCLQPGAVP-----GRDGSFGANVTPGTPIPGDGFKEGK 91
Db 1208 -----GITGQVPPGPIKGEKGDGSPGMGIPGVQAGPRDGIQAGK 1252

RESULT 8
OQCFRO PRELIMINARY; PRT; 287 AA.
ID OQCFRO;
AC OQCFRO;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to C1q-like.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040774; AAH40774.1;
SQ SEQUENCE 287 AA; 29292 MW; 8FF89EC1C7420415 CRC64;

Query Match
Best Local Similarity 9.2%; Score 120; DB 11; Length 287;
Matches 42; Conservative 10; Mismatches 57; Indels 12; Gaps 4;

OY 27 PSSASEIRKQKAKQLRQREV-DLYNC---MCLQPGAVPGRDGSFGANVTPGTPIG 82
Db 44 PAGAKAPPPGPGSTAL---EYWDLSANPPPPFPIQPKGDPGRPKPGRPGGPPG 100
OY 83 RDGFKEGECIRSEFESWTPNYKQCSWSLNYGIDLGKIACTFTKMSNSALRYLS 142
Db 101 PRGPGEKDGSRPL-----PGDLTTSAGAGVVGSGGTGGDTGEVTSALSAF 155
OY 143 G 143
Db 156 G 156

RESULT 9
OQ7265 PRELIMINARY; PRT; 1752 AA.
ID OQ7265;
AC OQ7265;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE 3 alpha procollagen.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=93186842; Pubmed=8444899;
RA Exposito J., Y., D'Alessio M., Di Liberto M., Ramirez F.;
RT "Complete primary structure of a sea-urchin type IV collagen and
RT analysis of the 5' end of its gene."
RL J. Biol. Chem. 268:5249-5254(1993).
DR EMBL; L02917; AAA50039.1;
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR001442; ProcollagenC4.
DR Pfam; PF01413; C4; 2.
DR Pfam; PF01391; Collagen; 25.
DR ProDom; PD000007; Collagen; 9.
DR ProDom; PD003923; ProcollagenC4; 1.
DR SMART; SM00111; C4; 2.
KW Collagen.
SQ SEQUENCE 1752 AA; 170210 MW; 1AESA21569346D CRC64;

Query Match
Best Local Similarity 9.2%; Score 120; DB 5; Length 1752;
Matches 46; Conservative 20; Mismatches 61; Indels 78; Gaps 9;

OY 3 PGAPASPORLRGLLLLLLPAPSSASEIRKQKAKQLRQREVVDLYNCMCLQPGAV 62
Db 1453 PGPPGROGR-----PGPG-----PPG-----LTGDKGT 1477
OY 63 PGDGSFGANVTPGTPIPGDGFKEGECIRSEF-----EESWT 103
Db 1478 PGVQGNPGVSGVPGGPGHKGEGFPGONGQPDPPGPKGAGIPGSSSGFFIRHSQT 1537
OY 104 PNYKQC-----SW-----SLNYGIDLGKIACTFTKMSNSALRYLSGLRL 147
Db 1538 TSIPCCPGTAKAMWIGSILTYQGNRGHGDJGKPGSC---LKRSTMPPLFC-NINN 1592
OY 148 KCRNACQRMWYFTFGAECGCLPT 172
Db 1593 VCHVASRNDYSYWLSTTE---PMPM 1614

RESULT 10
O18799 PRELIMINARY; PRT; 289 AA.
ID O18799;
AC O18799;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE C53B4.5 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Berks M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; Pubmed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z68215; GAA92453.1;
DR WormPeP; C53B4.5; CE03091.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; Col_cuticle_N; 1.
SQ SEQUENCE 289 AA; 29999A3FF9CC0B044 CRC64;

Query Match
Best Local Similarity 9.1%; Score 119; DB 5; Length 289;
Matches 29; Conservative 5; Mismatches 20; Indels 30; Gaps 2;

```



```

RESULT 13
ID 09NAR3 PRELIMINARY; PRT; 291 AA.
AC 09NAR3;
DR 01-OCT-2000 (TREMBlrel. 15, Created)
DR 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE C24F3.6 protein.
GN C24F3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBL_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurtry A.A.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL023716; CAB97232.1; -.
DR WormPeP; C24F3.6; CE18523.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; COL_cuticle.N.
DR InterPro; IPR002965; P_rich_extensions.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; COL_cuticle.N; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR ProDom; PD000007; Collagen; 2.
KW Collagen.
SQ
SEQUENCE 291 AA; 29191 MW; 8A8F3685823A3534 CRC64;

Query Match 9.1%; Score 118; DB 5; Length 291;
Best Local Similarity 34.5%; Pred. No. 0.0025;
Matches 29; Conservative 6; Mismatches 19; Indels 30; Gaps 2;

QY 25 PAPSASSEIPKQKQ-KAQLRQREVVDLYNGMCLQGPAGVPGRDSPGA----- 71
DB 205 PQPGAGPGEQGPQGPQ-----RGAPGEGKDGSPGGGEGKASGEPGP 249
QY 72 --NVTPGTPTGPRGDFGEC 93
DB 250 GRDGPGRHGGPGKDGPRGKGV 273

RESULT 14
ID 096JF7 PRELIMINARY; PRT; 832 AA.
AC 096JF7;
DR 01-DEC-2001 (TREMBlrel. 19, Created)
DR 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein KIAA1870 (Fragment).
GN KIAA1870.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Brain;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 8:85-95(2001).
DR EMBL; AB058773; BAB47499.1; -.

```

```

DR InterPro; IPR000087; Collagen.
DR InterPro; IPR000885; Fib_collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 9.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 832 AA; 83207 MW; 527640BD635A337F CRC64;

Query Match 9.1%; Score 118; DB 4; Length 832;
Best Local Similarity 47.8%; Pred. No. 0.0092;
Matches 33; Conservative 4; Mismatches 26; Indels 6; Gaps 3;

QY 25 PAPSASSEIPKQKQ-KAQLRQREVVDLYNGMCLQGPAGVPGRDSPGANVTPGTGPR 83
DB 367 PKGSGAGPGRKQKQKAGAPGRVQGLG--LPGRVYVGRQGLG---TAGPDGLGR 421
QY 84 DGFKEGKE 92
DB 422 DQAGQOQGE 430

RESULT 15
ID 081ZC6 PRELIMINARY; PRT; 1860 AA.
AC 081ZC6;
DR 01-MAR-2003 (TREMBlrel. 23, Created)
DR 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Collagen XXVII proalpha 1 chain precursor.
GN COL27A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Cartilage;
RA Pace J.M., Corrado M., Missero C., Byers P.H.;
RT "Identification, characterization and expression analysis of a new
RT fibrillar collagen gene, COL27A1.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY149237; AANA1263.1; -.
KW Signal.
FT SIGNAL 1 41 POTENTIAL.
FT CHAIN 625 1621 COLLAGEN XXVII PROALPHA 1 CHAIN.
SQ SEQUENCE 1860 AA; 186891 MW; 5F8CDFAF4B6014EC CRC64;

Query Match 9.1%; Score 118; DB 4; Length 1860;
Best Local Similarity 47.8%; Pred. No. 0.025;
Matches 33; Conservative 4; Mismatches 26; Indels 6; Gaps 3;

QY 25 PAPSASSEIPKQKQ-KAQLRQREVVDLYNGMCLQGPAGVPGRDSPGANVTPGTGPR 83
DB 1395 PKGSGAGPGRKQKQKAGAPGRVQGLG--LPGRVYVGRQGLG---TAGPDGLGR 1449
QY 84 DGFKEGKE 92
DB 1450 DQAGQOQGE 1458

Search completed: August 13, 2003, 13:27:21
Job time : 98 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:15:46 ; Search time 23 Seconds

(without alignments)  
496.847 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 1301  
Sequence: 1 MRPQGPASPORLRGLLL.....GDASTGWSVSRIIEELPK 243

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	122.5	9.4	246 1 C10C_MOUSE	002105 mus musculu
2	118.5	9.1	1464 1 CA11_HUMAN	P02452 homo sapien
3	117	9.0	754 1 CA54_CANFA	Q28247 canis fami1
4	116	8.9	1670 1 CA34_HUMAN	Q01955 homo sapien
5	115.5	8.9	1685 1 CA54_HUMAN	P29400 homo sapien
6	115.5	8.9	289 1 CQ47_HUMAN	Q9b12 homo sapien
7	115.5	8.9	1516 1 CA1H_HUMAN	P39600 homo sapien
8	115.5	8.9	1669 1 CA14_HUMAN	P02462 homo sapien
9	115	8.8	1466 1 CA13_HUMAN	P02461 homo sapien
10	115	8.8	1763 1 CA24_ARCSU	P27393 ascaris suu
11	113.5	8.7	1691 1 CA64_HUMAN	Q14031 homo sapien
12	113	8.7	2944 1 CA17_HUMAN	Q02388 homo sapien
13	112	8.6	245 1 C10C_HUMAN	P02747 homo sapien
14	111	8.5	747 1 CA12_BOVIN	P02459 bos taurus
15	110.5	8.5	671 1 CA11_RAT	P02454 ratu1us norv
16	110.5	8.5	1453 1 CA11_MOUSE	P01087 mus musculu
17	110.5	8.5	1460 1 CA11_CANFA	Q9x517 canis fami1
18	110	8.5	258 1 C10C_HUMAN	Q75973 homo sapien
19	110	8.5	299 1 CC34_CAEEL	P34687 caenorhabd1
20	110	8.5	684 1 CA39_HUMAN	Q14050 homo sapien
21	110	8.5	1049 1 CA13_BOVIN	P04258 bos taurus
22	110	8.5	1453 1 CA11_CHICK	P02457 gallus gall
23	110	8.5	1806 1 CA1B_HUMAN	P12107 homo sapien
24	109	8.4	1569 1 CA14_MOUSE	P02463 mus musculu
25	109	8.4	1758 1 CA14_CAEEL	P17139 caenorhabd1
26	108.5	8.3	1418 1 CA12_HUMAN	P02458 homo sapien
27	108.5	8.3	1459 1 CA12_MOUSE	P28881 mus musculu
28	107	8.2	744 1 CA18_HUMAN	P27658 homo sapien
29	107	8.2	765 1 MF10_MOUSE	Q923P0 bos taurus
30	106.5	8.2	453 1 MSRE_BOVIN	P21758 bos taurus
31	106.5	8.2	743 1 CA18_MOUSE	Q00780 mus musculu
32	106.5	8.2	779 1 CA18_BOVIN	P02453 bos taurus
33	106.5	8.2	1262 1 CA13_CHICK	P12105 gallus gall

34	106.5	8.2	1464 1 CA13_MOUSE	P08121 mus musculu
35	106.5	8.2	1758 1 CA24_CAEEL	P17140 caenorhabd1
36	106	8.1	296 1 CC01_CAEEL	P08124 caenorhabd1
37	106	8.1	301 1 CC02_CAEEL	P17656 caenorhabd1
38	106	8.1	302 1 CCDC_CAEEL	P17657 caenorhabd1
39	106	8.1	482 1 CA1B_RAT	P20909 ratu1us norv
40	106	8.1	744 1 CA18_RABIT	P14282 oryctolagus
41	106	8.1	1143 1 CA11_HUMAN	Q14993 homo sapien
42	106	8.1	1804 1 CA1B_MOUSE	Q61245 mus musculu
43	105.5	8.1	283 1 YQ33_CAEEL	Q09233 caenorhabd1
44	105.5	8.1	674 1 CA1A_BOVIN	P23206 bos taurus
45	105.5	8.1	674 1 CA1A_CHICK	P08125 gallus gall

## ALIGNMENTS

```

RESULT 1
C10C_MOUSE STANDARD; PRT; 246 AA.
ID C10C_MOUSE
AC Q02105;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Complement C1q subcomponent, C chain precursor.
GN C10G OR C10C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=93011118; PubMed=1396691;
RA Petry F., Reid K.B.M., Loos M.,
RT "Isolation, sequence analysis and characterization of cDNA clones
RT coding for the C chain of mouse C1q. Sequence similarity of
RT complement subcomponent C1q, collagen type VIII and type X and
RT precerebellin.";
RL Eur. J. Biochem. 209:129-134(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=96186528; PubMed=8606057;
RA Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;
RT "The mouse C1q genes are clustered on chromosome 4 and show
RT conservation of gene organization.";
RL Immunogenetics 43:370-376(1996).
CC -|- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD
CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE
CC COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT
CC CLIR(2)CIS(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1
CC TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE
CC FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
CC -|- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R
CC AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED
CC OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
CC A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
CC THE C CHAIN.
CC -|- SIMILARITY: Contains 1 collagenous domain.
CC -|- SIMILARITY: Contains 1 C1Q domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
DR EMBL: X66295; CAA46993.1; -
DR EMBL: X92960; CAA63535.1; -
DR PIR: S29328; S29328.

```

DR MGD: MGI:88225; C1q9.  
 DR InterPro: IPR001073; C1q.  
 DR pfam: PF00386; C1q; 1.  
 DR PRINTS: PR00007; Collagen; 1.  
 DR Prodom: PD00007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;  
 KW Repeat; Signal.  
 FT CHAIN 30 29  
 FT SIGNAL 1 29  
 FT DOMAIN 32 113  
 FT DOMAIN 114 246  
 FT DISULFID 33 33  
 FT MOD\_RES 37 37  
 FT MOD\_RES 40 40  
 FT MOD\_RES 43 43  
 FT MOD\_RES 61 61  
 FT MOD\_RES 64 64  
 FT MOD\_RES 73 73  
 FT MOD\_RES 76 76  
 FT MOD\_RES 79 79  
 FT MOD\_RES 82 82  
 FT MOD\_RES 97 97  
 FT MOD\_RES 100 100  
 FT MOD\_RES 106 106  
 FT MOD\_RES 109 109  
 SQ SEQUENCE 246 AA: 25966 MW: 2879EA1274BC88E0 CRC64:  
 Query Match 9.4%; Score 122.5; DB 1; Length 246;  
 Best Local Similarity 37.4%; Pred. No. 0.0072;  
 Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;  
 DB 5 GPASPORTRLRLILLLQLPAPSSASEIPKKGKAKQLRQRYVLYNMCQGPAGVG 64  
 4 GPSCPGQCGICLLFLALPRLRSAS-----ACGCGIPGMPGPGAG 47  
 OY 65 RDGS---PGANYIPCTPGIPGNDGPKGKGE 92  
 DB 48 KDHGKGLOGPKGPGIPGIPGPGKGGKGE 78  
 RESULT 2  
 CALL HUMAN STANDARD: PRT; 1464 AA.  
 AC P02452; Q14037; Q15176;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Collagen alpha 1(I) chain precursor.  
 GN COL1A1.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-472 FROM N.A.  
 RX MEDLINE=89025644; PubMed=3178743;  
 RA Tromp G., Kulvanliem H., Stacey A., Shikata H., Baldwin C.T.,  
 RA Jaenisch R., Prockop D.J.;  
 RT "Structure of a full-length cDNA clone for the prepro alpha 1(I)  
 RT chain of human type I procollagen.";  
 RL Biochem. J. 253:919-922(1988).  
 RN [2]  
 RP SEQUENCE OF 1-181 FROM N.A.  
 RX MEDLINE=84270697; PubMed=6462220;  
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,  
 RA Myers J., Williams C., Ramirez F.;  
 RT "Human pro alpha 1(I) collagen gene structure reveals evolutionary  
 RT conservation of a pattern of introns and exons.";

RL Nature 310:337-340(1984).  
 RN [3]  
 RP SEQUENCE OF 162-301.  
 RC TISSUE-Skin;  
 RX MEDLINE=71038625; PubMed=5529814;  
 RA Click E.M., Bornstein P.;  
 RT "Isolation and characterization of the cyanogen bromide peptides from  
 RT the alpha 1 and alpha 2 chains of human skin collagen.";  
 RL Biochemistry 9:4699-4706(1970).  
 RN [4]  
 RP SEQUENCE OF 263-268.  
 RC TISSUE-Skin;  
 RX MEDLINE=71001508; PubMed=4319110;  
 RA Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;  
 RT "A comparative study of glycopeptides derived from selected  
 RT vertebrate collagens. A possible role of the carbohydrate in fibril  
 RT formation.";  
 RL J. Biol. Chem. 245:5042-5048(1970).  
 RN [5]  
 RP SEQUENCE OF 425-1464 FROM N.A.  
 RX MEDLINE=84080385; PubMed=6689127;  
 RA Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,  
 RA Prockop D.J.;  
 RT "Nucleotide sequences of complementary deoxyribonucleic acids for the  
 RT pro alpha 1 chain of human type I procollagen. Statistical evaluation  
 RT of structures that are conserved during evolution.";  
 RL Biochemistry 22:5213-5223(1983).  
 RN [6]  
 RP SEQUENCE OF 1229-1454 FROM N.A.  
 RC TISSUE-Bone;  
 RX MEDLINE=88124208; PubMed=3340531;  
 RA Maekela J.K., Raassina M., Virta A., Vuorio E.;  
 RT "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide  
 RT domain.";  
 RL Nucleic Acids Res. 16:349-349(1988).  
 RN [7]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=88097389; PubMed=3480516;  
 RA Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gellinas R.E.;  
 RT "Regulatory elements in the first intron contribute to  
 RT transcriptional control of the human alpha 1(I) collagen gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8865-8873(1987).  
 RN [8]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=85130970; PubMed=2857713;  
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;  
 RT "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.  
 RT Promoter structure, Alu repeats, and polymorphic transcripts.";  
 RL J. Biol. Chem. 260:2315-2320(1985).  
 RN [9]  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE=88033098; PubMed=2822714;  
 RA Rossouw C.M.S., Verger W.P., du Plooy S.J., Bernard M.P., Ramirez F.,  
 RA de Wet W.J.;  
 RT "DNA sequences in the first intron of the human pro-alpha 1(I)  
 RT collagen gene enhance transcription.";  
 RL J. Biol. Chem. 262:15151-15157(1987).  
 RN [10]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=91184577; PubMed=2010058;  
 RA Kulvanliem H., Tromp G., Prockop D.J.;  
 RT "Mutations in collagen genes: causes of rare and some common diseases  
 RT in humans.";  
 RL FASEB J. 5:2052-2060(1991).  
 RN [11]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=97255959; PubMed=9101290;  
 RA Kulvanliem H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 RT associated collagen (type IX), and network-forming collagen (type X)  
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 RN [12]

RP REVIEW ON OI VARIANTS.  
 RX MEDLINE-91374476; PubMed-1895312;  
 RA Byers P.H., Wallis G.A., Willing M.C.;  
 RT "Osteogenesis imperfecta: translation of mutation to phenotype.";  
 RL J. Med. Genet. 28:433-442(1991).  
 RN [13]  
 RP REVIEW ON OI VARIANTS.  
 RX MEDLINE-97169389; PubMed-9016532;  
 RA Dalgleish R.;  
 RT "The human type I collagen mutation database.";  
 RL Nucleic Acids Res. 25:181-187(1997).  
 RN [14]  
 RP VARIANTS OI-II CYS-1166.  
 RX MEDLINE-86287390; PubMed-3016737;  
 RA Cohn D.H., Byers P.H., Steinmann B., Gellinas R.E.;  
 RT "Lethal osteogenesis imperfecta resulting from a single nucleotide  
 change in one human pro alpha 1(I) collagen allele.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).  
 RN [15]  
 RP VARIANTS OI-II ARG-569.  
 RX MEDLINE-87222295; PubMed-3108247;  
 RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;  
 RT "Lethal perinatal osteogenesis imperfecta due to the substitution of  
 arginine for glycine at residue 391 of the alpha 1(I) chain of type I  
 collagen.";  
 RL J. Biol. Chem. 262:7021-7027(1987).  
 RN [16]  
 RP VARIANTS OI-II CYS-926.  
 RX MEDLINE-88033031; PubMed-3667599;  
 RA Vogel B.E., Minor R.R., Freund M., Prockop D.J.;  
 RT "A point mutation in a type I procollagen gene converts glycine 748  
 of the alpha 1 chain to cysteine and destabilizes the triple helix in  
 a lethal variant of osteogenesis imperfecta.";  
 RL J. Biol. Chem. 262:14737-14744(1987).  
 RN [17]  
 RP VARIANTS OI-II ARG-842.  
 RX MEDLINE-88298828; PubMed-3403550;  
 RA Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;  
 RT "Substitution of arginine for glycine 664 in the collagen alpha 1(I)  
 chain in lethal perinatal osteogenesis imperfecta. Demonstration of  
 the peptide defect by in vitro expression of the mutant cDNA.";  
 RL J. Biol. Chem. 263:11627-11630(1988).  
 RN [18]  
 RP VARIANTS OI CYS-1195.  
 RX MEDLINE-89218628; PubMed-3244312;  
 RA Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;  
 RT "A cysteine for glycine substitution at position 1017 in an alpha  
 1(I) chain of type I collagen in a patient with mild dominantly  
 inherited osteogenesis imperfecta.";  
 RL Mol. Biol. Med. 5:197-207(1988).  
 RN [19]  
 RP VARIANTS OI-II VAL-434.  
 RX MEDLINE-89255493; PubMed-2470760;  
 RA Patterson E., Smiley E., Bonadio J.;  
 RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta  
 mutation.";  
 RL J. Biol. Chem. 264:10083-10087(1989).  
 RN [20]  
 RP VARIANTS OI-IV SER-1010.  
 RX MEDLINE-89308591; PubMed-2745420;  
 RA Martin J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koepflin D.A.;  
 RT "Osteogenesis imperfecta type IV. Detection of a point mutation in  
 one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";  
 RL J. Biol. Chem. 264:11893-11900(1989).  
 RN [21]  
 RP VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.  
 RX MEDLINE-89380165; PubMed-2777764;  
 RA Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;  
 RT "Characterization of point mutations in the collagen COL1A1 and  
 COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";  
 RL J. Biol. Chem. 264:15809-15812(1989).  
 RN [22]  
 RP VARIANT OI SER-1022.

RX MEDLINE-90062066; PubMed-2511192;  
 RA Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;  
 RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe  
 RT variant of osteogenesis imperfecta minimally destabilizes the triple  
 RT helix of type I procollagen. The effects of glycine substitutions on  
 RT thermal stability are either position of amino acid specific.";  
 RL J. Biol. Chem. 264:119694-119699(1989).  
 RN [23]  
 RP VARIANTS OI-II CYS-1082.  
 RX MEDLINE-89109573; PubMed-2913053;  
 RA Constantinou C.D., Nielsen K.B., Prockop D.J.;  
 RT "A lethal variant of osteogenesis imperfecta has a single base  
 RT mutation that substitutes cysteine for glycine 904 of the alpha 1(I)  
 RT chain of type I procollagen. The asymptomatic mother has an  
 RT unidentified mutation producing an overmodified and unstable type I  
 RT procollagen.";  
 RL J. Clin. Invest. 83:574-584(1989).  
 RN [24]  
 RP VARIANTS OI CYS-272; CYS-704 AND CYS-896.  
 RX MEDLINE-90009313; PubMed-2794057;  
 RA Starman B.J., Eyre D., Charbonneau H., Harrylock M., Wels M.A.;  
 RT "Wels L., Graham J.M., Byers P.H.;  
 RT "Osteogenesis imperfecta. The position of substitution for glycine by  
 RT cysteine in the triple helical domain of the pro alpha 1(I) chains of  
 RT type I collagen determines the clinical phenotype.";  
 RL J. Clin. Invest. 84:1206-1214(1989).  
 RN [25]  
 RP VARIANTS OI-II CYS-422.  
 Query Match 9.18; Score 118.5; DB 1; Length 1464;  
 Best Local Similarity 36.38; Pred. No. 0.013;  
 Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;  
 OY 3 PGSPAAAS--PQRRLGLLLLLQLPPSSASEIPKGGKQKQNLQREYVDLYNMCQGGPA 60  
 DB 357 PGSPRSSECPQGYRG-----EPGPPG-----PAG-----AAGPA 385  
 OY 61 GVPKRDGSPGAVNIPGPGIPGRDGFKEGK 91  
 DB 386 GNPAGDQPGKAKGANGAPGAGAPGPGANG 416  
 RESULT 3  
 CAS4\_CANFA STANDARD; PRT; 754 AA.  
 ID CAS4\_CANFA  
 AC 028247;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Collagen alpha 5(IV) chain (Fragment).  
 GN COL4A5.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Samoyed; TISSUE-Kidney;  
 RX MEDLINE-94224868; PubMed-8171024;  
 RA Zheng K., Thorner P.S., Marrano P., Bauman R., McInnes R.R.;  
 RT "Canine X chromosome-linked hereditary nephritis: a genetic model for  
 RT human X-linked hereditary nephritis resulting from a single base  
 RT mutation in the gene encoding the alpha 5 chain of collagen type  
 RT IV.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3989-3993(1994).  
 CC -I- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF  
 CC GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'  
 CC MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENACTIN/  
 CC NIDOGEN.  
 CC -I- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV) -  
 CC ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE  
 CC WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.  
 CC -I- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).

CC -1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS  
 CC DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE  
 CC G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY  
 CC CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL  
 CC TRIPLE-HELICAL 7S DOMAIN.  
 CC -1- P1M: Prolines are hydroxylated in some or all of the chains.  
 CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
 CC -1- P1M: Type IV collagens contain numerous cysteine residues which  
 CC are involved in inter- and intramolecular disulfide bonding. 12 of  
 CC these, located in the NC1 domain, are conserved in all known type  
 CC IV collagens.  
 CC -1- DISEASE: A DEFECT IN COL4A5 HAS BEEN FOUND TO BE THE CAUSE OF  
 CC CANINE X-LINKED HEREDITARY NEPHRITIS (HN), A DISEASE SIMILAR TO  
 CC THAT IN HUMANS (ALSO REFERRED TO AS ALPORT SYNDROME) CHARACTERIZED  
 CC BY PROGRESSIVE RENAL FAILURE AND NEUROSENSORY DEAFNESS.  
 CC -1- SIMILARITY: TO OTHER TYPE IV COLLAGENS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: 007888; AAB60258.1; -  
 CC PIR: A55267; A55267.  
 CC DR InterPro: IPR000087; Collagen.  
 CC DR InterPro: IPR001442; ProcollagenC4.  
 CC DR Pfam: PF01413; C4; 2.  
 CC DR Pfam: PF01391; Collagen; 8.  
 CC DR Prodom: PD000007; C1g\_helix; 1.  
 CC DR Prodom: PD003923; ProcollagenC4; 1.  
 CC DR SMART: SM00111; C4; 2.  
 CC DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;  
 CC KW Glycoprotein; Basement membrane; Collagen; Cell adhesion.  
 CC FT NON\_TER 1 1  
 CC FT DOMAIN <1 530 TRIPLE-HELICAL REGION  
 CC FT DISULFID 531 >754 NONHELICAL REGION (NC1).  
 CC FT DISULFID 552 643 OR 640 (BY SIMILARITY).  
 CC FT DISULFID 585 640 OR 643 (BY SIMILARITY).  
 CC FT DISULFID 597 603 BY SIMILARITY.  
 CC FT DISULFID 662 ? OR 754 (BY SIMILARITY).  
 CC FT DISULFID 696 754 BY SIMILARITY.  
 CC FT DISULFID 708 714 BY SIMILARITY.  
 CC FT NON\_TER 754 754  
 CC SQ SEQUENCE 754 AA; 73537 MW; D5E321C287FA925B CRC64;  
 CC Query Match 9.0%; Score 117; DB 1; Length 754;  
 CC Best Local Similarity 34.4%; Pred. NO. 0.0084;  
 CC Matches 33; Conservative 7; Mismatches 34; Indels 22; Gaps 4;  
 CC  
 CC QY 3 PGPAASQRLRLGLLLILLILLPAPSSASEIP-----KGQD-KAQLNREYVDLYNGMC 55  
 CC DB 332 PGQPGGRP-----GLPGEGPGRGLPGNGIGKGERGNPGQPGGLPGKGD-- 377  
 CC QY 56 LOGPAGVRGDSRGANVYIPGPGTIPGRDGRKGGG 91  
 CC DB 378 -QGPPGIQGNPGRPEGLNGMKDGLGVGPFGMGK 412  
 CC  
 CC RESULT 4  
 CC CA34\_HUMAN STANDARD; PRT; 1670 AA.  
 CC AC 001955; G9BQ72;  
 CC DT 01-OCT-1996 (Rel. 34, Created)  
 CC DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 CC DE Collagen alpha 3(IV) chain precursor (Goodpasture antigen).  
 CC GN COL4A3.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE=94364994; PubMed=8083201;  
 RA Mariyama M., Leinonen A., Mochizuki T., Tryggvason K., Reiders S.T.;  
 RT "Complete primary structure of the human alpha 3(IV) collagen chain.  
 RT Coexpression of the alpha 3(IV) and alpha 4(IV) collagen chains in  
 RT human tissues.";  
 RL J. Biol. Chem. 269:23013-23017(1994).  
 RN [2]  
 RN REVISIONS.  
 RA Leinonen A.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.; VARIANTS AS GLU-297; ARG-407; ARG-640; ARG-1167;  
 RP GLU-1207; GLN-1215; SER-1277; THR-1330; GLU-1334; GLU-1347 AND  
 RP CYS-1661, AND VARIANTS ARG-43; GLU-162; TYR-326; HIS-408; ARG-451;  
 RP PRO-574; GLU-1269 AND PRO-1474  
 RX MEDLINE=21064696; PubMed=11134255;  
 RA Heidet L., Arrondel C., Forestier L., Cohen-Solal L., Mollet G.,  
 RA Gutierrez B., Stavrou C., Gubler M.C., Antignac C.;  
 RT "Structure of the human type IV collagen gene COL4A3 and mutations in  
 RT autosomal Alport syndrome";  
 RL J. Am. Soc. Nephrol. 12:97-106(2001).  
 RN [4]  
 RN SEQUENCE OF 1386-1670 FROM N.A., AND PARTIAL SEQUENCE.  
 RP MEDLINE=93015826; PubMed=1400291;  
 RA Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.;  
 RT "Exon/intron structure of the human alpha 3(IV) gene encompassing the  
 RT Goodpasture antigen (alpha 3(IV)NC1). Identification of a potentially  
 RT antigenic region at the triple helix/NC1 domain junction.";  
 RL J. Biol. Chem. 267:19780-19784(1992).  
 RN [5]  
 RN SEQUENCE OF 1453-1670 FROM N.A.  
 RP MEDLINE=91353570; PubMed=1882640;  
 RA Morrison K.E., Mariyama M., Yang-Feng T.L., Reiders S.T.;  
 RT "Sequence and localization of a partial cDNA encoding the human alpha  
 RT 3 chain of type IV collagen.";  
 RL Am. J. Hum. Genet. 49:545-554(1991).  
 RN [6]  
 RN SEQUENCE OF 1331-1670 FROM N.A.  
 RP TISSUE-Kidney;  
 RX MEDLINE=92447878; PubMed=1737849;  
 RA Turner N., Mason P.D., Brown R., Fox M., Povey S., Rees A.,  
 RA Pusey C.D.;  
 RT "Molecular cloning of the human Goodpasture antigen demonstrates it  
 RT to be the alpha 3 chain of type IV collagen.";  
 RL J. Clin. Invest. 89:592-601(1992).  
 RN [7]  
 RN SEQUENCE OF 1644-1670 FROM N.A.  
 RP TISSUE-Kidney;  
 RA Ding J.;  
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RN SEQUENCE OF 1439-1670, AND ALTERNATIVE SPLICING.  
 RC TISSUE-Kidney;  
 RX MEDLINE=94124597; PubMed=8294492;  
 RA Feng L., Xia Y., Wilson C.B.;  
 RT "Alternative splicing of the NC1 domain of the human alpha 3(IV)  
 RT collagen gene. Differential expression of mRNA transcripts that  
 RT predict three protein variants with distinct carboxyl regions.";  
 RL J. Biol. Chem. 269:2342-2348(1994).  
 RN [9]  
 RN SEQUENCE OF 1-29 FROM N.A.  
 RX MEDLINE=98196854; PubMed=9537506;  
 RA Monota R., Sugimoto M., Ohashi T., Kigasawa K., Yoshioke H.,  
 RA Ninomiya Y.;  
 RT "Two genes, COL4A3 and COL4A4 coding for the human alpha3(IV) and  
 RT alpha4(IV) collagen chains are arranged head-to-head on chromosome  
 RT 2q36.";  
 RL FEBS Lett. 424:11-16(1998).  
 RN [10]



RP ALTERNATIVE SPLICING.  
 RX MEDLINE-93280184; PubMed-8505332;  
 RA Bernal D., Quinones S., Saus J.;  
 RT "The human mRNA encoding the Goodpasture antigen is alternatively  
 RT spliced";  
 RL J Biol. Chem. 268:12090-12094(1993).  
 RN [11]  
 RP VARIANT PRO-1474.  
 RX MEDLINE-95078827; PubMed-7987301;  
 RA Lemmink H.H., Mochizuki T., van den Heuvel L.P.W.J., Schroeder C.H.,  
 RA Barrientos A., Monens L.A.H., van Oost B.A., Brunner H.G.,  
 RA Reeders S.T., Smeets H.J.M.;  
 RT "Mutations in the type IV collagen alpha 3 (COL4A3) gene in autosomal  
 RT recessive Alport syndrome";  
 RL Hum. Mol. Genet. 3:1269-1273(1994).  
 CC -1- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF  
 CC GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'  
 CC MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENACTIVIN/  
 CC NIDOGN.  
 CC -1- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-  
 CC ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH  
 CC 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.  
 CC -1- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms-3;  
 CC Comment-Additional isoforms seem to exist. Isoforms differ in  
 CC the C-terminal part of the NCI domain;  
 CC Name-1;  
 CC IsoId=001955-1; Sequence-Displayed;  
 CC Name-2; Synonyms-V;  
 CC IsoId=001955-2; Sequence-VSP-001170;  
 CC Name-3; Synonyms-L5;  
 CC IsoId=001955-3; Sequence-VSP-001171;  
 CC -1- TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV COLLAGENS ARE  
 CC COLLOCALIZED AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDNEY, EYE,  
 CC COCHLEA, LUNG AND BRAIN.  
 CC -1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS  
 CC DOMAIN (NCI) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE  
 CC G-X-Y REPEATS IN THE LONG CENTRAL, TRIPLE-HELICAL DOMAIN (WHICH MAY  
 CC CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL  
 CC TRIPLE-HELICAL 7S DOMAIN.  
 CC -1- PTM: Prolines at the third position of the tripeptide repeating  
 CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
 CC -1- PTM: Isoform 2 contains an additional N-linked glycosylation site.  
 CC -1- PTM: Type IV collagens contain numerous cysteine residues which  
 CC are involved in inter- and intramolecular disulfide bonding. 12 of  
 CC these, located in the NCI domain, are conserved in all known type  
 CC IV collagens.  
 CC -1- PTM: Phosphorylated by the Goodpasture antigen-binding protein.  
 CC -1- DISEASE: Antibodies against the NCI domain of alpha3(IV) mediate  
 CC the autoimmune disease Goodpasture syndrome (MIM:233450), which is  
 CC characterized by hematuria and pulmonary hemorrhage.  
 CC -1- DISEASE: Defects in COL4A3 are a cause of autosomal recessive  
 CC Alport syndrome (AS) (MIM:203780), an hereditary disorder  
 CC characterized by progressive glomerulonephritis, renal failure,  
 CC hematuria, ocular abnormalities and deafness. The recessive form  
 CC occurs equally between males and females.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X80031; CA56335.1; -;  
 DR EMBL: AJ288487; CAC36101.1; -;  
 DR EMBL: AJ288488; CAC36101.1; JOINED.  
 DR EMBL: AJ288489; CAC36101.1; JOINED.  
 DR EMBL: AJ288490; CAC36101.1; JOINED.  
 DR EMBL: AJ288491; CAC36101.1; JOINED.  
 DR EMBL: AJ288492; CAC36101.1; JOINED.

DR EMBL: AJ288493; CAC36101.1; JOINED.  
 DR EMBL: AJ288494; CAC36101.1; JOINED.  
 DR EMBL: AJ288495; CAC36101.1; JOINED.  
 DR EMBL: AJ288496; CAC36101.1; JOINED.  
 DR EMBL: AJ288497; CAC36101.1; JOINED.  
 DR EMBL: AJ288498; CAC36101.1; JOINED.  
 DR EMBL: AJ288499; CAC36101.1; JOINED.  
 DR EMBL: AJ288500; CAC36101.1; JOINED.  
 DR EMBL: AJ288501; CAC36101.1; JOINED.  
 DR EMBL: AJ288502; CAC36101.1; JOINED.  
 DR EMBL: AJ288503; CAC36101.1; JOINED.  
 DR EMBL: AJ288504; CAC36101.1; JOINED.  
 DR EMBL: AJ288505; CAC36101.1; JOINED.  
 DR EMBL: AJ288506; CAC36101.1; JOINED.  
 DR EMBL: AJ288507; CAC36101.1; JOINED.  
 DR EMBL: AJ288508; CAC36101.1; JOINED.  
 DR EMBL: AJ288509; CAC36101.1; JOINED.  
 DR EMBL: AJ288510; CAC36101.1; JOINED.  
 DR EMBL: AJ288511; CAC36101.1; JOINED.  
 DR EMBL: AJ288512; CAC36101.1; JOINED.  
 DR EMBL: AJ288513; CAC36101.1; JOINED.  
 DR EMBL: AJ288514; CAC36101.1; JOINED.  
 DR EMBL: AJ288515; CAC36101.1; JOINED.  
 DR EMBL: AJ288516; CAC36101.1; JOINED.  
 DR EMBL: AJ288517; CAC36101.1; JOINED.  
 DR EMBL: AJ288518; CAC36101.1; JOINED.  
 DR EMBL: AJ288519; CAC36101.1; JOINED.  
 DR EMBL: AJ288520; CAC36101.1; JOINED.  
 DR EMBL: AJ288521; CAC36101.1; JOINED.  
 DR EMBL: AJ288522; CAC36101.1; JOINED.  
 DR EMBL: AJ288523; CAC36101.1; JOINED.  
 DR EMBL: AJ288524; CAC36101.1; JOINED.  
 DR EMBL: AJ288525; CAC36101.1; JOINED.  
 DR EMBL: AJ288526; CAC36101.1; JOINED.  
 DR EMBL: AJ288527; CAC36101.1; JOINED.  
 DR EMBL: AJ288528; CAC36101.1; JOINED.  
 DR EMBL: AJ288529; CAC36101.1; JOINED.  
 DR EMBL: AJ288530; CAC36101.1; JOINED.  
 DR EMBL: AJ288531; CAC36101.1; JOINED.  
 DR EMBL: AJ288532; CAC36101.1; JOINED.  
 DR EMBL: AJ288533; CAC36101.1; JOINED.  
 DR EMBL: AJ288534; CAC36101.1; JOINED.  
 DR EMBL: AJ288535; CAC36101.1; JOINED.  
 DR EMBL: AJ288536; CAC36101.1; JOINED.

Query Match 8.9%; Score 116; DR 1; Length 1670;  
 Best Local Similarity 35.18; Pred. No. 0.026;  
 Matches 33; Conservative 6; Mismatches 37; Indels 18; Gaps 3;  
 QY 5 GPASPORTLRLLDLLLPAPSSASEIPKQKQALROREVVVDLYNGKCIQGPAGVPG 64  
 Db 467 GKPEP-----GLTCTQCPYIPGPGCLGRLHGVKGIKPR-----GQAALIKG 511  
 QY 65 RDGSPGANVTPGPIPGIRD--GFKGEKGECLR 95  
 Db 512 SPGSPGNTGLPFGFPGAGDPGLKGEKGETLQ 545

RESULT 5  
 CA54\_HUMAN STANDARD; PRT; 1685 AA.  
 AC P29400; O16006; Q16126;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Collagen alpha 5(IV) chain precursor.  
 GN COL4A5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE-94165049; PubMed-8120014;  
 RA Zhou J., Leinonen A., Tryggvason K.;  
 RT "Structure of the human type IV collagen COL4A5 gene.";  
 RL J. Biol. Chem. 269:6608-6614(1994).  
 RN [2]  
 RN SEQUENCE OF 1-910 FROM N.A., AND VARIANT AS CYS-521.  
 RP TISSUE=Kidney;  
 RX MEDLINE-92316923; PubMed-1352287;  
 RA Zhou J., Hertz J.M., Leinonen A., Tryggvason K.;  
 RT "Complete amino acid sequence of the human alpha 5 (IV) collagen  
 chain and identification of a single-base mutation in exon 23  
 converting glycine 521 in the collagenous domain to cysteine in an  
 Alport syndrome patient.";  
 RL J. Biol. Chem. 267:12475-12481(1992).  
 RN [3]  
 RN SEQUENCE OF 85-1685 FROM N.A.  
 RP TISSUE=Placenta;  
 RX MEDLINE-90337990; PubMed-2380186;  
 RA Phlajaniemi T., Pohjalainen E.R., Myers J.C.;  
 RT "Complete primary structure of the triple-helical region and the  
 carboxyl-terminal domain of a new type IV collagen chain, alpha  
 5(IV).";  
 RL J. Biol. Chem. 265:13758-13766(1990).  
 RN [4]  
 RN SEQUENCE OF 924-1685 FROM N.A.  
 RP MEDLINE-91169491; PubMed-2004755;  
 RA Zhou J., Hostalka S.L., Chow L.T., Tryggvason K.;  
 RT "Characterization of the 3' half of the human type IV collagen alpha  
 5 gene that is affected in the Alport syndrome.";  
 RL Genomics 9:1-9(1991).  
 RN [5]  
 RN SEQUENCE OF 914-1685 FROM N.A.  
 RP MEDLINE-90160375; PubMed-1689491;  
 RA Hostalka S.L., Eddy R.L., Byers M.G., Hoehlyhae M., Shows T.B.,  
 RA Tryggvason K.;  
 RT "Identification of a distinct type IV collagen alpha chain with  
 restricted kidney distribution and assignment of its gene to the  
 locus of X chromosome-linked Alport syndrome.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1606-1610(1990).  
 RN [6]  
 RN SEQUENCE OF 1442-1471 FROM N.A.  
 RP MEDLINE-90252791; PubMed-2339699;  
 RA Myers J.C., Jones T.A., Pohjalainen E.R., Kadri A.S., Goddard A.D.,  
 RA Sheer D., Solomon E., Phlajaniemi T.;  
 RT "Molecular cloning of alpha 5(IV) collagen and assignment of the gene  
 to the region of the X chromosome containing the Alport syndrome  
 locus.";  
 RL Am. J. Hum. Genet. 46:1024-1033(1990).  
 RN [7]  
 RN SEQUENCE OF 1-20 FROM N.A.  
 RP Guo C., van Damme B., Vanrenterghem Y., Devriendt K., Cassiman J.-J.,  
 RA Marynen P.;  
 RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RN SEQUENCE OF 1258-1270 FROM N.A. (ISOFORM 2).  
 RP MEDLINE-94133540; PubMed-8301933;  
 RA Guo C., van Damme B., van Damme-Lombaerts R., van den Berghe H.,  
 RA Cassiman J.-J., Marynen P.;  
 RT "Differential splicing of COL4A5 mRNA in kidney and white blood  
 cells: a complex mutation in the COL4A5 gene of an Alport patient  
 deletes the NCI domain.";  
 RL Kidney Int. 44:1316-1321(1993).  
 RN [9]  
 RN REVIEW ON VARIANTS.  
 RP MEDLINE-97338662; PubMed-9195222;  
 RA Lemmink H.H., Schroeder C.H., Monnens L.A.H., Smeets H.J.M.;  
 RT "The clinical spectrum of type IV collagen mutations.";  
 RL Hum. Mutat. 9:477-499(1997).  
 RN [10]  
 RN VARIANT AS SER-1564.  
 RX MEDLINE-91169492; PubMed-1672282;  
 RA Zhou J., Barker D.F., Hostalka S.L., Gregory M.C., Atkin C.L.,  
 RA Tryggvason K.;

RT "Single base mutation in alpha 5(IV) collagen chain gene converting a  
 conserved cysteine to serine in Alport syndrome.";  
 RL Genomics 9:10-18(1991).  
 RN [11]  
 RN VARIANT AS ARG-325.  
 RX MEDLINE-92303559; PubMed-1376965;  
 RA Knebelmann B., Deschenes G., Gros F., Hors M.-C., Gruenfeld J.-P.,  
 RA Tryggvason K., Gubler M.-C., Antignac C.;  
 RT "Substitution of arginine for glycine 325 in the collagen alpha 5  
 (IV) chain associated with X-linked Alport syndrome: characterization  
 of the mutation by direct sequencing of PCR-amplified lymphoblast  
 cell DNA fragments.";  
 RL Am. J. Hum. Genet. 51:135-142(1992).  
 RN [12]  
 RN VARIANT AS GLU-325.  
 RX MEDLINE-93244772; PubMed-1363780;  
 RA Renieri A., Seri M., Myers J.C., Phlajaniemi T., Massella L.,  
 RA Rizzoni G.F., de Marchi M.;  
 RT "De novo mutation in the COL4A5 gene converting glycine 325 to  
 glutamic acid in Alport syndrome.";  
 RL Hum. Mol. Genet. 1:127-129(1992).  
 RN [13]  
 RN VARIANTS AS THR-1517; SER-1538 AND GLN-1563.  
 RX MEDLINE-94010948; PubMed-8406498;  
 RA Lemmink H.H., Schroeder C.H., Brunner H.G., Nelen M.R., Zhou J.,  
 RA Tryggvason K., Haggma-Schouten W.A.G., Roodvoets A.P., Rascher W.,  
 RA van Oost B.A., Smeets H.J.M.;  
 RT "Identification of four novel mutations in the COL4A5 gene of  
 patients with Alport syndrome.";  
 RL Genomics 17:485-489(1993).  
 RN [14]  
 RN VARIANTS AS GLU-400; VAL-406; VAL-638; ALA-638; ARG-653; ARG-796;  
 RP ARG-869; ARG-872 AND CYS-1241.  
 RX MEDLINE-95322976; PubMed-7599631;  
 RA Boye E., Flinter F., Zhou J., Tryggvason K., Bobrow M., Harris A.;  
 RT "Detection of 12 novel mutations in the collagenous domain of the  
 COL4A5 gene in Alport syndrome patients.";  
 RL Hum. Mutat. 5:197-204(1995).  
 RN [15]  
 RN VARIANT AS ARG-1649.  
 RP MEDLINE-96213750; PubMed-8651292;  
 RA Barker D.F., Pruchno C.J., Jiang X., Atkin C.L., Stone E.M.,  
 RA Denison J.C., Fain P.R., Gregory M.C.;  
 RT "A mutation causing Alport syndrome with tardive hearing loss is  
 common in the western United States.";  
 RL Am. J. Hum. Genet. 58:1157-1165(1996).  
 RN [16]  
 RN VARIANTS AS:  
 RX MEDLINE-96213754; PubMed-8651296;  
 RA Renieri A., Brutlini M., Galli L., Zanelli P., Neri T.M., Rossetti S.,  
 RA Turco A.E., Helskari N., Zhou J., Gusmano R., Massella L., Banfi G.,  
 RA Scolari F., Sessa A., Rizzoni G.F., Tryggvason K., Pignatelli P.F.,  
 RA Savi M., Ballabio A., de Marchi M.;  
 RT "X-linked Alport syndrome: an SSCP-based mutation survey over all 51  
 exons of the COL4A5 gene.";  
 RL Am. J. Hum. Genet. 58:1192-1204(1996).  
 RN [17]  
 RN VARIANTS AS, AND VARIANTS ASP-430; SER-444; SER-619; ASN-664 AND  
 RP MET-1428.  
 RX MEDLINE-97094179; PubMed-8940267;  
 RA Knebelmann B., Brelliat C., Forestier L., Arrondel C., Jaccaster D.,  
 RA Glacras I., Drouot L., Deschenes G., Gruenfeld J.-P., Broyer M.,  
 RA Gubler M.-C., Antignac C.;  
 RT "Spectrum of mutations in the COL4A5 collagen gene in X-linked Alport  
 syndrome.";  
 RL Am. J. Hum. Genet. 59:1221-1232(1996).  
 RN [18]  
 RN VARIANT AS ASP-1498.  
 RX MEDLINE-96233932; PubMed-8829632;  
 RA Tverskaya S., Bobrygina V., Tsalykova F., Ignatova M.,  
 RA Krasnopol'skaya X., Eygarov O.;  
 RT "Substitution of Ala980 in noncollagen domain of alpha 5(IV) collagen  
 chain associated with adult-onset X-linked Alport syndrome.";

RL Hum. Mutat. 7:149-150(1996).  
 RN [19]  
 RP VARIANT AS GLN-1677.  
 RX MEDLINE-97295089; PubMed-9150741;  
 RA Barker D.F., Denison J.C., Atkin C.L., Gregory M.C.;  
 RT "Common ancestry of three Ashkenazi-American families with Alport  
 syndrome and COL4A5 R1677Q.";  
 RL Hum. Genet. 99:681-684(1997).  
 RN [20]  
 RP VARIANTS AS ARG-174; ARG-177; ARG-325; CYS-1410; TRP-1421; THR-1517  
 RP AND ASP-1596.  
 RX MEDLINE-98112435; PubMed-9452056;  
 RA Neri T.M., Zanelli P., de Palma G., Savi M., Rossetti S., Turco A.E.,  
 RA Pignatelli G.F., Gaili L., Brutti M., Renieri A., Mingarelli R.,  
 RA Trivelli A., Pinciaroli A.R., Ragalolo M., Rizzoni G.F., de Marchi M.;  
 RT "Missense mutations in the COL4A5 gene in patients with X-linked  
 Alport syndrome.";  
 RL Hum. Mutat. Suppl. 1:S106-S109(1998).  
 RN [21]  
 RP VARIANTS AS VAL-420; 456-PRO--PRO-458 DEL; ASP-573; ASP-624; ASP-635;  
 RP 802-GLY-PRO-807 DEL; ARG-869; CYS-941; SER-1030; SER-1066; ASP-1143;  
 RP ARG-1196; GLU-1261; SER-1357 AND ARG-1649.  
 RX MEDLINE-99063529; PubMed-9848783;  
 RA Martin P., Helkari N., Zhou J., Leinonen A., Tunnelius T., Hertz J.M.,  
 RA Barker D.F., Gregory M.C., Atkin C.L., Strykarsdotter U., Neumann H.,  
 RA Sprigante J., Shows T.B., Pettersson E., Tryggvason K.;  
 RT "High mutation detection rate in the COL4A5 collagen gene in suspected  
 Alport syndrome using PCR and direct DNA sequencing.";  
 RL J. Am. Soc. Nephrol. 9:2291-2301(1998).  
 RN [22]  
 RP VARIANTS AS GLU-579; LYS-633; ASP-947; VAL-953; ARG-1107; ARG-1158;  
 RP SER-1170 AND TRP-1678, AND VARIANTS SER-444 AND ALA-739.  
 RX MEDLINE-20030197; PubMed-10561141;  
 RA Inoue Y., Nishio H., Shirakawa T., Nakanishi K., Nakamura H.,  
 RA Sumito K., Nishiyama K., Iijima K., Yoshikawa N.;  
 RT "Detection of mutations in the COL4A5 gene in over 90% of male  
 patients with X-linked Alport's syndrome by RT-PCR and direct  
 sequencing.";  
 RL Am. J. Kidney Dis. 34:854-862(1999).  
 RN [23]  
 RP VARIANT AS ARG-822.  
 Query Match 8.9%; Score 116; DB 1; Length 1685;  
 Best Local Similarity 35.1%; Pred. No. 0.027;  
 Matches 33; Conservative 6; Mismatches 37; Indels 18; Gaps 3;  
 QY 3 PGSPASPORTRLGILLILLQLPAPSSASERP-----KQKQAKLQREVVLDYNGMCIQ 57  
 DB 1256 PGSPGPRP-----GLPGPSPGPGPLPNGGKIG-EKGNPGQGLPGLPKGKDQ 1302  
 QY 58 GPAGVPGRDGSPGANVPGTPGIPGRDGFKEGKG 91  
 DB 1303 GPPGLQGNPGRPLNGMKDPPGLPGVGPFGMKG 1336  
 RESULT 6  
 COT7\_HUMAN STANDARD; PRT; 289 AA.  
 ID COT7\_HUMAN  
 AC 09BXJ2;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Complement-clq tumor necrosis factor-related protein 7 precursor.  
 GN C1QTNF7 OR CTRP7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.;  
 RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RX MEDLINE-22388257; PubMed-12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1 SIMILARITY: Contains 1 collagenous domain.  
 CC -1 SIMILARITY: Contains 1 C1Q domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; AF329839; AK17963.1; -;  
 DR EMBL; BC022187; AAH22187.1; -;  
 DR Genew; HGNC:14342; C1QTNF7.  
 DR InterPro; IPR001073; C1Q.  
 DR InterPro; IPR000087; Collagen.  
 DR Pfam; PF00386; C1q; 1.  
 DR Pfam; PF01391; Collagen; 2.  
 DR PRINTS; PR00007; COMPLEMENTC1Q.  
 DR SMART; SM00110; C1Q; 1.  
 DR PROSITE; PS01113; C1Q; 1.  
 KW Collagen; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 289  
 FT FT 38 139  
 FT DOMAIN 141 276  
 FT DOMAIN 141 276  
 SQ SEQUENCE 289 AA; 30683 MW; A61609FP86D26946 CRC64;  
 Query Match 8.9%; Score 115.5; DB 1; Length 289;  
 Best Local Similarity 46.3%; Pred. No. 0.0037;  
 Matches 31; Conservative 5; Mismatches 22; Indels 9; Gaps 3;  
 QY 30 ASEIPKQKAKQAKQREVVLDYNGMC-----LQSPAGVPGRDGSPGANVPGTPGIPGRD 85  
 DB 14 ASGQPRN---QLKGENYSPRY--ICSIPLPDPGPPGANGSPGPHRIGLPGRDG 68  
 QY 86 FKKEGKE 92  
 DB 69 RKKEGKE 75  
 RESULT 7  
 CAIR\_HUMAN STANDARD; PRT; 1516 AA.  
 ID CAIR\_HUMAN  
 AC P39060; O9UK38; O9Y607; O9Y608;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Collagen alpha 1(XVIII) chain precursor [Contains: Endostatin].  
 GN COL18A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98164096; PubMed=9503365;  
 RA Saarela J., Ylikarppa R., Rehn M., Purmonen S., Pihlajaniemi T.;  
 RT "Complete primary structure of two variant forms of human type XVIII  
 RT collagen and tissue-specific differences in the expression of the  
 RT corresponding transcripts".  
 RL Matrix Biol. 16:319-328(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20289799; PubMed=10830953;  
 RA Hattori M., Fujiyama A., Taylor T.D., Matanabe H., Yada T.,  
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,  
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,  
 RA Folleard K., Rump A., Schillhabel M., Schudy A., Lehmann R., Patterson D.,  
 RA Reichwald K., Kump A., Schillhabel M., Schudy A., Zimmermann W.,  
 RA Shintani A., Sasaki T., Nagamine K., Matsuyama S., Antonarakis S.E.,  
 RA Minoshima S., Shimizu N., Nordiek G., Horstischer K., Brandt P.,  
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,  
 RA Ramer J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,  
 RA Weinmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,  
 RA Lehnach H., Reinhardt R., Yaspo M.-L.;  
 RT "The DNA sequence of human chromosome 21.";  
 RL Nature 405:311-319(2000).  
 RN [3]  
 RP SEQUENCE OF 834-1516 FROM N.A.  
 RX MEDLINE=94245237; PubMed=8188291;  
 RA Oh S.P., Warman M.L., Seldin M.F., Cheng S., Knoll J.R., Timmons S.,  
 RA Olsen B.R.;  
 RT "Cloning of cDNA and genomic DNA encoding human type XVIII collagen  
 RT and localization of the alpha 1(XVIII) collagen gene to mouse  
 RL chromosome 10 and human chromosome 21.";  
 RN Genomics 19:494-499(1994).  
 RN [4]  
 RP SEQUENCE OF 1334-1516 FROM N.A.  
 RX TISSUE=Placenta;  
 RA Zhi-Yong H., Biao L., Wei-Jie Z., Xiang-Pu W.;  
 RT "Cloning and expression of human endostatin gene in Escherichia  
 RL coli.";  
 RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP INVOLVEMENT IN KNOBLOCH SYNDROME.  
 RX MEDLINE=20400145; PubMed=10942434;  
 RA Sertie A.L., Sossi V., Camargo A.A., Zatz M., Brahe C.,  
 RA Passos-Bueno M.R.;  
 RT "Collagen XVIII, containing an endogenous inhibitor of angiogenesis  
 RT and tumor growth, plays a critical role in the maintenance of retinal  
 RL structure and in neural tube closure.";  
 RL Hum. Mol. Genet. 9:2051-2058(2000).  
 RN [6]  
 RP VARIANT ASN-1437.  
 RX MEDLINE=21518361; PubMed=11606364;  
 RA Iugnetti P., Suzuki O., Godol P.H., Alves V.A., Sertie A.L.,  
 RA Zorick T., Soares F., Camargo A., Moreira E.S., di Loreto C.,  
 RA Moreira-Filho C.A., Simpson A., Oliva G., Passos-Bueno M.R.;  
 RT "A polymorphism in endostatin, an angiogenesis inhibitor, predisposes  
 RT for the development of prostatic adenocarcinoma.";  
 RL Cancer Res. 61:7375-7378(2001).  
 CC -1- FUNCTION: COL18A1 PROBABLY PLAYS A MAJOR ROLE IN DETERMINING THE  
 CC RETINAL STRUCTURE AS WELL AS IN THE CLOSURE OF THE NEURAL TUBE.  
 CC -1- FUNCTION: ENDOSTATIN POTENTIALLY INHIBITS ENDOTHELIAL CELL  
 CC PROLIFERATION AND ANGIOGENESIS. MAY INHIBIT ANGIOGENESIS BY  
 CC BINDING TO THE HEPARAN SULPHATE PROTEOGLYCAN INVOLVED IN GROWTH  
 CC FACTOR SIGNALING.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;

CC Name:Long; Synonyms=NC-493;  
 CC IsoId=P39060-1; Sequence=Displayed;  
 CC Name=Short; Synonyms=NC1-303;  
 CC IsoId=P39060-2; Sequence=VSP\_001155, VSP\_001156;  
 CC TISSUE SPECIFICITY: PRESENT IN MULTIPLE ORGANS WITH HIGHEST LEVELS  
 CC IN LIVER, LUNG AND KIDNEY.  
 CC -1- PTM: Prolines at the third position of the tripeptide repeating  
 CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
 CC -1- POLYMORPHISM: There is an association between a polymorphism in  
 CC position 1437 and prostate cancer. Heterozygous Asn-1437  
 CC individuals have a 2.5 times increased chance of developing  
 CC prostate cancer as compared with homozygous Asp-1437 individuals.  
 CC -1- DISEASE: Defects in COL18A1 are a cause of Knobloch syndrome (KNO)  
 CC [MIM:267750], an autosomal recessive disorder defined by the  
 CC occurrence of high myopia, vitreoretinal degeneration with retinal  
 CC detachment, macular abnormalities and occipital encephalocele.  
 CC -1- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH  
 CC INTERRUPTED HELICES (FACIT) FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>  
 CC or send an email to [license@sdb-sdb.ch](mailto:license@sdb-sdb.ch)).  
 CC -----  
 CC EMBL; AF018081; AAC39658.1; -  
 CC EMBL; AF018082; AAC39659.1; -  
 CC EMBL; AL163302; CAB90482.1; -  
 CC EMBL; U22548; AAS51864.1; -  
 CC EMBL; AF184060; AAF01310.1; ALT\_INIT.  
 CC PDB; 1BNL; 02-DEC-98.  
 CC GlycoSiteDB; P39060;  
 CC Gene; HGNC:2195; COL18A1.  
 CC MIM; 267750; -  
 CC GO; GO:0005581; C:collagen; TAS.  
 CC GO; GO:0006181; F:tumor suppressor; TAS.  
 CC GO; GO:0007397; P:histogenesis and organogenesis; TAS.  
 CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
 CC GO; GO:0007048; P:oncogenesis; TAS.  
 CC GO; GO:0007601; P:vision; TAS.  
 CC InterPro; IPR000087; Collagen.  
 CC InterPro; IPR00191; LamlnA\_g.  
 CC InterPro; IPR003129; TSPN.  
 CC Pfam; PF01391; Collagen; 7.  
 CC Pfam; PF02210; TSPN; 1.  
 CC ProDom; PPO00007; Ctg\_helix; 1.  
 CC SMART; SM00282; Lamc; 1.  
 CC SMART; SM00210; TSPN; 1.  
 CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation;  
 CC Cell adhesion; Collagen; Glycoprotein; Signal; Alternative splicing;  
 CC Polymorphism; 3D-structure.  
 CC SIGNAL 1 23  
 CC CHAIN 24 1516  
 CC CHAIN 1334 1516  
 CC DOMAIN 24 516  
 CC DOMAIN 517 550  
 CC DOMAIN 551 560  
 CC DOMAIN 561 640  
 CC DOMAIN 641 664  
 CC DOMAIN 665 786  
 CC DOMAIN 787 809  
 CC DOMAIN 810 892  
 CC DOMAIN 893 906  
 CC DOMAIN 907 948  
 CC DOMAIN 949 961  
 CC DOMAIN 962 1034  
 CC DOMAIN 1035 1044  
 CC DOMAIN 1045 1077  
 CC DOMAIN 1078 1089  
 CC DOMAIN 1090 1111  
 CC COLLAGEN ALPHA 1(XVIII) CHAIN.  
 CC ENDOSTATIN.  
 CC NONHELICAL REGION 1 (NC1).  
 CC TRIPLE-HELICAL REGION 1 (COL1).  
 CC NONHELICAL REGION 2 (NC2).  
 CC TRIPLE-HELICAL REGION 2 (COL2).  
 CC NONHELICAL REGION 3 (NC3).  
 CC TRIPLE-HELICAL REGION 3 (COL3).  
 CC NONHELICAL REGION 4 (NC4).  
 CC TRIPLE-HELICAL REGION 4 (COL4).  
 CC NONHELICAL REGION 5 (NC5).  
 CC TRIPLE-HELICAL REGION 5 (COL5).  
 CC NONHELICAL REGION 6 (NC6).  
 CC TRIPLE-HELICAL REGION 6 (COL6).  
 CC NONHELICAL REGION 7 (NC7).  
 CC TRIPLE-HELICAL REGION 7 (COL7).  
 CC NONHELICAL REGION 8 (NC8).  
 CC TRIPLE-HELICAL REGION 8 (COL8).

FT	DOMAIN	1112	1118		NONHELICAL REGION 9 (NC9).
FT	DOMAIN	1119	1173		TRIPLE-HELICAL REGION 9 (COL9).
FT	DOMAIN	1174	1186		NONHELICAL REGION 10 (NC10).
FT	DOMAIN	1187	1204		TRIPLE-HELICAL REGION 10 (COL10).
FT	DOMAIN	1205	1516		NONHELICAL REGION 11 (NC11).
FT	CARBOHYD	68	68		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	129	129		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	164	164		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	691	691		O-LINKED (GALNAC . . .) (POTENTIAL).
FT	CARBOHYD	1329	1329		/FTID-CAR_000150.
FT	DISULFID	1366	1506		BY SIMILARITY.
FT	DISULFID	1468	1498		BY SIMILARITY.
FT	SITE	1095	1097		CELL ATTACHMENT SITE (POTENTIAL).
FT	VANSPPLIC	1	180		Missing (In Isoform Short).
FT	VANSPPLIC				/FTID-VSP_001155.
FT	VANSPPLIC	181	215		HTTEGTLPAPRPSPPSGRWPAPLTGSVPPSS -> MA
FT	VANSPPLIC				PCPCMPRRRLDLVLAPLVLLGVRAASAEF (In
FT	VANSPPLIC				Isoform Short).
FT	VARIANT	1437	1437		/FTID-VSP_001156.
FT	VARIANT				D -> N (Increased risk of developing
FT	VARIANT				prostate cancer).
FT	VARIANT				/FTID-VAR_012709.
FT	CONFLICT	428	428		F -> S (IN REF. 2).
FT	CONFLICT	841	841		I -> V (IN REF. 2).
FT	CONFLICT	877	877		V -> L (IN REF. 3).
FT	CONFLICT	886	886		P -> R (IN REF. 3).
FT	CONFLICT	912	912		R -> R (IN REF. 3).
FT	CONFLICT	933	933		R -> L (IN REF. 3).
FT	CONFLICT	975	975		A -> L (IN REF. 3).
FT	CONFLICT	1064	1064		A -> P (IN REF. 3).
FT	CONFLICT	1084	1084		L -> K (IN REF. 3).
FT	CONFLICT	1120	1120		P -> A (IN REF. 3).
FT	CONFLICT	1123	1123		P -> A (IN REF. 3).
FT	CONFLICT	1126	1126		P -> PPGP (IN REF. 2).
FT	CONFLICT	1206	1206		G -> GO (IN REF. 3).
FT	CONFLICT	1304	1304		R -> G (IN REF. 3).
FT	CONFLICT	1314	1314		A -> G (IN REF. 3).
FT	CONFLICT	1323	1324		LR -> CG (IN REF. 3).
FT	CONFLICT	1443	1443		R -> T (IN REF. 4).
FT	CONFLICT	1483	1483		S -> Y (IN REF. 4).
SO	SEQUENCE	1516 AA;	153840 MW;		3C70F29A4476EE76 CRC64;
Query Match                      8.9%;    Score 115.5; DB 1;    Length 1516;					
Best Local Similarity          44.1%;    Pred. No. 0.026;					
Matches    26;    Conservative    8;    Mismatches    20;    Indels     5;    Gaps       2					
Oy	52 NGMOLQGA---GGVGGRGSGCANIPEPTGTPGDKGKGEGLRESFEESMTPNRK 107				
Db	691 NSSDPGPAAGLPGVPGRGPFGPGLPGPPGPGRGPPRTGO--KSLGEGAGAPGHR 747				
:               :   :          :   :   :   :   :   :					
RESULT 8					
CA14_HUMAN					
ID CA14_HUMAN	STANDARD:	PRT: 1669 AA.			
AC P02462;					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 01-FEB-1996 (Rel. 33, Last sequence update)					
DT 15-SEP-2003 (Rel. 42, Last annotation update)					
DE Collagen alpha 1(IIV) chain precursor.					
GN COL4A1.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
OX NCBI_TaxId=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=89340433; PubMed=2701944;					
RA Soininen R., Huotari M., Ganguly A., Prockop D.J., Trygvason K.;					
RT "Structural organization of the gene for the alpha 1 chain of human					
RT type IV collagen."					
RT J. Biol. Chem. 264:13565-13571(1989).					
RN [2]					

RP SEQUENCE OF 46-1257 FROM N.A.  
RC TISSUE-Placenta;  
RX MEDLINE=8083584; PubMed=3691802;  
RA Souhnen R., Haka-Risku T., Prockop D.J., Tryggvason K.;  
RT "Complete primary structure of the alpha 1-chain of human basement  
RL membrane (type IV) collagen.";  
RN FEBS Lett. 225:188-194(1987).  
[3]  
RP SEQUENCE OF 1-943 FROM N.A.  
RC TISSUE-Placenta;  
RX MEDLINE=88029471; PubMed=3311751;  
RA Bräzel D., Oberhauser I., Dierlinger H., Babel W., Glanville R.W.,  
RA Deltmann R., Kuehn K.;  
RT "Completion of the amino acid sequence of the alpha 1 chain of human  
RT basement membrane collagen (type IV) reveals 21 non-triplet  
RT interruptions located within the collagenous domain.";  
RN Eur. J. Biochem. 168:529-536(1987).  
[4]  
RP SEQUENCE OF 28-243.  
RX MEDLINE=86004708; PubMed=4043082;  
RA Glanville R.W., Qian R.Q., Stebold B., Ristell J., Kuehn K.;  
RT "Amino acid sequence of the N-terminal aggregation and cross-linking  
RT region (75 domain) of the alpha 1 (IV) chain of human basement  
RT membrane collagen.";  
RN Eur. J. Biochem. 152:213-219(1985).  
[5]  
RP SEQUENCE OF 534-1447.  
RX MEDLINE=85003629; PubMed=543307;  
RA Babel W., Glanville R.W.;  
RT "Structure of human basement-membrane (type IV) collagen. Complete  
RT amino acid sequence of a 914-residue-long pepsin fragment from the  
RT alpha 1(IV) chain.";  
RN Eur. J. Biochem. 143:545-556(1984).  
[6]  
RP SEQUENCE OF 1256-1669 FROM N.A.  
RX MEDLINE=85207819; PubMed=2581969;  
RA PildäJanleml T., Tryggvason K., Myers J.C., Kurkinen M., Lebo R.,  
RA Cheung M.-C., Prockop D.J., Boyd C.D.;  
RT "cDNA clones coding for the pro-alpha1(IV) chain of human type IV  
RT procollagen reveal an unusual homology of amino acid sequences in two  
RL halves of the carboxyl-terminal domain.";  
RN J. Biol. Chem. 260:7681-7687(1985).  
[7]  
RP SEQUENCE OF 1259-1669 FROM N.A.  
RX MEDLINE=85216555; PubMed=2582422;  
RA Brinker J.M., Gudas L.J., Loidl H.R., Wang S.-Y., Rosenbloom J.,  
RA Kefalides N.A., Myers J.C.;  
RT "Restricted homology between human alpha 1 type IV and other  
RT procollagen chains.";  
RN Proc. Natl. Acad. Sci. U.S.A. 82:3649-3653(1985).  
[8]  
RP SEQUENCE OF 1-28 FROM N.A.  
RX MEDLINE=89034231; PubMed=3182844;  
RA Souhnen R., Huotari M., Hostikka S.L., Prockop D.J., Tryggvason K.;  
RT "The structural genes for alpha 1 and alpha 2 chains of human type IV  
RT collagen are divergently encoded on opposite DNA strands and have an  
RT overlapping promoter region.";  
RN J. Biol. Chem. 263:17217-17220(1988).  
[9]  
RP SEQUENCE OF 1441-1669, AND DISULFIDE BONDS.  
RC TISSUE-Placenta;  
RX MEDLINE=89005112; PubMed=2844531;  
RA Stebold B., Deltmann R., Kuehn K.;  
RT "The arrangement of intra- and intermolecular disulfide bonds in the  
RT carboxyterminal, non-collagenous aggregation and cross-linking domain  
RL of basement-membrane type IV collagen.";  
RN Eur. J. Biochem. 176:617-624(1988).  
-1- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF  
CC GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'  
CC MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENACTIN/  
CC NIDOGEN.  
-1- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-  
CC ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE

WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.  
 - DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS  
 G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY  
 CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL  
 TRIPLE-HELICAL 7S DOMAIN.  
 - P1M: Lysines at the third position of the tripeptide repeating  
 unit (G-X-Y) are hydroxylated in all cases and bind carbohydrates.  
 - P1M: Prolines at the third position of the tripeptide repeating  
 unit (G-X-Y) are hydroxylated in some or all of the chains.  
 - P1M: Type IV collagens contain numerous cysteine residues which  
 are involved in inter- and intramolecular disulfide bonding. 12 of  
 these, located in the NC1 domain, are conserved in all known type  
 IV collagens.  
 -----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: M26576; AAA53098.1; JOINED.  
 CC EMBL: J04217; AAA53098.1; JOINED.  
 CC EMBL: M26550; AAA53098.1; JOINED.  
 CC EMBL: M26540; AAA53098.1; JOINED.  
 CC EMBL: M26542; AAA53098.1; JOINED.  
 CC EMBL: M26543; AAA53098.1; JOINED.  
 CC EMBL: M26544; AAA53098.1; JOINED.  
 CC EMBL: M26545; AAA53098.1; JOINED.  
 CC EMBL: M26546; AAA53098.1; JOINED.  
 CC EMBL: M26547; AAA53098.1; JOINED.  
 CC EMBL: M26537; AAA53098.1; JOINED.  
 CC EMBL: M26538; AAA53098.1; JOINED.  
 CC EMBL: M26548; AAA53098.1; JOINED.  
 CC EMBL: M26549; AAA53098.1; JOINED.  
 CC EMBL: M26551; AAA53098.1; JOINED.  
 CC EMBL: M26552; AAA53098.1; JOINED.  
 CC EMBL: M26553; AAA53098.1; JOINED.  
 CC EMBL: M26554; AAA53098.1; JOINED.  
 CC EMBL: M26555; AAA53098.1; JOINED.  
 CC EMBL: M26556; AAA53098.1; JOINED.  
 CC EMBL: M26557; AAA53098.1; JOINED.  
 CC EMBL: M26558; AAA53098.1; JOINED.  
 CC EMBL: M26559; AAA53098.1; JOINED.  
 CC EMBL: M26560; AAA53098.1; JOINED.  
 CC EMBL: M26561; AAA53098.1; JOINED.  
 CC EMBL: M26562; AAA53098.1; JOINED.  
 CC EMBL: M26563; AAA53098.1; JOINED.  
 CC EMBL: M26564; AAA53098.1; JOINED.  
 CC EMBL: M26565; AAA53098.1; JOINED.  
 CC EMBL: M26566; AAA53098.1; JOINED.  
 CC EMBL: M26567; AAA53098.1; JOINED.  
 CC EMBL: M26568; AAA53098.1; JOINED.  
 CC EMBL: M26569; AAA53098.1; JOINED.  
 CC EMBL: M26570; AAA53098.1; JOINED.  
 CC EMBL: M26571; AAA53098.1; JOINED.  
 CC EMBL: M26572; AAA53098.1; JOINED.  
 CC EMBL: M26573; AAA53098.1; JOINED.  
 CC EMBL: M26574; AAA53098.1; JOINED.  
 CC EMBL: M26575; AAA53098.1; JOINED.  
 CC EMBL: Y00706; CAA68698.1; JOINED.  
 CC EMBL: X05561; CAA29075.1; JOINED.  
 CC EMBL: M10940; AAA52006.1; JOINED.  
 CC PIR: S16876; CGH04B.  
 CC Genev: HGNC:2202; COL4A1.  
 CC MIM: 120130; COL4A1.  
 CC InterPro: IPR000087; Collagen.

DR InterPro: IPR001442; ProcollagenC4.  
 DR Pfam: PF01413; C4; 2.  
 DR Pfam: PF01391; Collagen; 24.  
 DR ProDom: PD000007; C1q\_helix; 6.  
 DR ProDom: PD003923; ProcollagenC4; 1.  
 DR SMART: SM0011; C4; 2.  
 KW Extracellular matrix; Connective tissue; Basement membrane;  
 Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.  
 FT SIGNAL 1 27  
 FT PROPEP 28 172  
 FT CHAIN 173 1669  
 FT DOMAIN 173 1440  
 FT DOMAIN 1441 1669  
 FT CARBOXID 126 126  
 FT DISULFID 1460 1551  
 FT DISULFID 1493 1548  
 FT DISULFID 1505 1511  
 FT DISULFID 1570 1665  
 FT DISULFID 1604 1662  
 FT DISULFID 1616 1662  
 FT CONFLICT 237 238  
 FT CONFLICT 241 241  
 FT CONFLICT 319 319  
 FT CONFLICT 719 719  
 FT CONFLICT 837 837  
 FT CONFLICT 842 842  
 FT CONFLICT 896 896  
 FT CONFLICT 904 904  
 FT CONFLICT 914 914  
 FT CONFLICT 998 998  
 FT CONFLICT 1010 1010  
 FT CONFLICT 1012 1012  
 FT CONFLICT 1358 1358  
 SQ SEQUENCE 1669 AA; 160611 MW; 3BBBA6DFB9B8A84 CRC64;  
 Query Match 8.9%; Score 115.5; DB 1; Length 1669;  
 Best Local Similarity 34.8%; Pred. No. 0.029; Mismatches 32; Indels 35; Gaps 4;  
 Matches 32; Conservative 5; Mismatches 20; Indels 35; Gaps 4;  
 QY 1 MRPGPAASPORLGLLILLQLP-APSSASEIPKQKQALRQREYVDLYNGMCLGGP 59  
 DB 1212 MGPPGPGQP-----GLPGSPGHATEGPKGD-----RGP 1240  
 QY 60 AGVPRDSSPGANVTPGTPGIRGRGFGKGG 91  
 DB 1241 GGGPLGLPLGP--MGPPGLPGIDGVKDXG 1269  
 RESULT 9  
 CA13\_HUMAN STANDARD; PRT; 1466 AA.  
 AC P02461; Q15112;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Collagen alpha 1(III) chain precursor.  
 GN COL3A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Skin fibroblast;  
 RX MEDLINE=89350838; PubMed=2764886;  
 RA Ala-Koko L., Kontusaari S., Baldwin C.T., Kulvanliemi H.,  
 RA Prockop D.J.;  
 RT "Structure of cDNA clones coding for the entire prepro alpha 1 (III)  
 RT chain of human type III procollagen. Differences in protein structure  
 RT from type I procollagen and conservation of codon preferences";  
 RL Biochem. J. 260:509-516(1989).  
 RN [2]  
 RP SEQUENCE OF 149-1225 FROM N.A.

RX MEDLINE-89386015; PubMed-2780304;  
 RA Janeczko R.A., Ramirez F.;  
 RT "Nucleotide and amino acid sequences of the entire human alpha 1  
 (III) collagen.";  
 RL Nucleic Acids Res. 17:6742-6742(1989).  
 RN [3]  
 RP SEQUENCE OF 168-398.  
 RX MEDLINE-77134724; PubMed-557335;  
 RA Seyer J.M., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of cyanogen  
 bromide peptides from the amino-terminal segment of type III collagen  
 of human liver.";  
 RL Biochemistry 16:1158-1164(1977).  
 RN [4]  
 RP REVISIONS.  
 RA Seyer J.M.;  
 RL Submitted (DEC-1977) to the PIR data bank.  
 RN [5]  
 RP SEQUENCE OF 399-727.  
 RX MEDLINE-79000343; PubMed-687591;  
 RA Seyer J.M., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of five  
 consecutive CNBr peptides from type III collagen of human liver.";  
 RL Biochemistry 17:3404-3411(1978).  
 RN [6]  
 RP SEQUENCE OF 728-964.  
 RX MEDLINE-80198282; PubMed-6246925;  
 RA Seyer J.M., Mainardi C., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of alpha 1  
 (III)-C85 from type III collagen of human liver.";  
 RL Biochemistry 19:1583-1589(1980).  
 RN [7]  
 RP SEQUENCE OF 950-1466 FROM N.A.  
 RX MEDLINE-88189827; PubMed-3357782;  
 RA Mankoo B.S., Dalgleish R.;  
 RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";  
 RL Nucleic Acids Res. 16:2337-2337(1988).  
 RN [8]  
 RP REVISION TO 1184.  
 RX MEDLINE-89098346; PubMed-3211760;  
 RA Molyneux K., Dalgleish R.;  
 RT "Human type III collagen 'variant' is a cDNA cloning artefact.";  
 RL Nucleic Acids Res. 16:11833-11833(1988).  
 RN [9]  
 RP SEQUENCE OF 1065-1466 FROM N.A.  
 RX MEDLINE-85087944; PubMed-6096827;  
 RA Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,  
 RT "Molecular cloning and carboxyl-propeptide analysis of human type III  
 procollagen.";  
 RL Nucleic Acids Res. 12:9383-9394(1984).  
 RN [10]  
 RP SEQUENCE OF 965-1200.  
 RX MEDLINE-81208139; PubMed-7016180;  
 RA Seyer J.M., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of alpha  
 1(III)-C89 from type III collagen of human liver.";  
 RL Biochemistry 20:2621-2627(1981).  
 RN [11]  
 RP SEQUENCE OF 1176-1466 FROM N.A.  
 RX MEDLINE-85157600; PubMed-2579949;  
 RA Chu M.-Y., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;  
 RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1  
 (III) collagen. Partial characterization of the 3' end region of the  
 gene.";  
 RL J. Biol. Chem. 260:4357-4363(1985).  
 RN [12]  
 RP SEQUENCE OF 1161-1200 FROM N.A.  
 RX MEDLINE-86187804; PubMed-3754462;  
 RA Miskulin M., Dalgleish R., Klueve-Beckerman B., Rennard S.I.,  
 RT "Human type III collagen gene expression is coordinately modulated  
 with the type I collagen genes during fibroblast growth.";

RL Biochemistry 25:1408-1413(1986).  
 RN [13]  
 RP SEQUENCE OF 1-170 FROM N.A.  
 RC TISSUE-Placenta;  
 RX MEDLINE-88303360; PubMed-3405773;  
 RA Toman D., Ricca G., de Crombrughe B.;  
 RT "Nucleotide sequence of a cDNA coding for the amino-terminal region  
 of human prepro alpha 1(III) collagen.";  
 RL Nucleic Acids Res. 16:7201-7201(1988).  
 RN [14]  
 RP SEQUENCE OF 1-176 FROM N.A.  
 RX MEDLINE-89378752; PubMed-2777083;  
 RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;  
 RT "Cloning and analysis of the 5' portion of the human type-III  
 procollagen gene (COL3A1).";  
 RL Gene 78:255-265(1989).  
 RN [15]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-97255959; PubMed-9101290;  
 RA Kuivaniemi H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 associated collagen (type IX), and network-forming collagen (type X)  
 cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 RN [16]  
 RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.  
 RX MEDLINE-93293988; PubMed-8514866;  
 RA Tromp G., Wu Y., Prockop D.J., Madhatter S.L., Kleinert C.,  
 RA Earley J.J., Zhuang J., Noerregaard O., Darling R.C., Abbott W.M.,  
 RA Cole C.W., Jaakkola P., Rymaszewski M., Pearce W.H., Yao J.S.-T.,  
 RA Majumdar K., Smolens S.N., Gatalica Z., Farrell R.E., Jimenez S.A.,  
 RA Jackson C.E., Michaels V.V., Kaye M., Kuivaniemi H.;  
 RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations  
 in the triple-helical domain of type III procollagen are an  
 infrequent cause of aortic aneurysms.";  
 RL J. Clin. Invest. 91:2539-2545(1993).  
 RN [17]  
 RP VARIANT THR-698.  
 RX MEDLINE-91045136; PubMed-2235526;  
 RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,  
 RA Wu Y., Ganguly A., Prockop D.J.;  
 RT "A polymorphism in exon 31 of the COL3A1 gene.";  
 RL Nucleic Acids Res. 18:6180-6180(1990).  
 RN [18]  
 RP VARIANT AORTIC ANEURYSM ARG-786.  
 RX MEDLINE-91056145; PubMed-2243125;  
 RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;  
 RT "A mutation in the gene for type III procollagen (COL3A1) in a family  
 with aortic aneurysms.";  
 RL J. Clin. Invest. 86:1465-1473(1990).  
 RN [19]  
 RP VARIANT EDS-IV ARG-828.  
 RX MEDLINE-94016385; PubMed-8411057;  
 RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;  
 RT "The substitution of glycine 661 by arginine in type III collagen  
 produces mutant molecules with different thermal stabilities and  
 causes Ehlers-Danlos syndrome type IV.";  
 RL J. Med. Genet. 30:690-693(1993).  
 RN [20]  
 RP VARIANT EDS-IV SER-957.  
 RX MEDLINE-89109135; PubMed-2492273;  
 RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;  
 RT "A single base mutation that substitutes serine for glycine 790 of  
 the alpha 1 (III) chain of type III procollagen exposes an arginine  
 and causes Ehlers-Danlos syndrome IV.";  
 RL J. Biol. Chem. 264:1349-1352(1989).  
 RN [21]  
 RP VARIANT EDS-IV VAL-960.  
 RX MEDLINE-95268429; PubMed-7749417;  
 RA Tromp G., de Paeppe A., Nuytink L., Madhatter S.L., Kuivaniemi H.;  
 RT "Substitution of valine for glycine 793 in type III procollagen in  
 Ehlers-Danlos syndrome type IV.";  
 RL Hum. Mutat. 5:179-181(1995).







OY 214 WGTGSDYPRKGDASTGMSY 233  
DB 1652 OIPNCPN-----GMSNL 1663

RESULT 11  
ID CA64\_HUMAN STANDARD; PRT; 1691 AA.  
AC 014031; Q12823; Q14053; Q9NOM5; Q9WTX3; Q9UJ76; Q9UNG6; Q9Y4L4;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE collagen alpha 6(IV) chain precursor.  
GN COL4A6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;

RP [1]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC TISSUE-Eye, and Kidney;  
RX MEDLINE=94171779; PubMed=8125972;  
RA Ohashi T., Sugimoto M., Mattei M.-G., Ninomiya Y.;  
RT Identification of a new collagen IV chain, alpha 6(IV), by cDNA  
RT isolation and assignment of the gene to chromosome Xq22, which is the  
RT same locus for COL4A5.";  
RL J. Biol. Chem. 269:7520-7526(1994).  
RN [2]  
RN SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=94230418; PubMed=8157548;  
RA Zhou J., Ding M., Zhao Z., Reeders S.T.;  
RT Complete primary structure of the sixth chain of human basement  
RT membrane collagen, alpha 6(IV). Isolation of the cDNAs for alpha 6(IV)  
RT and comparison with five other type IV collagen chains.";  
RL J. Biol. Chem. 269:13193-13199(1994).  
RN [3]  
RN SEQUENCE FROM N.A. (ISOFORMS A AND B), AND VARIANTS ALA-455 AND  
RP LYS-1110.  
RX MEDLINE=96299642; PubMed=8661006;  
RA Zhang X., Zhou J., Reeders S.T., Tryggvason K.;  
RT Structure of the human type IV collagen COL4A6 gene, which is mutated  
RT in Alport syndrome-associated leiomyomatosis.";  
RL Genomics 33:473-479(1996).  
RN [4]  
RN SEQUENCE FROM N.A.  
RA Bird C., Grafham D., Lawlor S., Wilson S.;  
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1-542 FROM N.A. (ISOFORM A).  
RX MEDLINE=93361972; PubMed=8356449;  
RA Zhou J., Mochizuki T., Smeets H., Antignac C., Laurila P.,  
RA de Paeppe A., Tryggvason K., Reeders S.T.;  
RT Deletion of the paired alpha 5(IV) and alpha 6(IV) collagen genes in  
RT inherited smooth muscle tumors.";  
RL Science 261:1167-1169(1993).  
CC -1- FUNCTION: Type IV collagen is the major structural component of  
CC glomerular basement membranes (GBM), forming a 'chicken-wire'  
CC meshwork together with laminins, proteoglycans and actinin/  
CC nidogen.  
CC -1- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV) -  
CC ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH  
CC 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.  
CC -1- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=A:  
CC IsoId=Q14031-1; Sequence=Displayed;  
CC Name=B:  
CC IsoId=Q14031-2; Sequence=VSP\_001174;  
CC -1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS  
CC DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE  
CC G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY  
CC CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL

CC TRIPLE-HELICAL 7S DOMAIN.  
CC -1- PTM: Prolines at the third position of the tripeptide repeating  
CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
CC -1- PTM: Type IV collagens contain numerous cysteine residues which  
CC are involved in inter- and intramolecular disulfide bonding. 12 of  
CC these, located in the NC1 domain, are conserved in all known type  
CC IV collagens.  
CC -1- SIMILARITY: TO OTHER TYPE IV COLLAGENS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: D21337; BAA04809.1; -;  
CC EMBL: U04845; AAB19569.2; -;  
CC EMBL: U47004; AAB19038.1; -;  
CC EMBL: U46959; AAB19038.1; JOINED.  
CC EMBL: U46961; AAB19038.1; JOINED.  
CC EMBL: U46962; AAB19038.1; JOINED.  
CC EMBL: U46963; AAB19038.1; JOINED.  
CC EMBL: U46964; AAB19038.1; JOINED.  
CC EMBL: U46965; AAB19038.1; JOINED.  
CC EMBL: U46966; AAB19038.1; JOINED.  
CC EMBL: U46967; AAB19038.1; JOINED.  
CC EMBL: U46968; AAB19038.1; JOINED.  
CC EMBL: U46969; AAB19038.1; JOINED.  
CC EMBL: U46970; AAB19038.1; JOINED.  
CC EMBL: U46971; AAB19038.1; JOINED.  
CC EMBL: U46972; AAB19038.1; JOINED.  
CC EMBL: U46973; AAB19038.1; JOINED.  
CC EMBL: U46974; AAB19038.1; JOINED.  
CC EMBL: U46975; AAB19038.1; JOINED.  
CC EMBL: U46976; AAB19038.1; JOINED.  
CC EMBL: U46977; AAB19038.1; JOINED.  
CC EMBL: U46978; AAB19038.1; JOINED.  
CC EMBL: U46979; AAB19038.1; JOINED.  
CC EMBL: U46980; AAB19038.1; JOINED.  
CC EMBL: U46981; AAB19038.1; JOINED.  
CC EMBL: U46982; AAB19038.1; JOINED.  
CC EMBL: U46983; AAB19038.1; JOINED.  
CC EMBL: U46984; AAB19038.1; JOINED.  
CC EMBL: U46985; AAB19038.1; JOINED.  
CC EMBL: U46986; AAB19038.1; JOINED.  
CC EMBL: U46987; AAB19038.1; JOINED.  
CC EMBL: U46988; AAB19038.1; JOINED.  
CC EMBL: U46989; AAB19038.1; JOINED.  
CC EMBL: U46990; AAB19038.1; JOINED.  
CC EMBL: U46991; AAB19038.1; JOINED.  
CC EMBL: U46992; AAB19038.1; JOINED.  
CC EMBL: U46993; AAB19038.1; JOINED.  
CC EMBL: U46994; AAB19038.1; JOINED.  
CC EMBL: U46995; AAB19038.1; JOINED.  
CC EMBL: U46996; AAB19038.1; JOINED.  
CC EMBL: U46997; AAB19038.1; JOINED.  
CC EMBL: U46998; AAB19038.1; JOINED.  
CC EMBL: U46999; AAB19038.1; JOINED.  
CC EMBL: U47000; AAB19038.1; JOINED.  
CC EMBL: U47001; AAB19038.1; JOINED.  
CC EMBL: U47002; AAB19038.1; JOINED.  
CC EMBL: U47003; AAB19038.1; JOINED.  
CC EMBL: U47004; AAB19038.1; JOINED.  
CC EMBL: U46960; AAB19039.1; JOINED.  
CC EMBL: U46961; AAB19039.1; JOINED.  
CC EMBL: U46962; AAB19039.1; JOINED.  
CC EMBL: U46963; AAB19039.1; JOINED.  
CC EMBL: U46964; AAB19039.1; JOINED.  
CC EMBL: U46965; AAB19039.1; JOINED.  
CC EMBL: U46966; AAB19039.1; JOINED.  
CC EMBL: U46967; AAB19039.1; JOINED.

DR EMBL: U46968; AAB19039.1; JOINED.  
 DR EMBL: U46969; AAB19039.1; JOINED.  
 DR EMBL: U46970; AAB19039.1; JOINED.  
 DR EMBL: U46971; AAB19039.1; JOINED.  
 DR EMBL: U46972; AAB19039.1; JOINED.  
 DR EMBL: U46973; AAB19039.1; JOINED.  
 DR EMBL: U46974; AAB19039.1; JOINED.  
 DR EMBL: U46975; AAB19039.1; JOINED.  
 DR EMBL: U46976; AAB19039.1; JOINED.  
 DR EMBL: U46977; AAB19039.1; JOINED.  
 DR EMBL: U46978; AAB19039.1; JOINED.  
 DR EMBL: U46979; AAB19039.1; JOINED.  
 DR EMBL: U46980; AAB19039.1; JOINED.  
 DR EMBL: U46981; AAB19039.1; JOINED.  
 DR EMBL: U46982; AAB19039.1; JOINED.  
 DR EMBL: U46983; AAB19039.1; JOINED.  
 DR EMBL: U46984; AAB19039.1; JOINED.  
 DR EMBL: U46985; AAB19039.1; JOINED.  
 DR EMBL: U46986; AAB19039.1; JOINED.  
 DR EMBL: U46987; AAB19039.1; JOINED.  
 DR EMBL: U46988; AAB19039.1; JOINED.  
 DR EMBL: U46989; AAB19039.1; JOINED.  
 DR EMBL: U46990; AAB19039.1; JOINED.  
 DR EMBL: U46991; AAB19039.1; JOINED.  
 DR EMBL: U46992; AAB19039.1; JOINED.  
 DR EMBL: U46993; AAB19039.1; JOINED.  
 DR EMBL: U46994; AAB19039.1; JOINED.  
 DR EMBL: U46995; AAB19039.1; JOINED.  
 DR EMBL: U46996; AAB19039.1; JOINED.  
 DR EMBL: U46997; AAB19039.1; JOINED.  
 DR EMBL: U46998; AAB19039.1; JOINED.  
 DR EMBL: U46999; AAB19039.1; JOINED.  
 DR EMBL: U47000; AAB19039.1; JOINED.  
 DR EMBL: U47001; AAB19039.1; JOINED.  
 DR EMBL: U47002; AAB19039.1; JOINED.  
 DR EMBL: U47003; AAB19039.1; JOINED.  
 DR EMBL: AL034369; CAA22265.1; -  
 DR EMBL: AL109943; CAB89263.1; -  
 DR EMBL: AL136080; CAB96748.1; -  
 DR EMBL: AL031177; CAA20120.1; -  
 DR EMBL: L22763; AAA16338.1; -  
 DR PIR: A54122; CGH06B.  
 DR Gene: HGNC:2208; COLA6.  
 DR MIM: 303631; -  
 DR GO: 0005587; C:collagen type IV; NAS.  
 DR GO: 0005201; E:extracellular matrix structural constituent; NAS.  
 DR GO: 0030198; P:extracellular matrix organization and biogenesis; NAS.  
 DR InterPro: IPR000087; Collagen.  
 DR InterPro: IPR001442; ProcollagenC4.  
 DR Pfam: PF01413; C4; 2.  
 DR Pfam: PF01391; Collagen; 20.  
 DR ProDom: PD000007; C1g\_helix; 4.  
 DR ProDom: PD003923; ProcollagenC4; 1.  
 DR SMART: SM00111; C4; 2.  
 DR KEGG: Extracellular matrix; Connective tissue; Basement membrane;  
 Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal;  
 Alternative splicing; Polymorphism.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 1691 COLLAGEN ALPHA 6(IV) CHAIN.  
 FT DOMAIN 23 46 7S DOMAIN.  
 FT DOMAIN 47 1463 TRIPLE-HELICAL REGION.

Query Match 8.7%; Score 113.5; DB 1; Length 1691;  
 Best Local Similarity 36.0%; Pred. NO. 0.045;  
 Matches 36; Conservative 9; Mismatches 22; Indels 33; Gaps 7;

4 GGPASPGRLRGILLTLQLPAPSSASEIPKQKOKALRQREVVDLYNGM----- 54  
 DB 524 GGPAGAP-----GLVGPL-----GPSG-----PKGK-----KGPILLSTIQAGMDGRDSCS 565  
 OY 55 -CIAGPAGVPGRDSPGANVIGTPGIP--GRDGRGKRG 91  
 DB 566 GGRGVTGEGPKDGVPG--LPGLRGLRGDGGGGRPGKRG 602

RESULT 12  
 CAL7\_HUMAN STANDARD; PRT; 2944 AA.  
 ID 002388; 014054; 016507;  
 AC 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Collagen alpha 1(VII) chain precursor (long-chain collagen) (LC  
 DE collagen).  
 GN COL7A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94327588; PubMed-8051117;  
 RA Christiano A.M., Greenspan D.S., Lee S., Uitto J.;  
 RT "Cloning of human type VII collagen. Complete primary sequence of the  
 RT alpha 1(VII) chain and identification of intragenic polymorphisms.";  
 RT J. Biol. Chem. 269:20256-20262(1994).  
 RN [2]  
 RP SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-93338437; PubMed-1307247;  
 RA Christiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,  
 RA Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.E.,  
 RA Uitto J.;  
 RT "The large non-collagenous domain (NC-1) of type VII collagen is  
 RT amino-terminal and chimeric. Homology to cartilage matrix protein,  
 RT the type III domains of fibronectin and the A domains of von  
 RT Willebrand factor.";  
 RT Hum. Mol. Genet. 1:475-481(1992).  
 RN [3]  
 RP SEQUENCE OF 815-1439 FROM N.A.  
 RX MEDLINE-93334380; PubMed-1871109;  
 RA Parente M.G., Chung L.C., Rymmenen J., Woodley D.T., Wynn K.W.,  
 RA Bauer E.A., Mattei M.-G., Chu M.-L., Uitto J.;  
 RT "Human type VII collagen: cDNA cloning and chromosomal mapping of the  
 RT gene.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).  
 RN [4]  
 RP SEQUENCE OF 369-1255 FROM N.A.  
 RX MEDLINE-93107742; PubMed-1469284;  
 RA Gammon W.R., Abernethy M.L., Padilla K.M., Prisyanyan P.S.,  
 RA Cook M.E., Wright J., Brigaman R.A., Hunt S.W. III;  
 RT "Noncollagenous (NC1) domain of collagen VII resembles multidomain  
 RT adhesion proteins involved in tissue-specific organization of  
 RT extracellular matrix.";  
 RT J. Invest. Dermatol. 99:691-696(1992).  
 RN [5]  
 RP SEQUENCE OF 340-675 FROM N.A.  
 RX MEDLINE-92231902; PubMed-1567409;  
 RA Tanaka T., Takahashi K., Furukawa F., Tamura S.;  
 RT "Molecular cloning and characterization of type VII collagen cDNA.";  
 RT Biochem. Biophys. Res. Commun. 183:958-963(1992).  
 RN [6]  
 RP SEQUENCE OF 2395-2944 FROM N.A.  
 RX MEDLINE-93271985; PubMed-8499916;  
 RA Greenspan D.S.;  
 RT "The carboxyl-terminal half of type VII collagen, including the non-  
 RT corresponding NC-2 domain and intron/exon organization of the  
 RT Hum. Mol. Genet. 2:273-278(1993).  
 RN [7]  
 RP SEQUENCE OF 1-87 FROM N.A.  
 RX MEDLINE-94375010; PubMed-8088784;  
 RA Christiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,  
 RA Uitto J., Greenspan D.S.;  
 RT "Structural organization of the human type VII collagen gene (COL7A1),

RT composed of more exons than any previously characterized gene.;"

RL Genomics 21:169-179(1994).

RP [18]

RA REVIEW ON DEB VARIANTS.

RX MEDLINE=98041696; PubMed=9375848;

RT Jaervikallio A., Pulkkinen L., Uitto J.;

RT "Molecular basis of dystrophic epidermolysis bullosa: mutations in

RT the type VII collagen gene (COL7A1).";

RL Hum. Mutat. 10:338-347(1997).

RN [19]

RP VARIANT DEB LYS-2798.

RX MEDLINE=93291877; PubMed=8513326;

RA Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,

RA Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;

RT A missense mutation in type VII collagen in two affected siblings

RT with recessive dystrophic epidermolysis bullosa.;"

RL Nat. Genet. 4:62-66(1993).

RN [10]

RP VARIANT DEB SER-2040.

RX MEDLINE=94224777; PubMed=8170945;

RA Christiano A.M., Rymaenen M., Uitto J.;

RT "Dominant dystrophic epidermolysis bullosa: identification of a

RT Gly->Ser substitution in the triple-helical domain of type VII

RT collagen.;"

RL Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).

RN [11]

RP VARIANT DEB CYS-2623.

RX MEDLINE=96081220; PubMed=8541842;

RA Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Uitto J.;

RT "Peribulbar epidermolysis bullosa: genetic linkage to COL7A1 and

RT identification of a glycine-to-cysteine substitution in the triple-

RT helical domain of type VII collagen.;"

RL Hum. Mol. Genet. 4:1579-1583(1995).

RN [12]

RP VARIANT DEB ARG-2043.

RX MEDLINE=95164985; PubMed=7861014;

RA Christiano A.M., Morricone A., Paradisi M., Angelo C., Mazzanti C.,

RA Cavalieri R., Uitto J.;

RT "A glycine-to-arginine substitution in the triple-helical domain of

RT type VII collagen in a family with dominant dystrophic epidermolysis

RT bullosa.;"

RL J. Invest. Dermatol. 104:438-440(1995).

RN [13]

RP VARIANTS DEB.

RX MEDLINE=96220218; PubMed=8644729;

RA Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;

RT "Glycine substitutions in the triple-helical region of type VII

RT collagen result in a spectrum of dystrophic epidermolysis bullosa

RT phenotypes and patterns of inheritance.;"

RL Am. J. Hum. Genet. 58:671-681(1996).

RN [14]

RP VARIANT DEB ARG-2575.

RX MEDLINE=96154068; PubMed=8592061;

RA Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Uitto J.;

RT "Molecular basis of recessive dystrophic epidermolysis bullosa:

RT genotype/phenotype correlation in a case of moderate clinical

RT severity.;"

RL J. Invest. Dermatol. 106:119-124(1996).

RN [15]

RP VARIANT DEB ARG-1782.

RX MEDLINE=96183562; PubMed=8618018;

RA Christiano A.M., McGrath J.A., Uitto J.;

RT "Influence of the second COL7A1 mutation in determining the

RT phenotypic severity of recessive dystrophic epidermolysis bullosa.;"

RL J. Invest. Dermatol. 106:766-770(1996).

RN [16]

RP VARIANT DEB ASP-2073.

RX MEDLINE=96310789; PubMed=8757758;

RA Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,

RA Uitto J., Pope F.M., Bady R.A.J.;

RT "Clinicopathological correlations of compound heterozygous COL7A1

RT mutations in recessive dystrophic epidermolysis bullosa.;"

RL J. Invest. Dermatol. 107:171-177(1996).

RN [17]

RP VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND

RP ARG-2575.

RX MEDLINE=97465605; PubMed=9326325;

RA Hovnanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost C.,

RA Fraileg S., Christiano A.M., Uitto J., Lathrop M., Barrandon Y.,

RA de Prost Y.;

RT "Characterization of 18 new mutations in COL7A1 in recessive

RT dystrophic epidermolysis bullosa provides evidence for distinct

RT molecular mechanisms underlying defective anchoring fibril

RT formation.;"

RL Am. J. Hum. Genet. 61:599-610(1997).

RN [18]

RP VARIANT DEB ARG-1652.

RX MEDLINE=98106792; PubMed=944387;

RA Gerhalml-Friedman P.B., Karpali S., Horvath A., Christiano A.M.;

RT "Identification of a glycine substitution and a splice site mutation

RT in the type VII collagen gene in a proband with milds recessive

RT dystrophic epidermolysis bullosa.;"

RL Arch. Dermatol. Res. 289:640-645(1997).

RN [19]

RP VARIANTS DEB ARG-2009 AND ARG-2043.

RX MEDLINE=97358588; PubMed=9215684;

RA Winberg J.-O., Hammami-Hausali N., Nilsen O., Anton-Lamprecht I.,

RA Naylor S.L., Kerbacher K., Zimmermann M., Krajci P.,

RA Gedde-Dahl T., Jr., Bruckner-Tuderman L.;

RT "Modulation of disease severity of dystrophic epidermolysis bullosa by

RT a splice site mutation in combination with a missense mutation in the

RT COL7A1 gene.;"

RL Hum. Mol. Genet. 6:1125-1135(1997).

RN [20]

RP VARIANTS DEB ASP-1519; ASP-2006; GLU-2015 AND ARG-2034.

RX MEDLINE=98334662; PubMed=9668111;

RA Hammami-Hausali N., Schumann H., Baghunath M., Kilgus O., Luethi U.,

RA Luger T., Bruckner-Tuderman L.;

RT "Some, but not all, glycine substitution mutations in COL7A1 result in

RT intracellular accumulation of collagen VII, loss of anchoring

RT fibrils, and skin blistering.;"

RL J. Biol. Chem. 273:19228-19234(1998).

RN [21]

RP VARIANTS DEB CYS-2008; ARG-2207 AND SER-2775.

RX MEDLINE=98410965; PubMed=9740253;

RA Kon A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Uitto J.;

RT "Novel COL7A1 mutations in dystrophic forms of epidermolysis

RT bullosa.;"

RL J. Invest. Dermatol. 111:534-537(1998).

RN [22]

RP VARIANT DEB ARG-1347.

RX MEDLINE=99019477; PubMed=9804332;

RA Terracina M., Posteraro P., Schubert M., Sonego G., Atzori F.,

RA Zambruno G., Bruckner-Tuderman L., Castiglia D.;

RT "Compound heterozygosity for a recessive glycine substitution and a

RT splice site mutation in the COL7A1 gene causes an unusually mild form

RT of localized recessive dystrophic epidermolysis bullosa.;"

RL J. Invest. Dermatol. 111:744-750(1998).

RN [23]

RP VARIANTS DEB TRP-2034; VAL-2040; ARG-2043; ARG-2064 AND ASP-2713.

RX MEDLINE=99072663; PubMed=9856843;

Query Match 8.78; Score 113; DB 1; Length 2944;

Best Local Similarity 33.78; Pred. No. 0.095;

Matches 34; Conservative 2; Mismatches 23; Indels 42; Gaps 4;

QY 3 PGP- -----AASPR-----LNGILLLLLOLPAPSSASEIRKQKQALRQREVVDLY 51

DB 1792 PGP- -----AASPR-----LNGILLLLLOLPAPSSASEIRKQKQALRQREVVDLY 51

QY 52 NGMCLOGPACVPGRDSFGANVITPGTGPICGRDFKGEKE 92

DB 1830 -----GKPEDGKRGKNGKNGERCGDGEGRKGEKED 1861

RESULT 13

C1QC\_HUMAN STANDARD; PRT; 245 AA.  
 ID C1QC\_HUMAN PRT; 245 AA.  
 AC P02747; Q96DL2; Q96H05;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Complement C1q subcomponent, C chain precursor.  
 GN C1QC OR C1QC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RA Sellar G.C., Blake D.J., Reid K.B.M.;  
 RT MEDLINE=91174759; PubMed=1706597;  
 RT "Characterization and organization of the genes encoding the A-, B-  
 RT and C-chains of human complement subcomponent C1q. The complete  
 RT derived amino acid sequence of human C1q.";  
 RL Biochem. J. 274:481-490(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cerebellum;  
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,  
 RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;  
 RT "NEO human cDNA sequencing project.";  
 RT Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Staleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pailey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 29-122.  
 RA MEDLINE=80020137; PubMed=486087;  
 RA Reid K.B.M.;  
 RT "Complete amino acid sequences of the three collagen-like regions  
 RT present in subcomponent C1q of the first component of human  
 RT complement.";  
 RL Biochem. J. 179:367-371(1979).  
 RN [5]  
 RP REVIEW OF C1Q DEFICIENCY.  
 RA MEDLINE=98450587; PubMed=9777412;  
 RA Petry F.;  
 RT "Molecular basis of hereditary C1q deficiency.";  
 RL Immunobiology 199:286-294(1998).  
 CC -1- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYME C1R AND C1S TO YIELD  
 CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE  
 CC COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE C1(2+)-DEPENDENT  
 CC C1R(2YC1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1  
 CC TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE

FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.  
 -1- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R  
 AND S IN THE MOLAR RATIO OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED  
 OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE  
 A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF  
 THE C CHAIN.  
 -1- PTM: O-linked glycans consist of Glc-Gal disaccharides bound to  
 the oxygen atom of post-translationally added hydroxyl groups.  
 -1- DISEASE: Defects in C1QG are a cause of C1q deficiency  
 [MIM:120575]. It is a rare genetic disorder which is associated  
 with recurrent infections and a high prevalence of lupus  
 erythematosus-like symptoms. It is characterized by a loss of  
 activation of the complement classical pathway.  
 -1- SIMILARITY: Contains 1 collagenous domain.  
 -1- SIMILARITY: Contains 1 C1q domain.  
 -----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 -----  
 EMBL: AK057792; BAB71575.1; -;  
 EMBL: BC009016; AAH09016.1; -;  
 DR PIR: S14351; C1HQC.  
 DR Genew: HGNC:1245; C1QG.  
 DR MIM: 120575; -;  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0007923; F:defense/immunity protein activity; NAS.  
 DR GO: GO:0006935; P:immune response; NAS.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF00391; Collagen; 1.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM01110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 DR Repeat: Signal; Disease mutation.  
 KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;  
 FT SIGNAL 1 28  
 FT CHAIN 1 28  
 FT DOMAIN 29 245  
 FT 31 112  
 FT 113 245  
 FT DISULFID 32 32  
 FT MOD\_RES 36 36  
 FT MOD\_RES 39 39  
 FT MOD\_RES 42 42  
 FT MOD\_RES 45 45  
 FT MOD\_RES 54 54  
 FT MOD\_RES 57 57  
 FT MOD\_RES 63 63  
 FT MOD\_RES 66 66  
 FT MOD\_RES 71 71  
 FT MOD\_RES 75 75  
 FT MOD\_RES 77 75  
 FT CARBOHYD 81 81  
 FT MOD\_RES 84 84  
 FT MOD\_RES 84 84  
 FT MOD\_RES 93 93  
 FT MOD\_RES 96 96  
 FT MOD\_RES 99 99  
 FT MOD\_RES 105 105  
 FT VARIANT 103 43  
 FT 14 14  
 FT CONFLICT 23 23  
 FT CONFLICT 57 57  
 FT CONFLICT 66 66  
 FT CONFLICT 72 72  
 FT CONFLICT 84 84  
 FT CONFLICT 87 87  
 COMPLEMENT C1Q SUBCOMPONENT, C CHAIN.  
 COLLAGEN-LIKE.  
 INTERCHAIN (WITH OTHER C CHAIN).  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 O-LINKED (GAL. . .).  
 O-LINKED (GAL. . .).  
 HYDROXYLATION.  
 O-LINKED (GAL. . .).  
 HYDROXYLATION.  
 HYDROXYLATION.  
 HYDROXYLATION.  
 G -> R (in C1Q deficiency).  
 /FTid=VAR\_008542.  
 K -> R (IN REF. 2).  
 P -> A (IN REF. 1).  
 K -> P (IN REF. 4).  
 P -> K (IN REF. 4).  
 K -> P (IN REF. 4).  
 P -> K (IN REF. 4).  
 N -> D (IN REF. 4).



```

FT CONFLICT 191 192 EA -> AS (IN REF. 3).
FT CONFLICT 195 195 T -> Q (IN REF. 4).
FT CONFLICT 215 215 S -> A (IN REF. 4).
FT CONFLICT 227 227 T -> A (IN REF. 4).
FT CONFLICT 251 251 P -> A (IN REF. 4).
FT CONFLICT 258 258 Q -> T (IN REF. 4).
FT CONFLICT 261 261 T -> S (IN REF. 4).
FT CONFLICT 492 492 G -> P (IN REF. 5).
SQ SEQUENCE 747 AA; 71329 MW; DDFCID7CDICAE77C CRC64;

Query Match 8.5%; Score 111; DB 1; Length 747;
Best Local Similarity 23.3%; Pred No. 0.029; Indels 84; Gaps 8;
Matches 47; Conservative 19; Mismatches 52;

DB 57 GGPAGVPGRDSPGANVTP---GTPGIPRGDFKGEKGE----- 92
DB 513 RGERGFPGRGSPGAGLOGPGLGPTGDTGPKGASGAPGAPGAGPGGLQMTLDAMK 572
DB 93 ---CLAESFESEWTPN-----YKQCSWS-----LMTGIDLGKIA--- 124
DB 573 VFCNNEGETCYVPNPASVPKKNMWSKSKDKKHIMFGETTINGGFHFSYGD--MLAPNT 630
DB 125 ---ECTFTKMSNSALRYLFGSLRLKCRNACCORWYFTENGAECSGPLPEAIITYLDG 181
DB 631 ADVQMTFLRLSTEG-----SONITYHCKN-----SIAYLDEA 663
DB 182 SPENASTINIHTSVSEGLCEG 203
DB 664 AGNLKALLIOGSNDVEIRAE 685

RESULT 15
CALI-RAT STANDARD; PRT; 671 AA.
AC P02454; P02455;
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 1(I) chain (Fragments).
GN COL1A1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN NM
RN NM SEQUENCE OF 1-19.
RX MEDLINE=69155173; PubMed=5777344;
RA Bornstein P.;
RT "Comparative sequence studies of rat skin and tendon collagen. II.
RT The absence of a short sequence at the amino terminus of the skin
RT alpha 1 chain."
RL Biochemistry 8:63-71(1969).
RN NM
RN NM SEQUENCE OF 5-19.
RX MEDLINE=67162268; PubMed=5337886;
RA Kang A.H., Bornstein P., Piez K.A.;
RT "The amino acid sequence of peptides from the cross-linking region of
RT rat skin collagen."
RL Biochemistry 6:788-795(1967).
RN NM
RN NM SEQUENCE OF 20-55.
RX MEDLINE=67165368; PubMed=4290711;
RA Bornstein P.;
RT "The incomplete hydroxylation of individual prolyl residues in
RT collagen."
RL J. Biol. Chem. 242:2572-2574(1967).
RN NM
RN NM SEQUENCE OF 56-102.
RX MEDLINE=71263178; PubMed=4327399;
RA Butler W.T., Ponds S.L.;
RT "Chemical studies on the cyanogen bromide peptides of rat skin
RT collagen. Amino acid sequence of alpha 1-CH4."
RL Biochemistry 10:2076-2081(1971).

```

```

RN NM
RN NM SEQUENCE OF 103-139.
RX MEDLINE=70085124; PubMed=5441206;
RA Butler W.T.;
RT "Chemical studies on the cyanogen bromide peptides of rat skin
RT collagen. The covalent structure of alpha 1-CH5, the major
RT hexose-containing cyanogen bromide peptide of alpha 1."
RL Biochemistry 9:44-50(1970).
RN NM
RN NM SEQUENCE OF 140-238.
RX MEDLINE=72136131; PubMed=4335087;
RA Ballan G., Click E.M., Bornstein P.;
RT "Structure of rat skin collagen alpha 1-CH8. Amino acid sequence of
RT the hydroxylamine-produced fragment HA1."
RL Biochemistry 10:4470-4478(1971).
RN NM
RN NM SEQUENCE OF 239-418.
RX MEDLINE=73006942; PubMed=4342027;
RA Ballan G., Click E.M., Hermodson M.A., Bornstein P.;
RT "Structure of rat skin collagen alpha 1-CH8. Amino acid sequence of
RT the hydroxylamine-produced fragment HA2."
RL Biochemistry 11:3798-3806(1972).
RN NM
RN NM SEQUENCE OF 419-567.
RX MEDLINE=74271984; PubMed=4366532;
RA Butler W.T., Underwood S.P., Finch J.E. Jr.;
RT "Chemical studies on the cyanogen bromide peptides of rat skin
RT collagen. Amino acid sequence of alpha 1-CH3."
RL Biochemistry 13:2946-2953(1974).
RN NM
RN NM SEQUENCE OF 568-651.
RX MEDLINE=74011954; PubMed=4126850;
RA Stoltz M., Timpl R., Furchmayr H., Kuehn K.;
RT "Structural and immunogenic properties of a major antigenic
RT determinant in neutral salt-extracted rat-skin collagen."
RL Eur. J. Biochem. 37:287-294(1973).
RN NM
RN NM SEQUENCE OF 651-671.
RX MEDLINE=73049495; PubMed=4636751;
RA Stoltz M., Timpl R., Kuehn K.;
RT "Non-helical regions in rat collagen alpha 1-chain."
RL FEBS Lett. 26:61-65(1972).
RN NM
RN NM SEQUENCE OF 529-567 FROM N.A.
RX MEDLINE=85122694; PubMed=6395893;
RA Genovese C., Rowe D., Kream B.;
RT "Construction of DNA sequences complementary to rat alpha 1 and alpha
RT 2 collagen mRNA and their use in studying the regulation of type I
RT collagen synthesis by 1,25-dihydroxyvitamin D."
RL Biochemistry 23:6210-6216(1984).
RN NM
RN NM FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
CC (FIBRILLAR FORMING COLLAGEN).
CC -I SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
CC -I TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
CC BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
CC HYDROXYAPATITE.
CC -I PTH: Proline residues at the third position in some or all of the
CC repeating unit (G-X-Y) are hydroxylated in some or all of the
CC chains.
CC -I PTH: O-linked glycan consists of a Glc-Gal disaccharide bound to
CC the oxygen atom of a post-translationally added hydroxyl group.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M11432; AAA40832.1; ALT_SEQ.
DR InterPro: IPR000087; Collagen.
DR InterPro: IPR001007; VWF_C.

```



**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:22:37 ; Search time 39 Seconds

(without alignments)  
599.205 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 1301  
Sequence: 1 MKPGPASPQRRLGILL.....GDASTGWSVSRRIIEELPK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_76:\*\*\*  
2: PIR2:\*\*\*  
3: PIR3:\*\*\*  
4: PIR4:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.5	9.4	246	2 S29328	complement subcomp
2	120	9.2	1752	2 A45407	collagen alpha 3(I)
3	119	9.1	289	2 T20177	hypothetical prote
4	118.5	9.1	1464	1 CGH015	collagen alpha 1(I)
5	117	9.0	327	2 T29031	hypothetical prote
6	117	9.0	754	2 A55267	collagen alpha 5(I)
7	116	8.9	888	2 S28791	collagen alpha 1(X)
8	116	8.9	1670	1 CGH04B	collagen alpha 3(I)
9	115.5	8.9	1669	1 CGH04B	collagen alpha 1(I)
10	115	8.8	1466	1 CGH07L	collagen alpha 1(I)
11	115	8.8	1763	2 S16366	collagen alpha 2(I)
12	114.5	8.8	311	2 T15268	hypothetical prote
13	114	8.8	304	2 T26185	hypothetical prote
14	114	8.8	304	2 T26185	hypothetical prote
15	114	8.8	1691	1 S22917	collagen alpha 5(I)
16	113.5	8.7	300	2 T24482	hypothetical prote
17	113.5	8.7	920	2 A45748	collagen alpha 1(V)
18	113.5	8.7	1549	2 I48103	type VII collagen
19	113.5	8.7	1691	2 CGH06B	collagen alpha 6(I)
20	113	8.7	2944	2 A54849	collagen alpha 1(V)
21	112	8.6	178	2 A39762	collagen alpha 1(X)
22	112	8.6	325	2 T18594	hypothetical prote
23	111.5	8.6	428	2 T24769	hypothetical prote
24	111	8.5	245	1 C14H0C	complement subcomp
25	111	8.5	358	2 T26281	hypothetical prote
26	110.5	8.5	298	2 T27644	hypothetical prote
27	110.5	8.5	310	2 T29731	hypothetical prote
28	110.5	8.5	458	2 T31631	hypothetical prote
29	110.5	8.5	671	1 CGRT1S	collagen alpha 1(I)

30	110.5	8.5	1453	2 S21626	collagen alpha 1(I)
31	110	8.5	298	2 JC1448	collagen col-34
32	110	8.5	299	2 T29956	hypothetical prote
33	110	8.5	1042	1 CGCH1S	collagen alpha 1(I)
34	110	8.5	1049	1 CGB07S	collagen alpha 1(I)
35	110	8.5	1568	2 T09074	semaphorin recepto
36	110	8.5	1806	1 CGH01E	collagen alpha 1(X)
37	109.5	8.4	177	2 S37749	collagen alpha 2(X)
38	109.5	8.4	290	2 T24586	hypothetical prote
39	109.5	8.4	330	2 S46657	collagen alpha 1(X)
40	109.5	8.4	488	2 A27353	collagen alpha 1(I)
41	109	8.4	1414	1 S23809	collagen alpha 2(I)
42	109	8.4	1418	2 T45467	collagen alpha 1(I)
43	109	8.4	1669	1 CGM64B	collagen alpha 1(I)
44	109	8.4	1744	2 S40991	collagen alpha 1(I)
45	108.5	8.3	323	2 A61396	collagen alpha 1(I)

#### ALIGNMENTS

##### RESULT 1

S29328  
complement subcomponent C1q chain C - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999

C/Accession: S29328

R:Petty, F.; Reid, K.B.M.; Loos, M.

Eur. J. Biochem. 209, 129-134, 1992

A:Title: Isolation, sequence analysis and characterization of cDNA clones coding for eceredellin.

A:Reference number: S29328; MWID:93011118; PMID:1396691

A/Accession: S29328

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-246 <PEP>

A:Cross-references: EMBL:X66295; NID:950228; PIDN:CAA46993.1; PID:950229

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal F:122-245/Domain: complement C1q carboxyl-terminal homology <C1q>

##### Query Match

Best Local Similarity 37.4%; Score 122.5; DB 2; Length 246;  
Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;

QY	5	GPASPORLGLLLLLLPAPSSASERPKQKALQREVVLDYNGMKLOGPAGVPG	64
DB	4	GRSCOPCGCGLLLPLPLRSQAS-----ACCTGIPGMGMPGAPG	47
QY	65	RDGS---PGANVIGTPGIPGRDGRGKGE	92
DB	48	KDGHDLQCPKRGEPGIPAVDGTGPGKQGE	78

##### RESULT 2

A45407  
collagen alpha 3(IV) chain - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999

C/Accession: A45407; A43903; A23940

R:Expósito, J.Y.; D'Alessio, M.; Di Liberto, M.; Ramirez, F.

J. Biol. Chem. 268, 5249-5254, 1993

A:Title: Complete primary structure of a sea urchin type IV collagen alpha chain and

A:Reference number: A45407; MWID:93186842; PMID:844899

A/Accession: A45407

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-1752 <EXP>

A>Note: sequence extracted from NCBI backbone (NCBI:126841)

R:Kessell, G.M.; Etkin, M.; Benson, S.

Dev. Biol. 148, 261-272, 1991

A:Title: Primary mesenchyme cells of the sea urchin embryo require an autonomously pr

A:Reference number: A43903; MWID:92038439; PMID:1936564

A/Accession: A43903

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-633-1537, 'G' <RES>  
A:Cross-references: GB:S64572; NID:g238616; PIDN:AA620270.1; PID:g238617  
A:Note: sequence extracted from NCBI backbone (NCBIN:64572, NCBI:P:64573)  
R:Venkatesan, M.; De Pablo, F.; Vogeli, G.; Simpson, R.T.  
Proc. Natl. Acad. Sci. U.S.A. 83, 3351-3355, 1986  
A:Title: Structure and developmentally regulated expression of a Strongylocentrotus purp  
A:Reference number: A23940; MUID:86205894; PMID:3458186  
A:Accession: A23940  
A:Molecule type: DNA  
A:Residues: 742-812 <VEN>  
A:Cross-references: EMBL:M13206  
C:Superfamily: collagen alpha 1(IV) chain  
C:Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix  
F:29-161/Domain: amino-terminal nonhelical, 7S <7SD>  
F:162-1523/Region: interrupted helical  
F:1524-1752/Domain: carboxyl-terminal nonhelical, NC1 <NC1>  
F:1534-1634/Domain: collagen IV carboxyl-terminal repeat <CT1>  
F:1644-1748/Domain: collagen IV carboxyl-terminal repeat <CT2>  
F:129/Modified site: allysine (lys) #status predicted

Query Match 9.2%; Score 120; DB 2; Length 1752;  
Best Local Similarity 22.4%; Pred. No. 0.025;  
Matches 46; Conservative 20; Mismatches 61; Indels 78; Gaps 9;

QY 3 PGRASAPQRRLGLLLLLDLPASSASEIPKQKQAKQREVVDLYNGMCIQPGAV 62  
DB 1453 PGRGPRGDR-----PPGQ-----PPG-----LWGDKGT 1477  
QY 63 PGRGSPGANVTPGTGIPGRGKGEKGEKRESF-----EESWT 103  
DB 1478 PGVGNRCVSGVPEPGLKQGRGNGQPGDGFPTKKEAGIPGSSGFFITRHSQT 1537  
QY 104 PNYKQ-----SW-----SSLNYGIDLKIACTPTKMSNALVLESGSLRL 147  
DB 1538 TSIPQCPQGTAKMHGYSILFVQGNENRGHGDLDGKPGSC-----LKRFTMPFLFC-NINN 1592  
QY 148 KCRNACCGRWYFTFNGACSGPLPI 172  
DB 1593 VCHVASRNDYSYWLSTYE---PMDM 1614

RESULT 3  
T20177  
hypothetical protein C53B4.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T20177  
R:Berks, M.  
Submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19233  
A:Accession: T20177  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-289 <WT1>  
A:Cross-references: EMBL:Z68215; PIDN:CAA92453.1; GSPDB:GN00022; CESP:C53B4.5  
A:Experimental source: clone C53B4  
C:Genetics:  
A:Gene: CESP:C53B4.5  
A:Map position: 4  
C:Superfamily: unassigned collagens

Query Match 9.1%; Score 119; DB 2; Length 289;  
Best Local Similarity 34.5%; Pred. No. 0.004;  
Matches 29; Conservative 5; Mismatches 20; Indels 30; Gaps 2;

QY 25 PAPSASAEIRKQKQAKQREVVDLYNGMCIQPGAVPGRDGS-----P 69  
DB 203 PGRGSPGANVTPGTGIPGRGKGEKGEKRESF-----EESWT 103  
QY 70 GANVTPGTGIPGRGKGEKGEKRESF-----EESWT 103

DB 248 GRDQPGRPGRGKGEKGEK 271  
RESULT 4  
CGHUIS  
collagen alpha 1(I) chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1981 #sequence\_revision 04-Oct-1996 #text\_change 31-Dec-2000  
C:Accession: I60114; S01143; A93335; I55254; A39443; I55237; A35233; S09400; B90567;  
5269; A29439; I53466; A02852; I37247  
R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.  
Gene 67, 105-115, 1988  
A:Title: Complete nucleotide sequence of the region encompassing the first twenty-five  
A:Reference number: I60114; MUID:88329734; PMID:284432  
A:Accession: I60114  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-369, 'L', 371-588 <DAL>  
A:Cross-references: GB:M20789; NID:g179593; PIDN:AA59373.1; PID:g179594  
R:Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Pr  
Biochem. J. 253, 919-922, 1988  
A:Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of hum  
A:Reference number: S01143; MUID:89025644; PMID:3178743  
A:Accession: S01143  
A:Molecule type: mRNA  
A:Residues: 1-472 <TRO>  
A:Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546;  
A:Note: submitted to the EMBL/GenBank/DBJ databases by Prockop, D.J., 13-JUN-1988  
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams,  
Nature 310, 337-340, 1984  
A:Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation  
A:Reference number: A93335; MUID:84270697; PMID:6462220  
A:Accession: A93335  
A:Molecule type: DNA  
A:Residues: 1-58, 'O', 60-181 <CHD>  
A:Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658  
R:Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet,  
J. Biol. Chem. 262, 15151-15157, 1987  
A:Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene  
A:Reference number: I55254; MUID:88033098; PMID:2822714  
A:Accession: I55254  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-45 <ROS>  
A:Cross-references: GB:J02829; NID:g180387; PIDN:AA51993.1; PID:g180388  
R:Bornslein, P.; McKay, J.; Morishima, J.K.; Devaryalu, S.; Gelinas, R.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987  
A:Title: Regulatory elements in the first intron contribute to transcriptional contro  
A:Reference number: A39443; MUID:88097389; PMID:3480516  
A:Accession: A39443  
A:Molecule type: DNA  
A:Residues: 1-34 <BOR>  
A:Cross-references: GB:J03559; NID:g180876; PIDN:AA52052.1; PID:g553238  
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.  
J. Biol. Chem. 260, 2315-2320, 1985  
A:Title: Fine structural analysis of the human pro-alpha 1(I) collagen gene. Promote  
A:Reference number: I55237; MUID:85130970; PMID:2857713  
A:Accession: I55237  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-34 <CH2>  
A:Cross-references: GB:M10627; NID:g180383; PIDN:AA51992.1; PID:g553226  
R:Wirtz, M.K.; Keene, D.R.; Hoti, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Holl  
J. Biol. Chem. 265, 6312-6317, 1990  
A:Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-term  
A:Reference number: A35233; MUID:90202908; PMID:2318855  
A:Accession: A35233  
A:Molecule type: protein  
A:Residues: 33-52 <WIR>  
A:Note: this propeptide fragment remained non-covalently bound to a defective, unclea  
R:Well, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.

EMBO J. 8, 1705-1710, 1989  
 A:Title: A base substitution in the exon of a collagen gene causes alternative splicing  
 A:Reference number: 509400; MUID:89356643; PMID:2767050  
 A:Accession: 509400  
 A:Molecule type: mRNA  
 A:Residues: 156-183 <MET>  
 R:Click, E.M.; Bornstein, P.  
 Biochemistry 9, 4699-4706, 1970  
 A:Title: Isolation and characterization of the cyanogen bromide peptides from the alpha1  
 A:Reference number: A90567; MUID:71036625; PMID:5529814  
 A:Contents: CNBr0-1, CNBr2, CNBr4, CNBr5  
 A:Accession: B90567  
 A:Molecule type: Protein  
 A:Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z'  
 A:Experimental source: skin  
 A:Note: evidence for 170-allysine  
 R:Beetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, F.  
 Eur. J. Biochem. 192, 153-159, 1990  
 A:Title: A critical crosslink region in human bone-derived collagen type I. Specific cle  
 A:Reference number: S11372; MUID:90382436; PMID:2169412  
 A:Accession: S11372  
 A:Molecule type: Protein  
 A:Residues: 175-187, 274-287, 'P', 289 <BAE>  
 A:Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion  
 R:Dak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Mizel, S.A.; Gonzalez  
 J. Biol. Chem. 266, 21827-21832, 1991  
 A:Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain  
 A:Reference number: I55342; MUID:92042092; PMID:1718984  
 A:Accession: I55342  
 A:Molecule type: Protein  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 258-268, 1347-1357 <DEA>  
 A:Cross-references: GB:567495; NID:9239007; PIDN:AAB20350.1; PID:9239008  
 A:Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report  
 R:Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.  
 J. Biol. Chem. 245, 5042-5048, 1970  
 A:Title: Comparative study of glycopeptides derived from selected vertebrate collagens.  
 A:Reference number: A92069; MUID:71001508; PMID:4319110  
 A:Accession: A92069  
 A:Molecule type: Protein  
 A:Residues: 263-268 <MOR>  
 A:Experimental source: skin  
 A:Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine  
 R:Labhard, M.E.; Hollister, D.W.  
 Matrix 10, 124-130, 1990  
 A:Title: Segmental amplification of the entire helical and telopeptide regions of the CT  
 A:Reference number: S15989; MUID:90326017; PMID:2374517  
 A:Accession: S15989  
 A:Molecule type: mRNA  
 A:Residues: 281-302, 402-420, 823-843, 925-944, 1026-1045, 1143-1162 <LAB>  
 R:Wirtz, M.K.; Rao, V.H.; Gnanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.  
 Connect. Tissue Res. 29, 1-11, 1993  
 A:Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of  
 A:Reference number: I52905; MUID:93339042; PMID:8339541  
 A:Accession: I52905  
 A:Molecule type: mRNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 342-352, 'C', 354-359 <MT2>  
 A:Cross-references: GB:564717; NID:9408195; PIDN:AAB27677.1; PID:9408196  
 A:Note: mutant sequence from patient with osteogenesis imperfecta  
 R:Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.  
 Biochemistry 22, 5213-5223, 1983  
 A:Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1  
 A:Reference number: A90476; MUID:84080385; PMID:6669127  
 A:Accession: A90476  
 A:Molecule type: mRNA  
 A:Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER>  
 A:Cross-references: GB:K01228; NID:9180391; PIDN:AAA51995.1; PID:9180392  
 A:Note: sequence partially completed for missing nucleotides by A29439  
 R:Chu, M.L.; Gardino, V.; Williams, C.J.; Ramirez, F.  
 J. Biol. Chem. 260, 691-694, 1985  
 A:Title: Multixon deletion in an osteogenesis imperfecta variant with increased type II

A:Reference number: A22161; MUID:85104934; PMID:2981843  
 A:Accession: A22161  
 A:Molecule type: DNA  
 A:Residues: 472-594, 'R', 596-607 <CH3>  
 A:Cross-references: GB:K03178; GB:K03179; NID:q179612; NID:q179613; PIDN:AAA51847.1;  
 A:Note: the authors translated the codon CGT for residue 595 as Pro  
 R:Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.  
 Am. J. Hum. Genet. 46, 1034-1040, 1990  
 A:Title: Variable expression of osteogenesis imperfecta in a nuclear family is explai  
 A:Reference number: A35336; MUID:90252792; PMID:2339700  
 A:Accession: A35336  
 A:Molecule type: mRNA  
 A:Residues: 710-720, 'E', 722-737, 'E', 739-745 <MAL>  
 A:Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu  
 R:Forlino, A.; Zolozzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mot  
 Hum. Mol. Genet. 3, 2201-2206, 1994  
 A:Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in th  
 A:Reference number: I54365; MUID:95187161; PMID:7881420  
 A:Accession: I54365  
 A:Molecule type: DNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 746-766, 'S', 768-781 <FOR>  
 A:Cross-references: GB:I47667; NID:q100903; PIDN:AAB59576.1; PID:q100904  
 R:Chesler, S.D.; Wallis, G.A.; Byers, P.H.  
 J. Biol. Chem. 268, 18218-18225, 1993  
 A:Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of  
 A:Reference number: A47426; MUID:93352646; PMID:8349697  
 A:Accession: A47426  
 A:Molecule type: mRNA  
 A:Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>  
 A:Cross-references: GB:564596; NID:9407589; PIDN:AAB27856.1; PID:9407590  
 A:Note: sequence extracted from NCBI backbone (NCBI:136444, NCBI:136445)  
 A:Note: does not represent an experimentally determined sequence but three different  
 A:Accession: B47426  
 A:Molecule type: mRNA  
 A:Residues: 1179-1464 <CH4>  
 A:Experimental source: normal dermal fibroblast culture  
 A:Accession: C47426  
 A:Molecule type: mRNA  
 A:Residues: 1179-1276, 'H', 1278-1464 <CH5>  
 A:Experimental source: fetal cell 86-237  
 A:Accession: D47426  
 A:Molecule type: mRNA  
 A:Residues: 1179-1336, 1339-1464 <CH6>  
 A:Experimental source: fetal cell 86-146  
 A:Accession: E47426  
 A:Molecule type: mRNA  
 A:Residues: 1179-1387, 'R', 1389-1464 <CH7>  
 A:Experimental source: fetal cell 88-251  
 R:Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.;  
 J. Biol. Chem. 263, 14605-14607, 1988  
 A:Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide  
 A:Reference number: I52699; MUID:89008319; PMID:3170557  
 A:Accession: I52699  
 A:Molecule type: DNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 1187-1194, 'C', 1196-1220 <COH>  
 A:Cross-references: GB:M23213; NID:9340842; PIDN:AAB59363.1; PID:9409622  
 A:Note: mutant sequence from a patient with mild osteogenesis imperfecta  
 R:Meekelae, J.K.; Raassna, M.; Virta, A.; Vuorio, E.  
 Nucleic Acids Res. 16, 349, 1988  
 A:Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.

Query Match 9.1%; Score 118.5; DB 1; Length 1464;  
 Best Local Similarity 36.3%; Pred. No. 0.028;  
 Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;  
 Oy 3 PGGNAA--PQRKGLLLLLLQPPASASSEIKGKQKQKLRREYVDYLNKGCLOGPA 60  
 DB 357 PGGGSGGGGGGGG-----EPGPG-----PAG-----AAGPA 385  
 Oy 61 GVGPRDSSPGANVPTGPIRGDRGFGKGG 91

DB 386 GNPAGDGPAGKANGACBACIAGAPFPFGK 416

RESULT 5  
T29031  
hypothetical protein F53612.7 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T29031  
R:Wu, X.; Graves, T.  
submitted to the EMBL Data Library, May 1997  
A:Description: The sequence of *C. elegans* cosmid F53612.  
A:Reference number: Z20555  
A:Accession: T29031  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-327 <MUX>  
A:Cross-references: EMBL:AF003139; PIDN:AA54156.1; GSPDB:GN00019; CESP:F53612.7  
A:Experimental source: strain Bristol N2; clone F53612  
A:Genetics:  
A:Gene: CESP:F53612.7  
A:Map position: 1  
A:Introns: 59/3; 138/1; 223/2  
A:Superfamily: unassigned collagens

Query Match 9.0%; Score 117; DB 2; Length 327;  
Best Local Similarity 33.3%; Pred. No. 0.0069;  
Matches 31; Conservative 2; Mismatches 22; Indels 38; Gaps 3;

OY 1 MRPGPASPQRRLGILLLLQLPAPSSASEIPKQKAKQAKQREVVDLYGMKLGCPA 60  
|||||  
DB 261 MGPGRP-----PGPRG-----PGKQCA-----GGRK 282

OY 61 GVPGRDGSFGANVDPETPIGRDGFKEGKGC 93  
|||||  
DB 283 GAPGDGNGPGRPGKPGPGAPGPDGSAGEKGC 315

RESULT 6  
A55267  
collagen alpha 5(IV) chain - dog (fragment)  
C:Species: *Canis lupus familiaris* (dog)  
C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 13-Aug-1999  
C:Accession: A55267  
R:Zheng, K.; Thorne, P.S.; Marrano, P.; Bauman, R.; McInnes, R.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3989-3993, 1994  
A:Title: Canine x chromosome-linked hereditary nephritis: a genetic model for human X-11  
en type IV.  
A:Reference number: A55267; MUID:94224868; PMID:8171024  
A:Accession: A55267  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-754 <ZHE>  
A:Cross-references: GB:U07888; NID:9469547; PIDN:AA560258.1; PID:9469548  
C:Superfamily: collagen alpha 1(IV) chain

Query Match 9.0%; Score 117; DB 2; Length 754;  
Best Local Similarity 34.4%; Pred. No. 0.018;  
Matches 33; Conservative 7; Mismatches 34; Indels 22; Gaps 4;

OY 3 PGGPASPQRRLGILLLLQLPAPSSASEIP-----KQKQ--KAQLRQREVVDLYGMK 55  
|||||  
DB 332 PGGPGRP-----GLPGDEGRGLGNGKIGKEKNGPQPGQPLGLKGD-- 377

OY 56 LQGPAGVPRDGSFGANVDPETPIGRDGFKEGKGC 91  
|||||  
DB 378 -QGPPIQGNPGRPGLNGMKGDPGLPGVGFPGFMKG 412

RESULT 7  
S28791  
collagen alpha 1(XI) chain - chicken (fragment)

C:Species: *Gallus gallus* (chicken)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Aug-1999  
C:Accession: S28791  
R:Nah, H.D.; Barembaum, M.; Upholt, W.B.  
J. Biol. Chem. 267, 22581-22586, 1992  
A:Title: The chicken alpha1(XI) collagen gene is widely expressed in embryonic tissue  
A:Reference number: S28791; MUID:93054557; PMID:1429607  
A:Accession: S28791  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-888 <NAH>  
A:Cross-references: EMBL:M88593; NID:9211619; PIDN:AAA48707.1; PID:9211620  
C:Superfamily: collagen alpha 1(IV) chain; fibrillar collagen carboxyl-terminal homolo  
F:665-887//Domain: fibrillar collagen carboxyl-terminal homology <CC>

Query Match 8.9%; Score 116; DB 2; Length 888;  
Best Local Similarity 34.1%; Pred. No. 0.027;  
Matches 31; Conservative 4; Mismatches 20; Indels 36; Gaps 3;

OY 3 PGGPAA--SPQRRLGILLLLQLPAPSSASEIPKQKAKQAKQREVVDLYGMKLGCPA 60  
|||||  
DB 479 PGGPAGKPGPEGLRGI-----PGVGE-----QGIP 504

OY 61 GVPGRDGSFGANVDPETPIGRDGFKEGKGC 91  
|||||  
DB 505 GAPGDGPPGHLGPPGLPELKGDPGSKGKGC 535

RESULT 8  
CGH038  
collagen alpha 3(IV) chain precursor, long splice form - human  
N:Alternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice for  
C:Species: *Homo sapiens* (man)  
C>Date: 28-Oct-1994 #sequence\_revision 03-Oct-1995 #text\_change 22-Jun-1999  
C:Accession: A54763; A43928; A44043; A45971; A39786  
R:Maruyama, M.; Leinonen, A.; Mochizuki, T.; Trygvason, K.; Reeder, S.T.  
J. Biol. Chem. 269, 23013-23017, 1994  
A:Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpress  
A:Reference number: A54763; MUID:94364994; PMID:8083201  
A:Accession: A54763  
A:Molecule type: mRNA  
A:Residues: 1-1670 <MAR>  
A:Cross-references: GB:X80031; NID:9577563; PID:9577564  
A:Experimental source: kidney  
R:Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.D.  
J. Clin. Invest. 89, 592-601, 1992  
A:Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the  
A:Reference number: A43928; MUID:92147878; PMID:1737849  
A:Accession: A43928  
A:Molecule type: mRNA  
A:Residues: 1331-1524, '1', 1526-1670 <TUR>  
A:Cross-references: GB:M81379  
A:Experimental source: kidney  
R:Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.  
J. Biol. Chem. 267, 19780-19784, 1992  
A:Title: Exon/Intron structure of the human alpha 3(IV) gene encompassing the Goodpas  
A:Reference number: A44043; MUID:93015826; PMID:1400291  
A:Accession: A44043  
A:Molecule type: DNA; mRNA  
A:Residues: 1386-1670 <OUT>  
A:Cross-references: GB:M92993; NID:9177895; PIDN:AAA21610.1; PID:9177896  
A:Note: sequence extracted from NCBI backbone (NCBI:115597)  
R:Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.  
J. Biol. Chem. 269, 17358, 1994  
A:Reference number: A44738; MUID:94274734; PMID:8006044  
A:Contents: annotation: erratum: correction to intronic sequence in A44043  
R:Bernal, D.; Quinones, S.; Saus, J.  
J. Biol. Chem. 268, 12090-12094, 1993  
A:Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.  
A:Reference number: A45971; MUID:93280184; PMID:8505332  
A:Accession: A45971  
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1427-1444 <BER>  
A:Note: Sequence extracted from NCBI backbone (NCBI:P133363); sequence incorrectly identified as: 1427-1444 <BER>  
R:Morrisson, K.E.; Matiyama, M.; Yang-Feng, T.L.; Reeders, S.T.  
Am. J. Hum. Genet. 49, 545-554, 1991  
A:Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain of A:Reference number: A39786; MUID:91353570; PMID:1862840  
A:Accession: A39786  
A:Molecule type: mRNA  
A:Residues: 1453-1593, 'A', 1595-1670 <MOR>  
A:Cross-references: GB:S55790; NID:9234418; PIDN:AA19637.1; PID:9234419  
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit (ed and subsequently O-glycosylated).  
C:Comment: In Goodpasture's syndrome, an autoimmune response develops against an epitope C:Genetics:  
A:Gene: GDB:COL4A3  
A:Cross-references: GDB:128351; OMIM:120070  
A:Map position: 2q36-2q37  
A:Insertions: 1385/1, 1418/1, 1488/1, 1547/2; 1585/3; 1643/2 #status incomplete  
A:Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strands with C:Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 3 monomer amino-terminal domains (with disulfide and desmosine cross-links), dimeric dimer associations in the interrupted helical domain (with disulfide and desmosine cross-links) C:Function:  
A:Description: minor structural component of extracellular basement membrane in kidney  
C:Superfamily: collagen alpha 1(IV) chain  
C:Keywords: alternative splicing; basement membrane; cell binding; coll; coll; extracel F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>  
F:29-42/Domain: amino-terminal nonhelical, NHI <NHI>  
F:43-1438/Region: Interrupted helical  
F:91-793/Region: cell attachment (R-G-D) motif  
F:996-998/Region: cell attachment (R-G-D) motif  
F:1154-1156/Region: cell attachment (R-G-D) motif  
F:1306-1308/Region: cell attachment (R-G-D) motif  
F:1345-1347/Region: cell attachment (R-G-D) motif  
F:1432-1434/Region: cell attachment (R-G-D) motif  
F:1439-1670/Domain: carboxyl-terminal nonhelical, NCI <NCI>  
F:1451-1551/Domain: collagen IV carboxyl-terminal repeat <CTR>  
F:1561-1665/Domain: collagen IV carboxyl-terminal repeat <CTR>  
F:31, 33, 39, 41, 125, 422, 476, 479, 682, 722, 809, 1387/Disulfide bonds: Interchain #status predicted  
F:253/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:1460-1548, 1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted  
F:1505-1511, 1616-1622/Disulfide bonds: #status predicted  
F:1570-1662, 1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted

Query Match 8.9%; Score 116; DB 1; Length 1670;  
Best Local Similarity 35.1%; Pred. No. 0.055;  
Matches 33; Conservative 6; Mismatches 37; Indels 18; Gaps 3;  
OY 5 GPASPORTLGLLLLLLPAPSSASEIPKROKALROREVVLDYNGMCLGPAGVP 64  
Db 467 GPKGEP-----GLCTGCPYIPGPPGLGLPGLGHSVGIPR-----GGAAGLKG 511  
OY 65 RQSGPAGNIPGPIPGKD---GFGKGECLR 95  
Db 512 SPSPGNTGLPFPFGPAGGDPGLKGEKGTQL 545  
RESULT 9  
CGH4B  
collagen alpha 1(IV) chain precursor - human  
N:Alternate names: procollagen alpha 1(IV) chain  
C:Species: Homo sapiens (man)  
C:Date: 28-May-1986 #sequence, revision 31-Dec-1992 #text, change 07-Dec-1999  
C:Accession: S16876; A32117; S02738; S00048; S25826; A23115; S00207; S39614; A02863; A58  
R:Solinen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Tryggvason, K.  
J. Biol. Chem. 264, 13565-13571, 1989  
A:Title: Structural organization of the gene for the alpha-1 chain of human type IV coll  
A:Reference number: S16876; MUID:89340433; PMID:2701944  
A:Accession: S16876  
A:status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 1-1669 <SO11>  
A:Cross-references: EMBL:J04217; GB:J05039; NID:9180800; PIDN:AAA53098.1; PID:9180803  
A:Note: The nucleotide sequence was submitted to the EMBL data library, October 1988  
R:Solinen, R.; Huotari, M.; Hostikka, S.L.; Prockop, D.J.; Tryggvason, K.  
J. Biol. Chem. 263, 17217-17220, 1988  
A:Title: The structural genes for alpha1 and alpha2 chains of human type IV collagen  
A:Reference number: A92690; MUID:89034231; PMID:3182844  
A:Accession: A32117  
A:Molecule type: DNA  
A:Residues: 1-28 <SO12>  
A:Cross-references: EMBL:J04217; NID:9180759; PIDN:AAA53097.1; PID:9553233  
R:Poeschl, E.; Pollner, R.; Kuehn, K.  
EMBO J. 7, 2687-2695, 1988  
A:Title: The genes for the alpha1(IV) and alpha2(IV) chains of human basement membran  
A:Reference number: S02738; MUID:89030632; PMID:2846280  
A:Accession: S02738  
A:status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-6, 'L', '8'-28 <POE>  
A:Cross-references: EMBL:X12784; NID:930072  
R:Brazel, D.; Oberhauser, I.; Dierlinger, H.; Babel, W.; Glanville, R.W.; Deutzmann, Eur. J. Biochem. 168, 529-536, 1987  
A:Title: Completion of the amino acid sequence of the alpha1 chain of human basement  
A:Reference number: S00048; MUID:88029471; PMID:3311751  
A:Accession: S00048  
A:Molecule type: mRNA  
A:Residues: 1-318, 'A', 320-944 <BRA1>  
A:Cross-references: EMBL:X05561; NID:930066; PIDN:CAA9075.1; PID:930067  
A:Accession: S25826  
A:Molecule type: protein  
A:Residues: 271-318, 'A', 320-554 <BRA2>  
R:Glanville, R.W.; Qian, R.O.; Siebold, B.; Ristell, J.; Kuehn, K.  
Eur. J. Biochem. 152, 213-219, 1985  
A:Title: Amino acid sequence of the N-terminal aggregation and cross-linking region (A:Reference number: A23115; MUID:86004708; PMID:4043082  
A:Accession: A23115  
A:Molecule type: protein  
A:Residues: 28-236, 'KE', 239-240, 'K', 242-243 <GLA>  
A:Experimental source: placenta  
A:Note: the amino end of the mature form is blocked  
R:Solinen, R.; Haka-Risku, T.; Prockop, D.J.; Tryggvason, K.  
FEBS Lett. 225, 188-194, 1987  
A:Title: Complete primary structure of the alpha(1)-chain of human basement membrane  
A:Reference number: S00207; MUID:88083584; PMID:3691802  
A:Accession: S00207  
A:Molecule type: mRNA  
A:Residues: 244-530 <SO13>  
A:Cross-references: EMBL:Y00706; NID:929548; PIDN:CAA68698.1; PID:929549  
R:Edle, J.A.; Goldik, R.; Mann, K.; Kuehn, K.  
EMBO J. 12, 4795-4802, 1993  
A:Title: The alpha-1-beta-1 integrin recognition site of the basement membrane collag  
A:Reference number: S39614; MUID:84038963; PMID:8223408  
A:Accession: S39614  
A:Molecule type: protein  
A:Residues: 371-554 <EBL>  
R:Babel, W.; Glanville, R.W.  
Eur. J. Biochem. 143, 545-556, 1984  
A:Title: Structure of human basement-membrane (type IV) collagen. Complete amino-acid  
A:Reference number: A02863; MUID:85003629; PMID:6434307  
A:Accession: A02863  
A:Molecule type: protein  
A:Residues: 534-718, 'D', 720-836, 'Y', 838-841, 'P', 843-903, 'O', 905-913, 'K', 915-997, 'K', 9  
A:Experimental source: placenta  
R:Glanville, R.W.; Rauter, A.  
Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981  
A:Title: Peptide fragments of human placental basement-membrane collagens showing inte  
A:Reference number: S16908; MUID:82005835; PMID:6792033  
A:Accession: A58517  
A:Molecule type: protein  
A:Residues: 534-537, 'G', 539, 'G', 541-542, 'X', 544-553, 1389-1405, 'XX', 1408-1409, 'X', 1411  
R:McWhright, R.S.; Benson, V.A.; Lovellio, K.T.; van der Nest, M.; Fietzek, P.P.  
Biochemistry 22, 4940-4948, 1983  
A:Title: Isolation and characterization of pepsin-solubilized human basement membrane





R;Seyer, J.M.; Kang, A.H.  
 Biochemistry 16, 1158-1164, 1977  
 A:Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide  
 A:Reference number: A90399; MUID:77134724; PMID:557335  
 A:Accession: A90399  
 A:Molecule type: protein  
 A:Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SE1>  
 A:Experimental source: liver  
 A:Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact  
 R;Seyer, J.M.  
 submitted to the Atlas, December 1977  
 A:Reference number: A94562  
 A:Accession: A94562  
 A:Molecule type: protein  
 A:Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SE2>  
 A:Experimental source: liver  
 A:Note: author submitted corrections to A90399  
 R;Hilwicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.  
 Am. J. Hum. Genet. 53, 62-70, 1993  
 A:Title: Parental somatic and germ-line mosaicism for a multexon deletion with unusual  
 ispring.  
 A:Reference number: 151868; MUID:93304430; PMID:8317500  
 A:Accession: 151868  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 186-194 <MIL>  
 A:Cross-references: GB:S62925; NID:g386425; PIDN:AAD13937.1; PID:g4261637  
 R;Chiodo, A.A.; Silience, D.O.; Cole, W.G.; Bateman, J.F.  
 Biochem. J. 311, 939-943, 1995  
 A:Title: Abnormal type III collagen produced by an exon-17 skipping mutation of the COL3  
 A:Reference number: 559511; MUID:96067614; PMID:7487954  
 A:Accession: 559511  
 A:Molecule type: mRNA  
 A:Residues: 302-423 <CH1>  
 A:Cross-references: GB:S79877; NID:g1195576; PIDN:AAB5615.1; PID:g1195577  
 R;Seyer, J.M.; Kang, A.H.  
 Biochemistry 17, 3404-3411, 1978  
 A:Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe  
 A:Reference number: A90414; MUID:79000343; PMID:687591  
 A:Accession: A90414  
 A:Molecule type: protein  
 A:Residues: 399-675, 'N', 677-727 <SE3>  
 A:Experimental source: liver  
 R;Lee, B.; Vitale, E.; Superli-Furga, A.; Steinmann, B.; Ramirez, F.  
 J. Biol. Chem. 266, 5256-5259, 1991  
 A:Title: G to T transversion at position +5 of a splice donor site causes skipping of th  
 A:Reference number: 155349; MUID:91161621; PMID:1672129  
 A:Accession: 155349  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 537-605 <LEE>  
 A:Cross-references: GB:M59112; NID:g180815; PIDN:AAA52041.1; PID:g180816  
 R;Seyer, J.M.; Mainardi, C.; Kang, A.H.  
 Biochemistry 19, 1583-1589, 1980  
 A:Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from ty  
 A:Reference number: A90438; MUID:80198282; PMID:6246925  
 A:Accession: A90438  
 A:Molecule type: protein  
 A:Residues: 728-895, 'A', 897-964 <SE4>  
 A:Experimental source: liver  
 R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan  
 J. Biol. Chem. 265, 17070-17077, 1990  
 A:Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping an  
 A:Reference number: A38303; MUID:91009133; PMID:2145268  
 A:Accession: A38303  
 A:Molecule type: mRNA  
 A:Residues: 861-1015 <COL>  
 A:Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:g  
 A:Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos sy  
 R;Manoo, B.S.; Dalgleish, R.  
 Nucleic Acids Res. 16, 2337, 1988  
 A:Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.  
 A:Reference number: 502119; MUID:88189827; PMID:3357782

A:Accession: 502119  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>  
 A:Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054  
 R;Seyer, J.M.; Kang, A.H.  
 Biochemistry 20, 2621-2627, 1981  
 A:Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from  
 A:Reference number: A90446; MUID:81208139; PMID:7016180  
 A:Accession: A90446  
 A:Molecule type: protein  
 A:Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 11  
 A:Experimental source: liver  
 R;Loidl, H.R.; Brinker, J.M.; May, M.; Phlajaniemi, T.; Morrow, S.; Rosenbloom, J.;  
 Nucleic Acids Res. 12, 9383-9394, 1984  
 A:Title: Molecular cloning and carboxyl-propeptide analysis of human type III procoll  
 A:Reference number: A93551; MUID:85087944; PMID:6096827  
 A:Accession: A93551  
 A:Molecule type: mRNA  
 A:Residues: 1065-1155, 'P', 1157-1466 <LO1>  
 A:Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1  
 R;Miskulin, M.; Dalgleish, R.; Kluge-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Br  
 Biochemistry 25, 1408-1413, 1986  
 A:Title: Human type III collagen gene expression is coordinately modulated with the t  
 A:Reference number: 152393; MUID:86187804; PMID:3754462  
 A:Accession: 152393  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1161-1200 <MIS>  
 A:Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416  
 R;Emmanuel, B.S.; Camilizaro, L.A.; Seyer, J.M.; Myers, J.C.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985  
 A:Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long  
 A:Reference number: 159025; MUID:85216505; PMID:3858826  
 A:Accession: 159025  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1165-1196 <EMA>  
 A:Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418  
 R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sipola, M.; Ramirez, F.  
 J. Biol. Chem. 260, 4357-4363, 1985  
 A:Title: Isolation of cDNA and genomic clones encoding human pro-alpha(III) collagen  
 A:Reference number: A92516; MUID:85157600; PMID:257949  
 A:Accession: A92516  
 A:Molecule type: DNA  
 A:Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU>  
 A:Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797;  
 A:Experimental source: liver  
 A:Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons give  
 ation  
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit  
 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequent  
 C:Genetics:  
 A:Gene: GDB:COL3A1  
 A:Cross-references: GDB:118729; OMIM:120180  
 A:Map position: 2q31-2q31  
 A:Intons: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/3; 1337/3; 141  
 A:Note: the list of introns is incomplete; defects in this gene can result in Ehlers-  
 C:Complex: type III collagen is a homotrimer of monomers initially linked by disulfid  
 er of their length, is formed with desmosine cross-links made from lysine and allysin  
 C:Function:  
 A:Description: structural component of extracellular fibrous polymer that maintains 1  
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo  
 C:Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein;  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-153/Domain: amino-terminal propeptide #status predicted <PRO>  
 F:31-91/Domain: von Willebrand factor type C repeat homology <WVC>  
 F:154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>  
 F:154-167/Region: amino-terminal nonhelical telopeptide  
 F:168-1196/Region: helical  
 F:1091-1093/Region: cell attachment (R-G-D) motif  
 F:1197-1221/Region: carboxyl-terminal nonhelical telopeptide  
 F:1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>

F:1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>  
 F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 F:153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted  
 F:154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 F:161/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 F:263/284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental  
 F:263/Binding site: carboxylate (Lys) (covalent) #status experimental  
 F:584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental  
 F:948-949/Cleavage site: Gly-Ile (collagenase) #status experimental  
 F:1106/Binding site: carboxylate (Lys) (covalent) #status predicted

Query Match 8.8%; Score 115; DB 1; Length 1466;  
 Best Local Similarity 36.1%; Pred. No. 0.058;  
 Matches 39; Conservative 8; Mismatches 47; Indels 14; Gaps 5;

OY 22 LQLPAPSSASEIPKQKQALRQREVLDY--NGMCLQPGAGVPRGDSPGANVTPGPG 79  
 DB 72 LDCFPF---EIPEGECVAVCPQPTAPTRPPNGCGPGKDPGPPIGPNBPPG 127

OY 80 IPRGDFGKGEKLESEF---EESWTPNYKQCSMSLNYGDLGKIA 124  
 DB 128 QPGSPGSPGPPGIC--ESCPTGPONYSPDYSDYKVS---GVAVGGLA 170

## RESULT 11

collagen alpha 2(IV) chain precursor - pig roundworm  
 C:Species: Ascaris suum (pig roundworm)  
 C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 13-Aug-1999  
 C:Accession: S16366  
 R:Pettili, J.; Kingston, I.B.  
 J. Biol. Chem. 266, 16149-16156, 1991

A:Title: The complete primary structure of a nematode alpha-2(IV) collagen and the partial reference number: S16366; MUID:91340768; PMID:1714907  
 A:Accession: S16366  
 A:Molecule type: mRNA  
 A:Residues: 1-1763 <DB1>  
 A:Cross-references: GB:M67507; NID:g159648; PIDD:AA18014.1; PTD:g159649  
 C:Genetics:  
 A:Introns: 229/3; 266/3; 305/3; 360/3; 424/1; 489/1; 548/1; 656/3; 790/1; 891/1; 963/1;  
 C:Superfamily: collagen alpha 1(IV) chain  
 C:Keywords: alternative splicing; basement membrane; cell binding; collod coll; disulfide  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-1763/Product: collagen alpha 2(IV) chain #status predicted <MAT>  
 F:27-42/Domain: non-collagenous NH1 #status predicted <NH1>  
 F:43-1529/Domain: collagenous #status predicted <COI>  
 F:1530-1763/Domain: cell attachment (R-G-D) motif  
 F:1530-1763/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <NC1>  
 F:1530-1638/Domain: repeat NC1 #status predicted <NC12>  
 F:1639-1763/Domain: repeat NC1 #status predicted <NC12>  
 F:31,34,39,41,536,539/Dsulfide bonds: Interchain #status predicted  
 F:126/Binding site: carboxylate (asn) (covalent) #status predicted  
 F:1593-1599,1702-1709/Dsulfide bonds: #status predicted

Query Match 8.8%; Score 115; DB 2; Length 1763;  
 Best Local Similarity 25.4%; Pred. No. 0.072;  
 Matches 66; Conservative 24; Mismatches 94; Indels 76; Gaps 16;

OY 5 GPASPQRRLGILLILLQLLPAPSSASEIPKQKQALRQREVLDYNGMCLQGPAGV 62  
 DB 1449 GPMGAP-GIREKGLPGDGLPGPSG---PPGAGAGR-----DGPQPGMGEGGA 1498

OY 63 PGRGSPGANVTPGTPGIPGKDGKGEKLESEF---EESWTPNYKQCS-----W- 111  
 DB 1499 PGLGFPGEIGIPGIPGIPGSPGPGPGPGPKDGLLVKHSQTSSEVQCPGAWKWDG 1558

OY 112 -----SSLNYGIDGKIAECFTKRSNSALRYLESSSLRLKCRAC-----COR 156  
 DB 1559 YSLIYIEGNEKSHMODJGHAGSC---LSRSTMPFLE---CDVNVAVYASRNDKSY 1609

OY 157 WYTFNGAECGAPLIEAIIIDGSPEMNSTINIHRTSVEGLCEGIGAGLVDY---AI 213  
 DB 1610 WLST-----TAPTPMNV-----SEGGIEPIYSKAVCEA-PANVIVVHSQTI 1651

OY 214 WYTCSDYPKGDASTGMNSV 233  
 DB 1652 QIPNCPN-----GWNLSL 1663

## RESULT 12

hypothetical protein F59E12.12 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 24-Nov-1999  
 C:Accession: T15268  
 R:Johnson, D.  
 Submitted to the EMBL Data Library, May 1997  
 A:Description: The sequence of C. elegans cosmid F59E12.  
 A:Reference number: 218318  
 A:Accession: T15268  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-311 <JOB>  
 A:Cross-references: EMBL:AF003386; NID:g2088833; PTD:g2088834; PIDD:AA54250.1; GSPDB  
 A:Experimental source: strain Bristol N2; clone F59E12  
 C:Genetics:  
 A:Gene: CESP:F59E12.12  
 A:Map position: 2  
 A:Introns: 24/2  
 C:Superfamily: unassigned collagens

Query Match 8.8%; Score 114.5; DB 2; Length 311;  
 Best Local Similarity 51.1%; Pred. No. 0.011;  
 Matches 23; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

OY 53 GWC-----LQGPAGVPRGDSPGANVTPGTPGIPGKDGKGEK 92  
 DB 227 GKCEVNAVAGPSPGPGIPGDPGLGTGPNQDDEGCPAGE 271

## RESULT 13

hypothetical protein W05B2.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T26185  
 R:Gardner, A.  
 Submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z20166  
 A:Accession: T26185  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-304 <WIL>  
 A:Cross-references: EMBL:Z81138; PIDD:CA803475.1; GSPDB:GNO0021; CESP:W05B2.1  
 A:Experimental source: clone W05B2  
 C:Genetics:  
 A:Gene: CESP:W05B2.1  
 A:Map position: 3  
 A:Introns: 27/3  
 C:Superfamily: unassigned collagens

Query Match 8.8%; Score 114; DB 2; Length 304;  
 Best Local Similarity 31.9%; Pred. No. 0.012;  
 Matches 29; Conservative 5; Mismatches 25; Indels 32; Gaps 2;

OY 3 PGPASPQRRLGILLILLQLLPAPSSASEIPKQKQALRQREVLDYNGMCLQGPAGV 62  
 DB 227 PGP-----PPGASPGAPGPGGAG-----APGKGP 254

OY 63 PGRGSPGANVTPGTPGIPGKDGKGEKGEK 93  
 DB 255 SGAPGQPGADNPGAPGPGGSGAGKGC 285

## RESULT 14

T26184



hypothetical protein W05B2.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: J76184  
R:Gardner, A.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z20156  
A:Accession: J76184  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-304 <WIL>  
A:Cross-references: EMBL:Z81138; PIDB:CA803474.1; GSPDB:GN00021; CESP:W05B2.6  
A:Experimental source: clone W05B2  
C:Genetics:  
A:Gene: CESP:W05B2.6  
A:Map position: 3  
A:Introns: 27/3  
C:Superfamily: unassigned collagens

Query Match	8.8%	Score 114;	DB 2;	Length 304;
Best Local Similarity	31.9%	Pred. NO. 0.012;		
Matches	29;	Conservative	5;	Mismatches 25;
			Indels	32;
			Gaps	2;
OY	3	PGGPAASQRKRLGILLILLIDLPAPSSASELPKQKQKQLQREYVDLNGMCTGAPGVC	62	
Db	227	PGGG-----PGAGGPGAGGGGGQG-----APGPGP	254	
OY	63	PGRDGSPGANYIPGTPGIGRGDGFKEGEGEC	93	
Db	255	SGAGGQPCADNPGAPGQPGSGGAGEGIC	285	

**RESULT 15**

522917  
collagen alpha 5(IV) chain precursor, renal splice form - human  
N:Alternate names: procollagen alpha 5(IV) chain  
N:Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence.revision 27-Feb-1997 #text.change 21-Jul-2000  
C:Accession: S22917; A54365; A57079; A37122; I54317; A34850; S18850; I56971; I76598; A37122

R:Zhou, J.; Hertz, J.M.; Leinonen, A.; Tryggvason, K.  
J. Biol. Chem. 267, 12475-12481, 1992

A:Title: Complete amino acid sequence of the human alpha-5(IV) collagen chain and identical syntenic protein.

A:Reference number: S22917; MUID:92316923; PMID:1352287

A:Accession: S22917

A:Molecule type: mRNA

A:Residues: 1-967 <ZH0>

A:Cross-references: GB:M90464; NID:g180826; PIDN:AAA52046.1; PID:g553234

R:Zhou, J.; Leinonen, A.; Tryggvason, K.  
J. Biol. Chem. 269, 6608-6614, 1994

A:Title: Structure of the human type IV collagen COLA5 gene.

A:Reference number: A54365; MUID:94165049; PMID:8120014

A:Accession: A54365

A:Molecule type: DNA

A:Residues: 1-922 <ZH2>

A:Cross-references: GB:U04470; NID:g463378; GB:U04520; NID:g463428; PIDN:AAC27816.1; PIDN:R12001

R:Zhou, J.; Mochiwaki, T.; Smets, H.; Allignac, C.; Laurila, P.; de Raeye, A.; Tryggvason, K.  
Science 261, 1167-1169, 1993

A:Title: Deletion of the paired alphas(IV) and alpha6(IV) collagen genes in inherited syndrome of osteogenesis imperfecta.

A:Reference number: A57079; MUID:93361972; PMID:8356449

A:Accession: A57079

A:Molecule type: DNA

A:Residues: 1-27 <ZH4>

A:Cross-references: GB:I237153; NID:g587203; PIDN:CAA85512.1; PID:g587204

R:Pihlajaniemi, T.; Pohjolainen, E.R.; Myers, J.C.  
J. Biol. Chem. 265, 13758-13766, 1990

A:Title: Complete primary structure of the triple-helical region and the carboxyl-terminal half of the human alpha-5(I) collagen gene.

A:Reference number: A37122; MUID:90337990; PMID:2380186

A:Accession: A37122

A:Molecule type: mRNA

A:Residues: 84-439; GS', 442-624, 'TALO', 629-666, 'FR', 669-887, 'R', 889-1264, 1271-1691 <PIH>

A:Cross-references: GB:U05558; EMBL:M58526; NID:g1314209

A:Note: submitted to the EMBL Data Library, February 1991  
A:Note: the authors translated the codon GCC for residue 115 as Val  
R:Reichert, A.; Seftl, M.; Myers, J.C.; Philajantemi, T.; Massella, L.; Rizzoni, G.; De Hum, M.O. Genet. 1, 127-129, 1992  
A:Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid  
A:Reference number: 154317; MUID:93244772; PMID:1363760  
A:Accession: 154317  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 313-324, 'E', 326-330 <REN>  
A:Cross-references: GB:S59334; NID:g2929946; PIDN:AAD13909.1; PID:g4261609  
R:Hostalka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyge, M.; Shows, T.B.; Tryggyvason, K. Proc. Natl. Acad. Sci. U.S.A. 87, 1606-1610, 1990  
A:Title: Identification of a distinct type IV collagen alpha chain with restricted ki  
A:Reference number: A34850; MUID:90160375; PMID:16894931  
A:Accession: A34850  
A:Molecule type: mRNA  
A:Residues: 914-1264, 1271-1691 <HOS>  
A:Cross-references: EMBL:M31115; NID:G180824; PIDN:AA52045.1; PID:g180825  
R:Zhu, J.; Hostalka, S.L.; Chow, L.T.; Tryggyvason, K. Genomics 9, 1-9, 1991  
A:Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene t  
A:Reference number: A37969; MUID:91169491; PMID:2004755  
A:Accession: 518850  
A:Molecule type: DNA  
A:Residues: 924-1264, 1271-1691 <ZHU>  
A:Cross-references: EMBL:M63455; EMBL:M63456; EMBL:M63457; EMBL:M63458; EMBL:M63459; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:g177922; PIDN:AA51558.1; R:Guo, C.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Berghe, H.; Cassiman, J.J. Kidney Int. 44, 1316-1321, 1993  
A:Title: Differential splicing of COL4A5 mRNA in kidney and white blood cells: a comp  
A:Reference number: I56971; MUID:94133540; PMID:8301933  
A:Accession: 156971  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1258-1276 <GUO1>  
A:Cross-references: GB:S69168; NID:g545095; PIDN:AAC60612.1; PID:g545096  
A:Note: kidney splice form  
A:Accession: 176598  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1284-1291, 'MFLGACLV' <GUO2>  
A:Cross-references: GB:S69169; NID:g545097; PIDN:AAC60613.1; PID:g545098  
A:Note: frameshift mutation in patient with Alport syndrome  
R:Myers, J.C.; Jones, T.A.; Pohjolahti, E.R.; Kadri, A.S.; Goddard, A.D.; Sheer, D.; Am. J. Hum. Genet. 46, 1024-1033, 1990  
A:Title: Molecular cloning of alpha5(IV) collagen and assignment of the gene to the r  
A:Reference number: A35335; MUID:90252791; PMID:2339659  
A:Accession: A35335  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1448-1477 <MYE>  
R:Nakazoto, H.; Battlori, S.; Ushijima, T.; Matsuur, T.; Koltabshl, Y.; Takada, T.; Kidney Int. 46, 1307-1314, 1994  
A:Title: Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in prim  
A:Reference number: I56975; MUID:95156893; PMID:7853788  
A:Accession: 156975  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1595-1602 <NAK>  
A:Cross-references: GB:S75903; NID:g913882; PIDN:AAB33374.1; PID:g913883  
A:Note: premature termination mutation from a patient with Alport syndrome; one other  
R:Lemlik, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Tryggyvason, K. Genomics 17, 485-489, 1993  
A:Title: Identification of four novel mutations in the COL4A5 gene of patients with A  
A:Reference number: I54188; MUID:94010948; PMID:8406458  
A:Accession: 154188  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1604-1607, 'VHDAKVC' <LEM>  
A:Cross-references: GB:S65767; NID:g425563; PIDN:AAD13967.1; PID:g4261667  
A:Note: frameshift mutation from a patient with Alport syndrome; five other mutations  
A:Comment: Prolines and lysines at the third position of the tripeptide repeating uni

ed and subsequently O-glycosylated.

C:Genetics:

A:Gene: GDB:COL4A5; ATR

A:Cross-references: GDB:120596; OMIM:303630

A:Map position: Xq22-Xq22

A:Introns: 27/3; 47/3; 77/3; 92/3; 107/3; 128/3; 146/3; 155/3; 182/3; 203/3; 215/3; 229/3; 799/1; 837/1; 893/1; 923/1; 973/1; 1006/1; 1036/1; 1082/3; 1125/1; 1152/1; 1185/1

A:Note: the alpha 5(IV) and alpha 6(IV) chain genes are encoded on opposite strands with

C:Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 5

monomer amino-terminal domains (with disulfide and desmosine cross-links), dimeric

er associations in the interrupted helical domain (with disulfide and desmosine cross-

C:Function:

A:Description: minor structural component of extracellular basement membrane

C:Superfamily: collagen alpha 1(IV) chain

C:Keywords: Alport syndrome; basement membrane; coiled coil; extracellular matrix; glyco

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-1691/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <MAT1

F:27-1264,1271-1691/Product: collagen alpha 5(IV) chain, leukocyte splice form #status

F:27-41/Domain: amino-terminal nonhelical, NC2 #status predicted <NC2>

F:42-1462/Region: interrupted helical

F:1463-1691/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <NC1>

F:1473-1573/Domain: collagen IV carboxyl-terminal repeat <CT1>

F:1583-1687/Domain: collagen IV carboxyl-terminal repeat <CT2>

F:29,32,38,40,124,451,481,484/Disulfide bonds: Interchain #status predicted

F:125/Binding site: carbohydrate (asn) (covalent) #status predicted

F:1482-1570,1515-1573/Disulfide bonds: (or 1482-1573, 1515-1570) #status predicted

F:1527-1533,1638-1644/Disulfide bonds: #status predicted

F:1592-1684,1626-1687/Disulfide bonds: (or 1592-1687, 1626-1684) #status predicted

Query Match 8.8%; Score 114; DB 1; Length 1691;

Best Local Similarity 35.4%; Pred. No. 0.084;

Matches 34; Conservative 7; Mismatches 39; Indels 16; Gaps 4;

OY 3 PGPAA--SPQRLGLLILLQLPAPSSASEIP-----KGKQAQLRQREYVDLYNGMC 55

DB 1256 PGPGRDPGPTGFG-----LPGREGPGLPGNGIKG-EKGNPGOPGLPGLK 1306

OY 56 LOGPAGVGRDGPANYPGTPGIPGDRGKGEK 91

DB 1307 DOGPPGLQGNPGRGLNGKGDPLGVGPPGMRK 1342

Search completed: August 13, 2003, 13:28:06

Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:28:12 ; Search time 85 seconds  
(without alignments)  
453.771 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MRRQGPAPASPORTLRGILLIL.....GDASTGWSVSRITIEELPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 6

Total number of hits satisfying chosen parameters: 6118

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	100.0	243	21	AAV99441 Human PRO1755 (UNQ)
2	243	100.0	243	21	AAV99462 Human PRO1550 amln
3	243	100.0	243	22	AAU29206 Human PRO polypept
4	243	100.0	243	22	AAAB87586 Human PRO1550. Ho
5	243	100.0	243	22	AAAB66190 Protein of the inv
6	243	100.0	243	22	AAAB66211 Protein of the inv
7	243	100.0	243	23	ABP68636 Human pancreatic c
8	243	100.0	243	23	ABG95811 Human secreted/tra
9	243	100.0	243	23	ABG78938 Human breast tumou

10	243	100.0	243	23	ABB95545 Human angiogenesis
11	243	100.0	243	23	AAE20462 Human tumour-asso
12	243	100.0	243	23	ABB84939 Human PRO1550 prot
13	243	100.0	243	24	ABU71294 Human PRO1550 prot
14	243	100.0	243	24	ABU71566 Human secreted pol
15	243	100.0	243	24	ABU72012 Novel human secret
16	243	100.0	243	24	ABU72169 Human PRO polypept
17	243	100.0	243	24	ABU65751 Human secreted/tra
18	243	100.0	243	24	ABU66084 Novel human secret
19	243	100.0	243	24	ABU67588 Human secreted/tra
20	243	100.0	243	24	ABG75948 Human antigenic ta
21	243	100.0	243	24	ABU65446 Human PRO polypept
22	243	100.0	243	24	ABU37761 Human tumour-relat
23	243	100.0	243	24	ABU58582 Human PRO polypept
24	243	100.0	243	24	ABU56118 Human secreted/tra
25	243	100.0	243	24	ABU57113 Human PRO polypept
26	243	100.0	243	24	ABU10692 Human secreted/tra
27	243	100.0	278	23	ABP68637 Human pancreatic c
28	243	100.0	278	23	ABG78939 Human breast tumou
29	243	100.0	278	23	ABU37762 Human tumour-relat
30	197	81.1	197	23	ABG78940 Human breast tumou
31	197	81.1	197	23	ABU37763 Human tumour-relat
32	197	81.1	232	23	ABG78941 Human breast tumou
33	197	81.1	232	24	ABU37764 Human tumour-relat
34	170	70.0	210	23	ABG96339 Human ovarian canc
35	170	70.0	243	23	ABG36667 Human secretory pr
36	170	70.0	243	23	ABG96340 Human ovarian canc
37	170	70.0	243	23	ABJ05554 Breast cancer-asso
38	170	70.0	243	23	ABR80978 Human REMODELIN po
39	170	70.0	243	24	ABR48227 Human bladder canc
40	170	70.0	243	24	ABG75758 Human REMODELIN pr
41	170	70.0	243	24	ABU56607 Lung cancer-associ
42	170	70.0	276	20	AAW88934 Polypeptide fragme
43	170	70.0	276	20	ABBS1005 Human secreted pro
44	170	70.0	278	21	ABO8836 Amino acid sequenc
45	170	70.0	278	22	AAW25746 Human protein sequ

#### ALIGNMENTS

RESULT 1	AAV99441	standard; Protein; 243 AA.
XX	AAV99441	
AC	AAV99441:	
XX		
DT	08-AUG-2000	(first entry)
XX		
DE	Human PRO1755 (UNQ828)	amino acid sequence SPQ ID NO:352.
XX		
KW	Human: PRO polypeptide; membrane bound protein; receptor; diagnosis;	
KW	transmembrane; secretion; Immunoadhesion; Pharmaceutical; screening.	
OS	Homo sapiens.	
XX		
PN	W0200012708-A2.	
XX		
PD	09-MAR-2000.	
XX		
PF	01-SEP-1999;	99MO-US20111.
XX		
PR	01-SEP-1998;	98US-0098716.
PR	01-SEP-1998;	98US-0098749.
PR	01-SEP-1998;	98US-0098750.
PR	02-SEP-1998;	98US-0098803.
PR	02-SEP-1998;	98US-0098821.
PR	02-SEP-1998;	98US-0098843.
PR	09-SEP-1998;	98US-0099536.
PR	09-SEP-1998;	98US-0099596.
PR	09-SEP-1998;	98US-0099598.
PR	09-SEP-1998;	98US-0099602.
PR	09-SEP-1998;	98US-0099642.

```

PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 22-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.

PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106034.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108844.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108856.
PR 18-NOV-1998; 98US-0108904.

( GETH ) GENENTECH INC.
PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI: 2000-237871/20.
XX N-PSDB; AAA37123.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
XX secreted PRO polypeptides, useful for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 12; Fig 204; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding then have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
XX
XX Sequence 243 AA;
SO
Query Match 100.0%; Score 243; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 5,1e-220;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLGLLILLLILQLPAPSSASEIRKQKQKQALRQREVVDLYNGMCIQGA 60
DB 1 MRPOGPASPORLGLLILLLILQLPAPSSASEIRKQKQKQALRQREVVDLYNGMCIQGA 60
QY 61 GVPGRDGSFGANVITGPPIGPDGDFKGEKGECLRESFESWTNPKQCSWSSILNTYIDL 120

```

|||||  
Db 61 GVPGRDSDPGANVLPGPPIGRGPFGEKGEKLESESESWFTPNYKQCSMSLNYGIDL 120  
QY 121 GKIAECTFTKMRNSALRVLFSSGLRLKCRNACCORWFETNGACSGPLPIEATIIDQ 180  
Db 121 GKIAECTFTKMRNSALRVLFSSGLRLKCRNACCORWFETNGACSGPLPIEATIIDQ 180  
QY 181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMSVSRIITEE 240  
Db 181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMSVSRIITEE 240  
QY 241 LPK 243  
Db 241 LPK 243

RESULT 2  
AA99462  
ID AA99462 standard; Protein: 243 AA.  
XX  
AC AA99462;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Human PRO1550 amino acid sequence SEQ ID NO:431.  
XX  
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmacological; screening.  
OS Homo sapiens.  
XX  
PN WO200012708-A2.  
XX  
PD 09-MAR-2000.  
XX  
PE 01-SEP-1999; 99NO-US20111.  
XX  
PR 01-SEP-1998; 98US-0098716.  
PR 01-SEP-1998; 98US-0098749.  
PR 01-SEP-1998; 98US-0098750.  
PR 02-SEP-1998; 98US-0098803.  
PR 02-SEP-1998; 98US-0098821.  
PR 02-SEP-1998; 98US-0098843.  
PR 09-SEP-1998; 98US-0099536.  
PR 09-SEP-1998; 98US-0099596.  
PR 09-SEP-1998; 98US-0099598.  
PR 09-SEP-1998; 98US-0099602.  
PR 09-SEP-1998; 98US-0099642.  
PR 10-SEP-1998; 98US-0099741.  
PR 10-SEP-1998; 98US-0099754.  
PR 10-SEP-1998; 98US-0099792.  
PR 10-SEP-1998; 98US-0099808.  
PR 10-SEP-1998; 98US-0099812.  
PR 10-SEP-1998; 98US-0099815.  
PR 10-SEP-1998; 98US-0099816.  
PR 15-SEP-1998; 98US-0100385.  
PR 15-SEP-1998; 98US-0100388.  
PR 15-SEP-1998; 98US-0100390.  
PR 15-SEP-1998; 98US-0100584.  
PR 16-SEP-1998; 98US-0100627.  
PR 16-SEP-1998; 98US-0100661.  
PR 16-SEP-1998; 98US-0100662.  
PR 16-SEP-1998; 98US-0100664.  
PR 17-SEP-1998; 98US-0100683.  
PR 17-SEP-1998; 98US-0100684.  
PR 17-SEP-1998; 98US-0100710.  
PR 17-SEP-1998; 98US-0100711.  
PR 17-SEP-1998; 98US-0100919.  
PR 17-SEP-1998; 98US-0100930.  
PR 18-SEP-1998; 98US-0100848.  
PR 18-SEP-1998; 98US-0100849.  
PR 18-SEP-1998; 98US-0101014.

PR 18-SEP-1998; 98US-0101068.  
PR 18-SEP-1998; 98US-0101071.  
PR 22-SEP-1998; 98US-0101279.  
PR 23-SEP-1998; 98US-0101471.  
PR 23-SEP-1998; 98US-0101472.  
PR 23-SEP-1998; 98US-0101474.  
PR 23-SEP-1998; 98US-0101475.  
PR 23-SEP-1998; 98US-0101476.  
PR 23-SEP-1998; 98US-0101477.  
PR 23-SEP-1998; 98US-0101479.  
PR 24-SEP-1998; 98US-0101738.  
PR 24-SEP-1998; 98US-0101741.  
PR 24-SEP-1998; 98US-0101743.  
PR 24-SEP-1998; 98US-0101915.  
PR 24-SEP-1998; 98US-0101916.  
PR 29-SEP-1998; 98US-0102207.  
PR 29-SEP-1998; 98US-0102240.  
PR 29-SEP-1998; 98US-0102307.  
PR 29-SEP-1998; 98US-0102310.  
PR 29-SEP-1998; 98US-0102331.  
PR 30-SEP-1998; 98US-0102484.  
PR 30-SEP-1998; 98US-0102487.  
PR 30-SEP-1998; 98US-0102570.  
PR 30-SEP-1998; 98US-0102571.  
PR 01-OCT-1998; 98US-0102684.  
PR 01-OCT-1998; 98US-0102687.  
PR 02-OCT-1998; 98US-0102685.  
PR 06-OCT-1998; 98US-0103258.  
PR 06-OCT-1998; 98US-0103449.  
PR 07-OCT-1998; 98US-0103449.  
PR 07-OCT-1998; 98US-0103678.  
PR 07-OCT-1998; 98US-0103315.  
PR 07-OCT-1998; 98US-0103328.  
PR 07-OCT-1998; 98US-0103395.  
PR 07-OCT-1998; 98US-0103396.  
PR 07-OCT-1998; 98US-0103401.  
PR 08-OCT-1998; 98US-0103633.  
PR 08-OCT-1998; 98US-0103679.  
PR 08-OCT-1998; 98US-0103711.  
PR 08-OCT-1998; 98US-0104257.  
PR 14-OCT-1998; 98US-0104257.  
PR 20-OCT-1998; 98US-0104967.  
PR 20-OCT-1998; 98US-0105000.  
PR 20-OCT-1998; 98US-0105104.  
PR 21-OCT-1998; 98US-0105104.  
PR 22-OCT-1998; 98US-0105169.  
PR 22-OCT-1998; 98US-0105266.  
PR 26-OCT-1998; 98US-0105633.  
PR 26-OCT-1998; 98US-0105694.  
PR 27-OCT-1998; 98US-0105807.  
PR 27-OCT-1998; 98US-0105881.  
PR 27-OCT-1998; 98US-0105882.  
PR 27-OCT-1998; 98US-0106052.  
PR 28-OCT-1998; 98US-0106023.  
PR 28-OCT-1998; 98US-0106029.  
PR 28-OCT-1998; 98US-0106030.  
PR 28-OCT-1998; 98US-0106032.  
PR 28-OCT-1998; 98US-0106033.  
PR 28-OCT-1998; 98US-0106178.  
PR 29-OCT-1998; 98US-0106248.  
PR 29-OCT-1998; 98US-0106384.  
PR 29-OCT-1998; 98US-0108500.  
PR 30-OCT-1998; 98US-0106464.  
PR 03-NOV-1998; 98US-0106856.  
PR 03-NOV-1998; 98US-0106905.  
PR 03-NOV-1998; 98US-0106919.  
PR 03-NOV-1998; 98US-0106932.  
PR 03-NOV-1998; 98US-0106934.  
PR 10-NOV-1998; 98US-0107783.  
PR 17-NOV-1998; 98US-0108775.  
PR 17-NOV-1998; 98US-0108779.  
PR 17-NOV-1998; 98US-0108787.  
PR 17-NOV-1998; 98US-0108788.

XX	PA	(GETH ) GENENTECH INC.
XX	PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
XX	DR	WPI: 2000-237871/20.
XX	DR	N-PSDB; AAA37144.
XX	XX	New mammalian DNA sequences encoding transmembrane, receptor or
PT	secreted PRO polypeptides, useful for screening of potential peptide or	
PT	small molecule inhibitors of the relevant receptor/ligand interactions	
XX	PS	Claim 12; Fig 246; 773bp; English.
XX	CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC	receptor or secreted PRO polypeptides given in AA99340 to AA99462. The	
CC	transmembrane and receptor PRO proteins can be used for screening of	
CC	potential peptide or small molecule inhibitors of the relevant	
CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
CC	encoding them have various industrial applications, including uses as	
CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent	
CC	PCR primers and hybridisation probes used in the isolation of the PRO	
CC	polypeptides from the present invention.	
XX	SQ	Sequence    243 AA;
Query Match	100.0%; Score 243; DB 21; Length 243;	
Best Local Similarity	100.0%; Pred. No. 5.1e-220;	
Matches 243; Conservative	0; Mismatches 0; Indels	0; Gaps 0
OY	1	MRPGSPASPORLRRLRLLLILLILQLPAPSSASRIPKGGKAOLROREVDVLYNMCLOGPA 60
Db	1	MRPGSPASPORLRKLRLLLILLILQLPAPSSASRIPKGGKAOLROREVDVLYNMCLOGPA 60
OY	61	GVPGRDGPANVIPTGPIGRDFKGEGECLESEFESESWTPPNYKQCSWSLNYGIDL 120
Db	61	GVPGRDGPANVIRGTGPIGRDFKGEGECLESEFESESWTPPNYKQCSWSLNYGIDL 120
OY	121	GRIACECTTKRRSNALNVLFSGSLRLRCRNACCORRWTFTEFGAECSGPLPLEAIYYLDQ 180
Db	121	GRIACECTTKRRSNALRVLFSGSLRLCRNACCORRWTFTEFGAECSGPLPLEAIYYLDQ 180
OY	181	GSPENNSTINIHRTSVGELEGIGAGLVDAIVWGTCSDYRKDGASTGMNSVRITIE 240
Db	181	GSPENNSTINIHRTSVGELEGIGAGLVDAIVWGTCSDYRKDGASTGMNSVRITIE 240
OY	241	LPK 243
Db	241	LPK 243
RESULT 3		
ID	AAU29206	standard; Protein; 243 AA.
AC	AAU29206;	
DE	18-DEC-2001	(first entry)
DE	Human PRO polypeptide sequence #183.	

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US06520.  
 XX  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 29-MAR-2000; 2000US-193053P.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194443P.  
 PR 04-APR-2000; 2000US-194447P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196820P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-602746/68.  
 XX  
 DR N-PSDB; AAS46107.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 PS Claim 11; Fig 366; 774pp; English.  
 XX  
 CC Sequences AU29024-AU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of

CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.

SO Sequence 243 AA:

Query Match 100.0%; Score 243; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-220;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRQGPASPORLRLGLLLLLLPAPSSASEIPKQKQAKQREVVLYNGMCLQGPA 60  
 DB 1 MRQGPASPORLRLGLLLLLLPAPSSASEIPKQKQAKQREVVLYNGMCLQGPA 60  
 QY 61 GVPGRDPSGANVYIPGPIPGRDGFKGKGEKCELRSEFSWTPNTKQCSWSLNYGIDL 120  
 DB 61 GVPGRDPSGANVYIPGPIPGRDGFKGKGEKCELRSEFSWTPNTKQCSWSLNYGIDL 120  
 QY 121 GKIAECTFTKMRNSALRYLFFSGSLRLKCRNACCQWYFTFNGAECSGPLPIEATIIYLDQ 180  
 DB 121 GKIAECTFTKMRNSALRYLFFSGSLRLKCRNACCQWYFTFNGAECSGPLPIEATIIYLDQ 180  
 QY 181 GSEPMNSTINIHRTSSVEGLCEIGAGLDVAIWGTCSDPKGDASTGMNSVSRITIEE 240  
 DB 181 GSEPMNSTINIHRTSSVEGLCEIGAGLDVAIWGTCSDPKGDASTGMNSVSRITIEE 240  
 QY 241 LPK 243  
 DB 241 LPK 243

RESULT 4  
 AAB87586

ID AAB87586 standard; protein; 243 AA.

AC AAB87586;

DT 15-MAY-2001 (first entry)

DE Human PRO1550.

KW Human; PRO protein; mapping.

OS Homo sapiens.

PN WO200116318-A2.

PF 24-AUG-2000; 2000WO-US23328.

XX 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 07-DEC-1999; 99US-0169495.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 11-JAN-2000; 2000US-0175481.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 03-MAR-2000; 2000US-0187202.  
 PR 25-APR-2000; 2000US-0199397.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 05-JUN-2000; 2000US-0209832.  
 XX

PA (GETH ) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Matanabe CK, Wood WI;

DR WPI; 2001-183260/18.

DR N-PSDB; AAF92118.

PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
 PT molecular biology, including use as hybridization probes, and in  
 PT chromosome and gene mapping.

PS Claim 12; Fig 122; 278bp; English.

CC The present sequence is a human PRO polypeptide (secreted and  
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
 CC anti-PRO antibodies are useful for preparation of a medicament useful in  
 CC the treatment of a condition which is responsive to the PRO protein,  
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
 CC employed as molecular weight markers for protein electrophoresis. The PRO  
 CC coding sequence has applications in molecular biology, including use as  
 CC hybridisation probes, and in chromosome and gene mapping.

SO Sequence 243 AA:

Query Match 100.0%; Score 243; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-220;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRQGPASPORLRLGLLLLLLPAPSSASEIPKQKQAKQREVVLYNGMCLQGPA 60  
 DB 1 MRQGPASPORLRLGLLLLLLPAPSSASEIPKQKQAKQREVVLYNGMCLQGPA 60  
 QY 61 GVPGRDPSGANVYIPGPIPGRDGFKGKGEKCELRSEFSWTPNTKQCSWSLNYGIDL 120  
 DB 61 GVPGRDPSGANVYIPGPIPGRDGFKGKGEKCELRSEFSWTPNTKQCSWSLNYGIDL 120  
 QY 121 GKIAECTFTKMRNSALRYLFFSGSLRLKCRNACCQWYFTFNGAECSGPLPIEATIIYLDQ 180  
 DB 121 GKIAECTFTKMRNSALRYLFFSGSLRLKCRNACCQWYFTFNGAECSGPLPIEATIIYLDQ 180  
 QY 181 GSEPMNSTINIHRTSSVEGLCEIGAGLDVAIWGTCSDPKGDASTGMNSVSRITIEE 240  
 DB 181 GSEPMNSTINIHRTSSVEGLCEIGAGLDVAIWGTCSDPKGDASTGMNSVSRITIEE 240  
 QY 241 LPK 243  
 DB 241 LPK 243

RESULT 5

AAB66190

ID AAB66190 standard; protein; 243 AA.

AC AAB66190;

DT 02-APR-2001 (first entry)

DE Protein of the invention #102.

KW Secreted; transmembrane; gene therapy.

OS Unidentified.

PN WO200078961-A1.

PF 28-DEC-2000.

PR 18-FEB-2000; 2000WO-US04342.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.







PT	New isolated secreted and transmembrane PRO polypeptide useful for	XX
PT	modulating biological activity of a cell, or for treating	XX
PT	sports-related joint problems, osteoarthritis or rheumatoid arthritis	XX
XX	Claim 20; Fig 122; 399pp; English.	XX
CC	The invention relates to an isolated secreted and transmembrane PRO	CC
CC	polypeptide having 80 % sequence identity to a sequence appearing	CC
CC	as ABG9581-BG95934 or their associated signal peptide, or a sequence of	CC
CC	an extracellular domain of the proteins with their associated signal	CC
CC	peptide or lacking its associated signal peptide. Also included are	CC
CC	the nucleic acids encoding the proteins, vectors, host cells,	CC
CC	fusion proteins and antibodies which specifically bind to the proteins.	CC
CC	The proteins are useful for detecting a polypeptide designated as A, B, C	CC
CC	or D in a sample suspected of containing an A, B, C or D polypeptide,	CC
CC	by contacting the sample with a polypeptide designated as E, F, G, H or	CC
CC	I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H	CC
CC	or D/I polypeptide conjugate in the sample, where the formation of the	CC
CC	conjugate is indicative of the presence of an A, B, C or D polypeptide	CC
CC	in the sample, where A is a PRO10272 polypeptide, B is a PRO20110	CC
CC	polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,	CC
CC	E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040	CC
CC	polypeptide, H is a PRO20233 polypeptide and I is a PRO1890	CC
CC	polypeptide. The sample comprises a cell suspected of expressing the A,	CC
CC	B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with	CC
CC	a detectable label or is attached to a solid support. The proteins are	CC
CC	useful for linking a bioactive molecule to a cell expressing a	CC
CC	polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive	CC
CC	molecule is a toxin, a radiolabel or an antibody. The bioactive molecule	CC
CC	causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies	CC
CC	against them are useful for modulating a biological activity of a cell	CC
CC	expressing a polypeptide designated as A, B, C or D or E, F, G, H, or	CC
CC	I. The cell is killed. The proteins are useful for identifying	CC
CC	agonists or antagonists, for the preparation of a medicament useful in	CC
CC	the treatment of a condition which is responsive to the proteins, as	CC
CC	molecular weight markers for protein electrophoresis purposes, and as	CC
CC	therapeutic agents for treating sports-related joint problems,	CC
CC	articular cartilage defects, osteoarthritis or rheumatoid arthritis.	CC
CC	Nucleic acids encoding the proteins are useful as hybridisation probes,	CC
CC	in chromosome and gene mapping, in the generation of anti-sense RNA and	CC
CC	DNA, for the preparation of the proteins, to generate transgenic or	CC
CC	knockout animals which are useful in the development and screening of	CC
CC	therapeutic useful reagents, for chromosome identification, and in gene	CC
CC	therapy. The antibody is useful as a therapeutic agent, in a diagnostic	CC
CC	assay and for affinity purification of the protein from recombinant	CC
CC	cell culture natural sources. The present sequence represents a novel	CC
CC	secreted or transmembrane protein of the invention.	CC
XX		XX
SQ	Sequence 243 AA;	
Query Match	100.0%; Score 243; DB 223; Length 243;	
Best Local Similarity	100.0%; Pred. NO. 5,1e-220;	
Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1 MRPGASPAPORLKGILLTLLTLLQLPAPSSASEIPKQKAOALQREVVLYNGMCLQGPA 60	
DB	1 MRPGASPAPORLKGILLTLLTLLQLPAPSSASEIPKQKAOALQREVVLYNGMCLQGPA 60	
QY	61 GVPGRDSSPGANVTPGTGIPGRDGFKEKEGCELCRESEESTPNTYKQCSWSSLYNGIDL 120	
DB	61 GVPGRDSSPGANVTPGTGIPGRDGFKEKEGCELCRESEESTPNTYKQCSWSSLYNGIDL 120	
QY	121 GKILKEGFTTKRRSSALRLVLESGSLRLKCRNACCGRWFTFPGARGCSGLPIEATITLYDQ 180	
DB	121 GKILKEGFTTKRRSSALRLVLESGSLRLKCRNACCGRWFTFPGARGCSGLPIEATITLYDQ 180	
QY	121 GKILKEGFTTKRRSSALRLVLESGSLRLKCRNACCGRWFTFPGARGCSGLPIEATITLYDQ 180	
DB	121 GKILKEGFTTKRRSSALRLVLESGSLRLKCRNACCGRWFTFPGARGCSGLPIEATITLYDQ 180	
QY	181 GSPENMNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYKPGASTGWNVSRIIEE 240	
DB	181 GSPENMNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYKPGASTGWNVSRIIEE 240	
QY	241 LPK 243	

D	b		241 LPR 243
R	E	S	RESULT 9
A	B	G	ABG78938
I	D		ABG78938 standard; Protein; 243 AA.
X	X		
A	C		ABG78938;
X	X		
D	T		15-NOV-2002 (first entry)
X	X		
D	E		Human breast tumour polypeptide #29.
X	X		
K	M		Human: breast tumour protein; breast cancer; cytostatic; vaccine.
O	S		Homo sapiens.
X	X		
P	N		US2002085998-A1.
X	X		
P	D		04-JUL-2002.
X	X		
P	F		13-APR-2001; 2001US-0834759.
X	X		
E	R		26-DEC-1998; 98US-0222575.
X	X		02-APR-1999; 99US-0285480.
P	R		23-JUN-1999; 99US-0339338.
P	R		02-SEP-1999; 99US-0389681.
P	R		03-NOV-1999; 99US-0433826.
P	R		17-APR-2000; 2000US-0551621.
P	R		08-JUN-2000; 2000US-0590751.
P	R		22-JUN-2000; 2000US-0604287.
X	X		20-JUL-2000; 2000US-0620405.
X	X		(CORI-) CORIXA CORP.
P	I		Jiang Y, Dillion DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT,
P	I		Henderson RA;
D	R		WPI; 2002-635657/68.
X	X		N-PSDB; ABS64028, ABS64029.
P	T		Novel breast cancer polynucleotides and polypeptides encoded by the
P	T		polynucleotides, useful for detecting the presence of breast cancer in
P	T		a patient, and in pharmaceutical compositions, for treating breast
P	T		cancer -
X	X		
P	S		Claim 2; Page 235-236; 247pp; English.
X	X		
C	C		The invention relates to an isolated breast tumour polynucleotide and the
C	C		polypeptide it encodes. The polynucleotide and polypeptide are useful for
C	C		detecting the presence of breast cancer in a patient, and in
C	C		pharmaceutical compositions for treating breast cancer. The sequences are
C	C		useful for stimulating an immune response in a patient and can therefore
C	C		be used in production of vaccines. The sequences are also useful for
C	C		detecting the presence of a cancer in a patient, by obtaining a
C	C		biological sample from the patient, contacting the biological sample with
C	C		a composition of the invention and detecting the amount of polynucleotide
C	C		that hybridizes to the sample. This sequence represents a human breast
C	C		tumour polypeptide of the invention.
X	X		
S	Q		Sequence 243 AA:
Q	Y		Query Match 100.0%; Score 243; DB 23; Length 243;
D	b		Best local Similarity 100.0%; Pred. No. 5,1e-220;
			Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0
			1 MRPGPAASPORLRLGLLLILLQLLPASSASEIRKGRKAKQLRQREVVDLYNMCLOGPA 60
			1 MRPGPAASPORLRLGLLLILLQLLPASSASEIRKGRKAKQLRQREVVDLYNMCLOGPA 60
			61 CYPGRGSGANVIGTGTGIRGRDGFKEKECECLRESFESBSPNYKQCSWSLANTGIDL 120
			61 CYPGRGSGANVIGTGTGIRGRDGFKEKECECLRESFESBSPNYKQCSWSLANTGIDL 120

```

QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCNACCQRMVFTFNGAECGPIPIEAIITLDQ 180
DQ 121 GKIAECTFTKRSNSALRVLFSGSLRLKCNACCQRMVFTFNGAECGPIPIEAIITLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSYPRGDASTGWNVSRIITIEE 240
DQ 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSYPRGDASTGWNVSRIITIEE 240
QY 241 LPK 243
DQ 241 LPK 243

RESULT 10
AB95545
ID ABB95545 standard; Protein: 243 AA.
AC ABB95545;
XX
XX 19-JUL-2002 (first entry)
DE Human angiogenesis related protein PRO1550 SEQ ID NO: 246.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiatic; cytosatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US21735.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 28-JUL-2000; 2000US-220664P.
XX 02-AUG-2000; 2000WO-US20710.
XX 17-AUG-2000; 2000US-222695P.
XX 23-AUG-2000; 2000US-223352P.
XX 24-AUG-2000; 2000WO-US23338.
XX 07-SEP-2000; 2000US-23078P.
XX 15-SEP-2000; 2000US-000000P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 20-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06566.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866034.
XX 25-MAY-2001; 2001US-0866034.
XX 30-MAY-2001; 2001US-0870574.
XX 30-MAY-2001; 2001WO-US17443.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.

```

```

PR 28-JUN-2001; 2001WO-US00000.
XX
XX (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GUER/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
XX
XX N-PSDB; ABL95683.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 246; 567P; English.
XX
XX
XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a PRO protein of the invention.
XX
XX
XX Sequence 243 AA:
XX
XX Query Match 100.0%; Score 243; DB 23; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 5, 1e-220;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MRPGPAPASPORLRGLLILLILLDLPAPSSASEIPKQKAKOLQREVVLDYNGMCLGPA 60
XX DQ 1 MRPGPAPASPORLRGLLILLILLDLPAPSSASEIPKQKAKOLQREVVLDYNGMCLGPA 60
XX
XX QY 61 GVPGRDSSPGANVYIPGPIGRDGFGEKGECELRSEFESWPNPKQCSWSSLNTGIDL 120
XX DQ 61 GVPGRDSSPGANVYIPGPIGRDGFGEKGECELRSEFESWPNPKQCSWSSLNTGIDL 120
XX
XX QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCNACCQRMVFTFNGAECGPIPIEAIITLDQ 180
XX DQ 121 GKIAECTFTKRSNSALRVLFSGSLRLKCNACCQRMVFTFNGAECGPIPIEAIITLDQ 180
XX
XX QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSYPRGDASTGWNVSRIITIEE 240
XX DQ 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSYPRGDASTGWNVSRIITIEE 240
XX
XX QY 241 LPK 243
XX DQ 241 LPK 243

RESULT 11
AAE20462
ID AAE20462 standard; Protein: 243 AA.
AC AAE20462;

```

```

XX 01-JUL-2002 (first entry)
DF
XX
XX Human tumour-associated antigenic target-170 (TAT170) protein.
DE
XX Human; tumour-associated antigenic target-170; TAT170; cytostatic;
KM gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
XX antibody-dependent enzyme mediated prodruq therapy.
OS
XX Homo sapiens.
FH Key Location/Qualifiers
FH Peptide 1..30
FH /label= signal_peptide
FT Protein 31..243
FT /label= Mature_TAT170_protein
FT Modified-site 67..72
FT /note= "N-myristoylation site"
FT Modified-site 117..122
FT /note= "N-myristoylation site"
FT Modified-site 163..168
FT /note= "N-myristoylation site"
FT Modified-site 186..189
FT /note= "N-myristoylation site"
FT Modified-site 199..204
FT /note= "Asn is N-glycosylated"
FT Modified-site 203..208
FT /note= "N-myristoylation site"
FT Modified-site 203..208
FT /note= "N-myristoylation site"
XX
XX WO200216602-A2.
XX
XX 28-FEB-2002.
XX
XX 23-AUG-2001; 2001WO-US26626.
XX
XX 24-AUG-2000; 2000WO-US23328.
XX 01-DEC-2000; 2000WO-US32678.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
XX 29-JUN-2001; 2001WO-US21066.
XX 09-JUL-2001; 2001WO-US21735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Polakis P;
PI Williams PM, Wood WI, Wu TD, Zhang Z;
XX
XX WPI; 2002-292065/33.
XX N-PSDB; AAD32717.
XX
XX New antibodies that bind tumor-associated antigenic target (TAT)
XX polypeptides, useful for treating and diagnosing tumor (e.g. breast,
XX lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle,
XX pigs, goats, rabbits or humans
XX
XX Claim 1; Fig 7; 124pp; English.
XX
XX The present invention relates to an isolated antibody that binds to
XX tumor-associated antigenic target (TAT) polypeptide. The antibody is
XX used for treating and diagnosing tumors (e.g. breast, lung, liver or
XX stomach tumors) in mammals, e.g. dogs, cats, cattle, horses, sheep,
XX pigs, goats, rabbits, or preferably humans. The antibody may also be
XX used in antibody-dependent enzyme mediated prodruq therapy (ADEPT).
XX The antibody is also useful for the therapeutic treatment or for the
XX diagnostic detection of cancer. TAT cDNA is useful in gene therapy.
XX The present sequence is human TAT170 protein. TAT170 cDNA is designated
XX as DNA76393-1664.
XX
XX Sequence 243 AA:
XX
XX Query Match 100.0%; Score 243; DB 23; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 5,1e-220;

```

```

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPGPASPQRLRLGILLILLIQLPAPSSASEIPKQKQALRREVVLYNGMCIQSPA 60
DB 1 MRPGPASPQRLRLGILLILLIQLPAPSSASEIPKQKQALRREVVLYNGMCIQSPA 60
QY 61 GYPGDSGPANVIRPGTGTGIRGQFKKEKGECLRESEESWTPYKCCSSSLNYGIDL 120
DB 61 GYPGDSGPANVIRPGTGTGIRGQFKKEKGECLRESEESWTPYKCCSSSLNYGIDL 120
QY 121 GKIACTFTKMRNSALRVLFSGSLRLKCRNACCRWFTFTNGACSGPLIEATITVDQ 180
DB 121 GKIACTFTKMRNSALRVLFSGSLRLKCRNACCRWFTFTNGACSGPLIEATITVDQ 180
QY 181 GSPEMNSTINIHRTSSVGEICGEGAGLVDAIIVGTCSDYPKGDASTGMSVSRITIEE 240
DB 181 GSPEMNSTINIHRTSSVGEICGEGAGLVDAIIVGTCSDYPKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 12
ABB84939
ID ABB84939 standard; Protein; 243 AA.
XX
XX ABB84939;
XX
XX 16-MAY-2002 (first entry)
XX
XX Human PRO1550 protein sequence SEQ ID NO:246.
XX
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
XX vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
XX
XX Homo sapiens.
XX
XX WO200200690-A2.
XX
XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747253.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.

```



PR 17-DEC-1997; 97US-069870P.  
PR 18-DEC-1997; 97US-068017P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077649P.  
PR 20-MAR-1998; 98US-078886P.  
PR 20-MAR-1998; 98US-078939P.  
PR 27-MAR-1998; 98US-079664P.  
PR 27-MAR-1998; 98US-079786P.  
PR 31-MAR-1998; 98US-080107P.  
PR 31-MAR-1998; 98US-080194P.  
PR 01-APR-1998; 98US-080327P.  
PR 01-APR-1998; 98US-080333P.  
PR 08-APR-1998; 98US-081049P.  
PR 08-APR-1998; 98US-081070P.  
PR 09-APR-1998; 98US-081195P.  
PR 15-APR-1998; 98US-081838P.  
PR 21-APR-1998; 98US-082568P.  
PR 21-APR-1998; 98US-082569P.  
PR 22-APR-1998; 98US-082704P.  
PR 22-APR-1998; 98US-082797P.  
PR 28-APR-1998; 98US-083322P.  
PR 29-APR-1998; 98US-083495P.  
PR 29-APR-1998; 98US-083496P.  
PR 29-APR-1998; 98US-083499P.  
PR 29-APR-1998; 98US-083559P.  
PR 05-MAY-1998; 98US-084366P.  
PR 06-MAY-1998; 98US-084414P.  
PR 07-MAY-1998; 98US-084639P.  
PR 07-MAY-1998; 98US-084640P.  
PR 07-MAY-1998; 98US-084643P.  
PR 15-MAY-1998; 98US-085579P.  
PR 15-MAY-1998; 98US-085800P.  
PR 15-MAY-1998; 98US-085820P.  
PR 15-MAY-1998; 98US-085822P.  
PR 18-MAY-1998; 98US-085700P.  
PR 22-MAY-1998; 98US-086023P.  
PR 22-MAY-1998; 98US-086486P.  
PR 28-MAY-1998; 98US-087098P.  
PR 28-MAY-1998; 98US-087208P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088033P.  
PR 05-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088722P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088740P.  
PR 10-JUN-1998; 98US-088811P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088825P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088863P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089090P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.

PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090461P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090688P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 26-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091010P.  
PR 01-JUL-1998; 98US-091359P.  
PR 02-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091486P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091632P.  
PR 04-JUL-1998; 98US-094006P.  
PR 04-AUG-1998; 98US-095282P.  
PR 10-AUG-1998; 98US-095998P.  
PR 10-AUG-1998; 98US-096012P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096959P.  
PR 26-AUG-1998; 98US-097022P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-098014P.  
PR 01-SEP-1998; 98US-098716P.  
PR 01-SEP-1998; 98US-098723P.  
PR 02-SEP-1998; 98US-098803P.  
PR 02-SEP-1998; 98US-098821P.  
PR 02-SEP-1998; 98US-098843P.  
PR 09-SEP-1998; 98US-099602P.  
PR 10-SEP-1998; 98US-099741P.  
PR 10-SEP-1998; 98US-099754P.  
PR 10-SEP-1998; 98US-099763P.  
PR 10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 243; DB 24; Length 243;  
Best Local Similarity 100.0%; Pred. No. 5,1e-220; Indels 0; Gaps 0;  
Matches 243; Conservative 0; Mismatches 0;  
QY 1 MRPOGPASPORLNGLLILLIQLPAPSSASEIRKQKQALROREVDLYNGACLOGPA 60  
DB 1 MRPOGPASPORLNGLLILLIQLPAPSSASEIRKQKQALROREVDLYNGACLOGPA 60  
QY 61 GVPGRDSSPGANVPIPGPIGNDGFGKGEKCECLRESFESBWTBNYKQCSWSLNYGIDL 120  
DB 61 GVPGRDSSPGANVPIPGPIGNDGFGKGEKCECLRESFESBWTBNYKQCSWSLNYGIDL 120  
QY 121 GKIAECTFTKMRNSALRYLESSLRKCRACCORRYFPFNGACSGPIPIEALITYLDQ 180  
DB 121 GKIAECTFTKMRNSALRYLESSLRKCRACCORRYFPFNGACSGPIPIEALITYLDQ 180  
QY 181 GSPENNSTINIHRTSSVEGLCEGICAGLVDAIVWGTCSDPKPKDASTGNNSVRIITIEE 240  
DB 181 GSPENNSTINIHRTSSVEGLCEGICAGLVDAIVWGTCSDPKPKDASTGNNSVRIITIEE 240

OY 241 LPK 243  
241 LPK 243  
Db 241 LPK 243

RESULT 14  
ABU71566  
ID ABU71566 standard; Protein; 243 AA.  
XX  
AC ABU71566;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Human secreted polypeptide PRO1550.  
XX  
KW Human; gene therapy; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003013855-A1.  
XX  
PD 16-JAN-2003.  
XX  
PF 03-MAY-2002; 2002US-0063616.  
XX  
PR 30-DEC-1998; 98KR-0062142.  
PR 08-MAR-1999; 99MO-US05028.  
PR 14-MAY-1999; 99MO-US10733.  
PR 30-DEC-1999; 99MO-US31274.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 21-MAR-2000; 2000MO-US07532.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 10-NOV-2000; 2000MO-US30873.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 20-DEC-2000; 2000MO-US34956.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 14-MAY-1999; 99US-0311832.  
PR 25-AUG-1999; 99US-0380137.  
PR 25-AUG-1999; 99US-0380138.  
PR 25-AUG-1999; 99US-0380139.  
PR 25-AUG-1999; 99US-0380142.  
PR 15-SEP-1999; 99US-0397342.  
PR 18-OCT-1999; 99US-0403297.  
PR 12-NOV-1999; 99US-0423844.  
PR 22-AUG-2000; 2000US-0644848.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 08-NOV-2000; 2000US-0709238.  
PR 20-DEC-2000; 2000US-0747259.  
PR 22-MAR-2001; 2001US-0816744.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 30-MAY-2001; 2001US-0870574.  
PR 05-JUN-2001; 2001US-0874503.  
PR 29-JUN-2001; 2001US-0869599.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-DEC-2001; 2001US-0006867.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Eaton DL, Flyvoraof E, Gerritsen ME, Goddard A, Godowski PJ,  
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX WPI; 2003-330485/31.  
XX N-PSDB; ACAS8870.  
XX  
PT New isolated antibody specifically binding a PRO polypeptide, useful

PT for the preparation of a medicament for treating disorders with the  
PT aberrant expression or activity of the PRO polypeptide, such as tumor  
XX conditions and cancer  
XX  
PS Disclosure; Page 194-195; 406pp; English.  
XX  
XX The invention relates to an antibody that binds to a polypeptide with a  
CC fully defined sequence given in the specification. The methods and  
CC compositions (containing antibodies that specifically bind a PRO  
CC polypeptide) of the present invention are useful for the preparation of a  
CC medicament for the treatment of disorders associated with the aberrant  
CC expression or activity of the PRO polypeptide, such as tumour conditions  
CC and cancer. They can also be used to generate transgenic or knockout  
CC animals useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
CC molecular weight markers for protein electrophoresis, chromosome  
CC identification and tissue typing. The PRO polypeptides are useful to  
CC induce angiogenesis e.g wound healing; in the treatment of sports-related  
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
CC antibodies may be used in various diagnostic, competitive binding and/or  
CC immunoprecipitation assays. The present sequence represents the amino  
CC acid sequence of a PRO polypeptide of the invention.  
XX  
XX Sequence 243 AA;  
SQ  
XX  
XX Query Match 100.0%; Score 243; DB 24; Length 243;  
Best Local Similarity 100.0%; Pred No. 5,1e-220;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MRPGPAASFORLRLGLLLLLLLLPAPSSASEIPKQKQAKLRQREVVDLYNMCLOGPA 60  
Db 1 MRPGPAASFORLRLGLLLLLLLLPAPSSASEIPKQKQAKLRQREVVDLYNMCLOGPA 60  
OY 61 GYVGRDGSFGANVYIPPTGPIGRDGRKGEKGEELRSPFESPTPNKQCSWSSLYNGIDL 120  
Db 61 GYVGRDGSFGANVYIPPTGPIGRDGRKGEKGEELRSPFESPTPNKQCSWSSLYNGIDL 120  
OY 121 GKIAECTFTKMRNSALRYVFSGLRLKRCNNACCOMYFENGAECSGPIPIAIIYLLDQ 180  
Db 121 GKIAECTFTKMRNSALRYVFSGLRLKRCNNACCOMYFENGAECSGPIPIAIIYLLDQ 180  
OY 181 GSEPMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPKGDASTGMSVSRITIEE 240  
Db 181 GSEPMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPKGDASTGMSVSRITIEE 240  
OY 241 LPK 243  
XX 241 LPK 243  
Db 241 LPK 243  
XX  
XX  
XX RESULT 15  
XX ABU72012  
XX ID ABU72012 standard; Protein; 243 AA.  
XX  
XX AC ABU72012;  
XX  
XX DT 11-JUN-2003 (first entry)  
XX  
XX DE Novel human secreted and transmembrane protein PRO1550.  
XX  
XX KW Human; secreted and transmembrane polypeptide;  
XX KW chromosome mapping; gene mapping; transgenic animal; knockout animal;  
XX KW therapeutic agent screening; chromosome identification; tissue typing;  
XX KW gene therapy.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US2003018183-A1.  
XX  
XX PD 23-JAN-2003.  
XX  
XX PF 01-MAY-2002; 2002US-0063512.

XX 06-DEC-2001; 2001US-0006867.

XX (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerlitsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WR;

XX WPI: 2003-330984/31.  
DR N-PSDB: ACA60423.

XX New secreted and transmembrane PRO polypeptides and nucleic acid  
PT molecules encoding the polypeptides' useful in gene therapy or  
PT preparing a medicament for treating a condition that is responsive to  
PT the PRO polypeptide or antibody

PS Disclosure: Fig 122; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO  
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
CC for treating a condition that is responsive to the PRO polypeptide or  
CC antibody. The PRO nucleotide sequences may be used as hybridisation  
CC probes in chromosome and gene mapping, or in generating antisense RNA  
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,  
CC in assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knockout animals, which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides and nucleic acid molecules are also useful in gene  
CC therapy, and as molecular weight markers for protein electrophoresis  
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
CC PRO, or for the affinity purification of PRO from recombinant cell  
CC culture or natural sources. This is the amino acid sequence of a novel  
CC human secreted and transmembrane PRO polypeptide.

XX Sequence 243 AA;

Query Match 100.0%; Score 243; DB 24; Length 243;

Best Local Similarity 100.0%; Pred. No. 5.1e-220;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRPGPASPQRLRGLLILLILQLPAPSSASEIRPKGKQKQALRQREVVDLYNGMCLGSPA	60
DB	1	MRPGPASPQRLRGLLILLILQLPAPSSASEIRPKGKQKQALRQREVVDLYNGMCLGSPA	60
QY	61	GVPERDSSPGANVTPGTPGIFGRDGFKEGECLESFESWTPTNYKQCSWSLNTGIDL	120
DB	61	GVPERDSSPGANVTPGTPGIFGRDGFKEGECLESFESWTPTNYKQCSWSLNTGIDL	120
QY	121	GKIAECTFTKMRNSALRYLSSGLRLKCRNACCQRMWTFPFGAECGSLPIEAIITYIDQ	180
DB	121	GKIAECTFTKMRNSALRYLSSGLRLKCRNACCQRMWTFPFGAECGSLPIEAIITYIDQ	180
QY	181	GSPEMNSTINIRHTSSVYGLCEGIGAGLVDAIVWGTCSDDPKGDASTGWSVSRIITEE	240
DB	181	GSPEMNSTINIRHTSSVYGLCEGIGAGLVDAIVWGTCSDDPKGDASTGWSVSRIITEE	240
QY	241	LPK 243	
DB	241	LPK 243	

Search completed: August 13, 2003, 13:38:08  
Job time : 86 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:35:38 ; Search time 39 Seconds  
(without alignments)  
599.205 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243

Sequence: 1 MRPGAPASPQRLRGLLL...GDASTGMSVSRITIELLPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 9616862 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1982

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR\_76:\*

1: pirl1:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	3.7	133	2	probable membrane
2	9	3.7	144	2	probable membrane
3	9	3.7	247	2	myelin/oligodendro
4	9	3.7	779	1	collagen alpha 1(I
5	9	3.7	996	2	apollipoprotein E r
6	9	3.7	1464	1	collagen alpha 1(I
7	8	3.3	112	2	sporozoite antigen
8	8	3.3	141	1	lurotopin beta chai
9	8	3.3	165	1	choriogenadotropin
10	8	3.3	169	2	hypothetical prote
11	8	3.3	177	2	collagen alpha 2(X
12	8	3.3	249	2	collagen alpha 2(X
13	8	3.3	254	2	4-1BB ligand - hum
14	8	3.3	291	2	homeotic protein X
15	8	3.3	296	2	hypothetical prote
16	8	3.3	302	2	hypothetical prote
17	8	3.3	307	2	ribosome-binding p
18	8	3.3	330	2	collagen alpha 1(X
19	8	3.3	333	2	hypothetical prote
20	8	3.3	360	2	collagen dpy-2 - C
21	8	3.3	365	2	soluble-type glyco
22	8	3.3	368	2	flmtrial protein l
23	8	3.3	378	2	probable RING zinc
24	8	3.3	391	2	hypothetical prote
25	8	3.3	399	2	hypothetical prote
26	8	3.3	424	2	glutamate-1-semial
27	8	3.3	457	1	T-cell surface gly
28	8	3.3	487	1	steroide 21-monooxy
29	8	3.3	487	2	cytochrome P450 -

30	8	3.3	500	2	S66522	cartilage matrix p
31	8	3.3	636	2	S41067	collagen alpha 1(I
32	8	3.3	674	2	S23297	collagen alpha 1(X
33	8	3.3	809	2	A46747	Na+/H+-exchanging
34	8	3.3	917	2	S09646	collagen alpha 2(V
35	8	3.3	984	2	S67527	collagen kinase (EC
36	8	3.3	1018	1	CGH02A	collagen alpha 2(V
37	8	3.3	1029	1	S21369	collagen alpha 2(V
38	8	3.3	1102	2	JH0717	guanylate cyclase
39	8	3.3	1108	2	A55915	protein F54D8.1 (I
40	8	3.3	1120	2	H88449	neural cell adhesi
41	8	3.3	1265	1	A37967	Niemann-Pick C dis
42	8	3.3	1278	2	T30188	collagen alpha 1(X
43	8	3.3	1388	1	A53317	collagen alpha 2(I
44	8	3.3	1414	1	S23809	bullous pemphigoid
45	8	3.3	1433	2	A46053	

#### ALIGNMENTS

RESULT 1  
S57038  
Probable membrane protein YJR023c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19  
C:Species: Saccharomyces cerevisiae  
C>Date: 08-Jul-1995 #sequence.revision 08-Sep-1995 #text\_change 19-Apr-2002  
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.  
Submitted to the Protein Sequence Database, September 1995  
A:Accession: S57038  
A:Reference number: S56771  
A:Accession: S57038  
A:Molecule type: DNA  
A:Residues: 1-133 <ZAG>  
A:Cross-references: EMBL:449522; NID:q1015659; PID:q1015661  
R:Zagalski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; He  
submitted to the Protein Sequence Database, September 1995  
A:Reference number: S57040  
A:Accession: S57041  
A:Molecule type: DNA  
A:Residues: 1-93 <HUA>  
A:Cross-references: EMBL:449522; MIPS:YJR023c  
R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.  
submitted to the EMBL Data Library, May 1995  
A:Reference number: S55183  
A:Accession: S55212  
A:Molecule type: DNA  
A:Residues: 1-133 <DEH>  
A:Cross-references: EMBL:X87611  
C:Genetics:  
A:Cross-references: SGD:S0003784  
A:Map position: 10R  
C:Superfamily: Saccharomyces probable membrane protein YJR023c  
C:Keywords: transmembrane protein

Query Match 3.7%; Score 9; DB 2; Length 133;  
Best local Similarity 100.0%; Pred. No. 0.59;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24  
DB 22 LLLLLLQL 30

RESULT 2  
T18867  
Hypothetical protein C02F4.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence.revision 15-Oct-1999 #text\_change 21-Jan-2000  
R:Cummings, P.  
Submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19034

A:Accession: T18867  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-144 <NTL>  
 A:Cross-references: EMBL:281032; PIDs: CAB02722.1; GSPDB: GN00022; CESP: C02F4.3  
 A:Experimental source: clone C02F4  
 A:Genetics:  
 A:Gene: CESP: C02F4.3  
 A:Map position: 4  
 A:Inserts: 3/1  
 C:Superfamily: Caenorhabditis elegans hypothetical protein C02F4.3

Query Match  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 LLLLLLQL 24  
 |||||  
 Db 67 LLLLLLQL 75

## RESULT 3

A55717

Myelin/oligodendrocyte glycoprotein precursor - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 08-Oct-1999

C:Accession: A55717; C47712

R:Daubas, P.; Pham-Dinh, D.; Dautigny, A.

Genomics 23, 36-41, 1994

A:Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein gene

A:Reference number: A55717; MUID:5510110; PMID:7829100

A:Accession: A55717

A:Molecule type: DNA

A:Residues: 1-247 &lt;DAU&gt;

A:Cross-references: GB: I29498

R:Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Rousset, G.; Pontarotti, P.; Roedel, N.; Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993

A:Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin

A:Reference number: A47712; MUID:93376728; PMID:8367453

A:Accession: C47712

A:Molecule type: mRNA

A:Residues: 30-95, 'E', 97-247 &lt;PHA&gt;

A:Cross-references: GB: I20942; NID: g399588; PIDs: AAA03180.1; PID: g399589

A:Genetics:

A:Gene: MCG

A:Map position: 17

A:Note: encoded within the MHC

C:Function:

A:Description: may be involved in lipid interaction; may be involved in cell-cell commun

C:Keywords: glycoprotein; myelin; transmembrane protein

F:1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F:30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted &lt;MAT&gt;

F:151-179/Domain: transmembrane #status predicted &lt;TM&gt;

F:204-229/Domain: transmembrane #status predicted &lt;TM&gt;

F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 LLLLLLQL 24  
 |||||  
 Db 16 LLLLLLQL 24

## RESULT 4

CG9015

collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 24-Apr-1984 #sequence\_revision 31-Dec-1993 #text\_change 31-Mar-2000

C:Accession: A91193; A9129; A91387; A91201; A91200; A43048; A02853

R:Reuterberg, J.; Timpl, R.; Furtmayr, H.

Eur. J. Biochem. 27, 231-237, 1972

A:Title: Structural characterization of N-terminal antigenic determinants in calf and  
 A:Reference number: A91193; MUID:72255334; PMID:4115172  
 A:Accession: A91193  
 A:Molecule type: protein  
 A:Residues: 1-19 <RAU>  
 A:Experimental source: skin  
 A:Note: The epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is co  
 R:Flitzek, P.P.; Kuehn, K.  
 Eur. J. Biochem. 52, 77-82, 1975  
 A:Title: The covalent structure of collagen: amino-acid sequence of the cyanogen-brom  
 A:Reference number: A91229; MUID:76022320; PMID:1164916  
 A:Accession: A91229

A:Molecule type: protein

A:Residues: 20-145 <FIE>

A:Experimental source: skin

A:Note: Lys-103 is hydroxylated and binds glucosylgalactose

R:Flitzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.

FEBS Lett. 26, 74-76, 1972

A:Title: The covalent structure of collagen: amino acid sequence of alpha1-CB3 from c

A:Reference number: A91387; MUID:73049499; PMID:4673951

A:Accession: A91387

A:Molecule type: protein

A:Residues: 146-294 <FIE>

A:Experimental source: skin

R:Flitzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.

Eur. J. Biochem. 38, 396-400, 1973

A:Title: The covalent structure of collagen. 2. The amino-acid sequence of alpha1-CB7

A:Reference number: A91211; MUID:74086118; PMID:4359390

A:Accession: A91211

A:Molecule type: protein

A:Residues: 295-562 <FIE>

A:Experimental source: skin

R:Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.

Eur. J. Biochem. 30, 169-183, 1972

A:Title: The covalent structure of collagen. The amino-acid sequence of the 112 resid

A:Reference number: A91201; MUID:73042276; PMID:4343808

A:Accession: A91201

A:Molecule type: protein

A:Residues: 563-675 <WEN>

A:Experimental source: skin

R:Flitzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.

Eur. J. Biochem. 30, 163-168, 1972

A:Title: The amino acid sequence of the carboxyterminal nonhelical cross link region

A:Reference number: A43048

A:Accession: A43048

A:Molecule type: protein

A:Residues: 759-779 <RA2>

A:Experimental source: skin

C:Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hyd

C:Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) ar

C:Comment: The order of the eight CMr peptides in the alpha 1(I) chain of bovine skl

9, 149, 268, and 217 residues.

C:Comment: The complete chain contains 1052 residues.

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

C:Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglyutamic acid; trine

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

63 PGRDGPQA 71  
 |||||  
 Db 586 PGRDGPQA 594

```

RESULT 5
apolioprotein E receptor 2 precursor - mouse
J0237
A:Alternate names: apoER2
C:Species: Mus musculus (house mouse)
C>Date: 05-Dec-1998 #sequence revision 05-Dec-1998 #text change 18-Aug-2000
C:Accession: J0237
R:Kim, H.J.; Kim, D.H.; Magoori, K.; Saeki, S.; Yamamoto, T.T.
J. Biochem. 124, 451-456, 1998
A:Title: Evolution of the apolioprotein E receptor 2 gene by exon loss.
A:Reference number: J0237; MUID:96352006; PMID:9685741
A:Accession: J0237
A:Molecule type: mRNA
A:Residues: 1-996 <KID>
A:Cross-references: DDBJ:D85463
C:Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;
C:Keywords: glycoprotein
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-996/Product: apolioprotein E receptor 2 #status predicted <MAT>
F:41-75/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:80-116/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:121-157/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:161-195/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:200-237/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:251-286/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:291-325/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:331-368/Domain: LDL receptor ligand-binding repeat homology <LDL>
F:373-407/Domain: EGF homology <EGF>
F:585-628/Domain: LDL receptor YWTD-containing repeat homology <YWT>
F:723-767/Domain: EGF homology <EGF1>
F:858-881/Domain: transmembrane #status predicted <TMM>
F:805,840/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      3.7%; Score 9; DB 2; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 LLLLLLLQL 24
        |||||||
Db       14 LLLLLLLQL 22

RESULT 6
CGH015
collagen alpha 1(I) chain precursor - human
N:Alternate names: procollagen alpha 1(I) chain
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1991 #sequence revision 04-Oct-1996 #text change 31-Dec-2000
C:Accession: I60114; S01143; A53333; I55254; A39943; I55237; A35233; S09400; B90567; S11
5269; A29439; I53466; A02852; I37247
R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.J.
Gene 67, 105-115, 1988
A:Title: Complete nucleotide sequence of the region encompassing the first twenty-five e
A:Reference number: I60114; MUID:88325734; PMID:2843432
A:Accession: I60114
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369, 'L', 371-589 <DAI>
A:Cross-references: GB:M20789; NID:g179593; PIDN:AA59373.1; PID:g179594
R:Tromp, G.; Kuyaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock
Blochem. J. 253, 919-922, 1988
A:Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human
A:Reference number: S01143; MUID:89025644; PMID:31878743
A:Accession: S01143
A:Molecule type: mRNA
A:Residues: 1-472 <TRQ>
A:Cross-references: EMBL:X07884; NID:930015; PIDN:CA30731.1; PID:g30016; GB:M36546; NID
A:Note: submitted to the EMBL/Genbank/DBJ databases by Prockop, D.J., 13-JUN-1988
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
Nature 310, 337-340, 1984
A:Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of

```

```

A:Reference number: A93335; MUID:84270697; PMID:6462220
A:Accession: A93335
A:Molecule type: DNA
A:Residues: 1-58, 'Q', 60-181 <CHD>
A:Cross-references: EMBL:X00820; NID:935657; PIDN:CA23394.1; PID:g35658
R:Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet,
J. Biol. Chem. 262, 15151-15157, 1987
A:Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene
A:Reference number: I55254; MUID:88033098; PMID:2822714
A:Accession: I55254
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <ROS>
A:Cross-references: GB:J02829; NID:g180387; PIDN:AA51993.1; PID:g180388
R:Bornstein, P.; McKay, J.; Morishima, J.K.; Devareyalu, S.; Gellinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A:Title: Regulatory elements in the first intron contribute to transcriptional contro
A:Reference number: A39943; MUID:88097389; PMID:3480516
A:Accession: A39943
A:Molecule type: DNA
A:Residues: 1-34 <BOR>
A:Cross-references: GB:J03559; NID:g180876; PIDN:AA52052.1; PID:g553238
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A:Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promote
A:Reference number: I55237; MUID:85130970; PMID:2857713
A:Accession: I55237
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-34 <CH2>
A:Cross-references: GB:M10627; NID:g180383; PIDN:AA51992.1; PID:g553226
R:Wirtz, M.; Keene, D.R.; Horst, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Holl
J. Biol. Chem. 265, 6312-6317, 1990
A:Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-term
rome, type VII
A:Reference number: A35233; MUID:90202908; PMID:2318855
A:Accession: A35233
A:Molecule type: protein
A:Residues: 33-52 <MRP>
A:Note: this propeptide fragment remained non-covalently bound to a defective, unclea
R:Well, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.
EMBO J. 8, 1705-1710, 1989
A:Title: A base substitution in the exon of a collagen gene causes alternative splici
A:Reference number: S09400; MUID:89356643; PMID:2767050
A:Accession: S09400
A:Molecule type: mRNA
A:Residues: 156-183 <MEI>
R:Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A:Title: Isolation and characterization of the cyanogen bromide peptides from the alp
A:Reference number: A90567; MUID:71038625; PMID:5529814
A:Contents: CNBR0-1, CNBR2, CNBR4, CNBR5
A:Accession: B90567
A:Molecule type: protein
A:Residues: 162-188, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 233,
A:Experimental source: skin
A:Note: evidence for 170-allysine
R:Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller
Eur. J. Biochem. 192, 153-159, 1990
A:Title: A critical crosslink region in human-bone-derived collagen type I. Specific
A:Reference number: S11372; MUID:90382436; PMID:2169412
A:Accession: S11372
A:Molecule type: protein
A:Residues: 175-187, 274-287, 'P', 289 <BAE>
A:Note: sequence of collagen alpha 1(3)(I) isolated from bone after pepsin digestion
R:Deak, S.B.; Scholz, P.M.; Amerita, P.S.; Constantinou, C.D.; Levi-Mizel, S.A.; Ganza
J. Biol. Chem. 266, 21827-21832, 1991
A:Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen ch
cooperative melting of intact type I collagen.
A:Reference number: I55342; MUID:92042092; PMID:1718984
A:Accession: I55342
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA

```

A:Residues: 258-268,1347-1357 <DEA>  
A:Cross-references: GB:S6795; NID:9239007; PIDN:AAB20350.1; PID:9239008  
A:Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report  
R.Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.  
J. Biol. Chem. 245, 5042-5048, 1970  
A:Title: Comparative study of glycopeptides derived from selected vertebrate collagens.  
A:Reference number: A92069; PMID:71001508; PMID:4319110  
A:Accession: A92069  
A:Molecule type: protein  
A:Residues: 263-268 <MOR>  
A:Experimental source: skin  
A:Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine  
R.Labhard, M.E.; Hollister, D.W.  
Matrix 10, 124-130, 1990  
A:Title: Segmental amplification of the entire helical and telopeptide regions of the ct  
A:Reference number: S15989; PMID:90326017; PMID:2374517  
A:Accession: S15989  
A:Molecule type: mRNA  
A:Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>  
R.Wirtz, M.K.; Rao, V.H.; Glaville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.  
Connect. Tissue Res. 29, 1-11, 1993  
A:Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of  
A:Reference number: I52905; PMID:93339042; PMID:8339541  
A:Accession: I52905  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 342-352, 'C', 354-359 <MID>  
A:Cross-references: GB:S64717; NID:9408195; PIDN:AAB27677.1; PID:9408196  
A:Note: mutant sequence from patient with osteogenesis imperfecta  
R.Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Elkemberry, E.F.; Prockop, D.J.  
Biochemistry 22, 5213-5223, 1983  
A:Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1  
A:Reference number: A90476; PMID:84080385; PMID:6689127  
A:Accession: A90476  
A:Molecule type: mRNA  
A:Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER>  
A:Cross-references: GB:K01228; NID:9180391; PIDN:AA51995.1; PID:9180392  
A:Note: sequence partially completed for missing nucleotides by A29439  
R.Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.  
J. Biol. Chem. 260, 691-694, 1985  
A:Title: Multixon deletion in an osteogenesis imperfecta variant with increased type I  
A:Reference number: A22161; PMID:85104934; PMID:2981843  
A:Accession: A22161  
A:Molecule type: DNA  
A:Residues: 472-594, 'R', 596-607 <CH3>  
A:Cross-references: GB:K03178; GB:K03179; NID:9179613; NID:9179613; PIDN:AA51847.1; PID  
A:Note: the authors translated the codon CAG for 721 and CGT for 738 as Glu  
R.Forlino, A.; Zolozzi, F.; Valli, M.; Pignatelli, P.F.; Cetta, G.; Brunelli, P.C.; Motte  
Hum. Mol. Genet. 3, 2201-2206, 1994  
A:Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the C  
A:Reference number: I54365; PMID:95187161; PMID:7881420  
A:Accession: I54365  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 746-766, 'S', 768-781 <FOR>  
A:Cross-references: GB:L47667; NID:91009093; PIDN:AAB59576.1; PID:91009094  
R.Chessler, S.D.; Wallis, G.A.; Byers, P.H.  
J. Biol. Chem. 268, 18218-18225, 1993  
A:Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty  
A:Reference number: A47426; PMID:9352646; PMID:9349697  
A:Accession: A47426  
A:Molecule type: mRNA  
A:Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>  
A:Cross-references: GB:S64596; NID:9407589; PIDN:AAB27856.1; PID:9407590

A:Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBI:136445)  
A:Note: does not represent an experimentally determined sequence but three different  
A:Accession: B47426  
A:Molecule type: mRNA  
A:Residues: 1179-1464 <CH4>  
A:Experimental source: normal dermal fibroblast culture  
A:Accession: C47426  
A:Molecule type: mRNA  
A:Residues: 1179-1276, 'H', 1278-1464 <CH5>  
A:Experimental source: fetal cell 86-237  
A:Accession: D47426  
A:Molecule type: mRNA  
A:Residues: 1179-1336, 1339-1464 <CH6>  
A:Experimental source: fetal cell 86-146  
A:Accession: E47426  
A:Molecule type: mRNA  
A:Residues: 1179-1387, 'R', 1389-1464 <CH7>  
A:Experimental source: fetal cell 88-251  
R.Cohn, D.H.; Apone, S.; Byre, D.R.; Starman, B.J.; Andraassen, P.; Charbonneau, H.;  
J. Biol. Chem. 263, 14605-14607, 1988  
A:Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptid  
A:Reference number: I55269; PMID:89008319; PMID:3170557  
A:Accession: I55269  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1187-1194, 'C', 1196-1220 <CH8>  
A:Cross-references: GB:M23213; NID:9340842; PIDN:AAB59363.1; PID:9499622  
A:Note: mutant sequence from a patient with mild osteogenesis imperfecta  
R.Meckelae, J.K.; Raassina, M.; Virts, A.; Vuorio, E.  
Nucleic Acids Res. 16, 349, 1988  
A:Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.  
Query Match 3.7%; Score 9; DB 1; Length 1464;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1024 PGRDSPA 1032  
63 PGRDSPA 71  
1024 PGRDSPA 1032  
RESULT 7  
A60111  
sporozoite antigen - Eimeria tenella (fragment)  
C:Species: Eimeria tenella  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 17-Jul-1994  
C:Accession: A60111  
R:Miller, G.A.; Bhogal, B.S.; McCandliss, R.; Strausberg, R.L.; Jessee, E.J.; Anderso  
Infect. Immun. 57, 2014-2020, 1989  
A:Title: Characterization and vaccine potential of a novel recombinant coccidial anti  
A:Reference number: A60111; PMID:8927516; PMID:2659532  
A:Accession: A60111  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <MID>  
Query Match 3.3%; Score 8; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 16 LILLILLO 23  
LILLILLO 10  
RESULT 8  
LUTRUB  
luteolin beta chain precursor [validated] - human  
M:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizin  
C:Species: Homo sapiens (man)  
C:Date: 13-Jul-1981 #sequence\_revision 24-Nov-1999 #text\_change 20-Apr-2001  
C:Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552  
R:Rinalde, K.; Vamvakopoulos, N.C.; Fiddes, J.C.

Nature 307, 37-40, 1984  
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin and  
 A:Reference number: 137231; PMID:84093590; PMID:6690982  
 A:Accession: 137994  
 A:Status: preliminary; translated from GB/EMBL/DBJ; not compared with conceptual trans  
 A:Molecule type: DNA  
 A:Residues: 1-141 <FAL>  
 A:Cross-references: GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893  
 R:Wells, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.  
 N. Engl. J. Med. 326, 179-183, 1992  
 A:Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of  
 A:Reference number: 158013; PMID:92085985; PMID:1727547  
 A:Accession: 158013  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 72-73, 'R', 75-76 <WEI>  
 A:Cross-references: GB:S71273; NID:g240572; PIDN:AAD1960.1; PID:g4262812  
 R:Salim, M.R.; Li, C.H.  
 A:Note: mutant sequence from patient with hypogonadism  
 Biochim. Biophys. Acta 412, 70-81, 1975  
 A:Title: Human pituitary luteotropin. Isolation, properties, and the complete amino acid se  
 A:Reference number: A90604; PMID:76062547; PMID:1191677  
 A:Accession: A90604  
 A:Molecule type: protein  
 A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SAI>  
 R:Shome, B.; Parlow, A.F.  
 J. Clin. Endocrinol. Metab. 36, 618-621, 1973  
 A:Title: The primary structure of the hormone-specific, beta subunit of human pituitary  
 A:Reference number: A92759; PMID:73090987; PMID:4685398  
 A:Accession: A92759  
 A:Molecule type: protein  
 A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SHO>  
 R:Closset, J.; Hennen, G.; Leguin, R.M.  
 FEBS Lett. 29, 97-100, 1973  
 A:Title: Human lutealizing hormone the amino acid sequence of the beta subunit.  
 A:Reference number: A91389; PMID:73221227; PMID:4719207  
 A:Contents: annotation; partial sequence  
 R:Ward, D.N.  
 unpublished results, cited by Closset, J., Hennen, G., and Leguin, R.M., FEBS Lett. 29,  
 A:Reference number: A94466  
 A:Accession: A94466  
 A:Molecule type: protein  
 A:Residues: 21-38, 'Q', 40-46 <MAR>  
 A:Note: 28-Val, 33-Arg, and 35-Thr were also found  
 R:Shome, B.; Parlow, A.F.  
 submitted to the Atlas, April 1975  
 A:Reference number: A94552  
 A:Contents: annotation; binding site  
 C:Genetics:  
 A:Gene: GDB:LMB  
 A:Cross-references: GDB:119364; OMIM:152780  
 A:Map position: 19q13.3-19q13.3  
 C:Superfamily: pituitary glycoprotein hormone beta chain  
 C:Keywords: blocked amino end; glycoprotein; hormone; pituitary  
 F:1-20/Domain: signal sequence #status predicted <IG>  
 F:21-141/Product: luteotropin beta #status experimental <URB>  
 F:22/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat  
 F:29-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted  
 F:50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 3.38; Score 8; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 GLULILLL 22  
 Db 6 GLULILLL 13

## RESULT 9

## KTRHB

Chorionodotropon beta chain precursor [validated] - human  
 N:Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain

C:Species: Homo sapiens (man)  
 C:Date: 23-Oct-1991 #sequence-revision 23-Oct-1981 #text-change 08-Dec-2000  
 C:Accession: A93230; 169972; 155224; 155250; 170007; 170008; A92303; A92181; A92142;  
 R:Ridder, J.C.; Goodman, H.M.  
 Nature 286, 684-687, 1980  
 A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolu  
 A:Reference number: A93230; PMID:81012134; PMID:6774259  
 A:Accession: A93230  
 A:Molecule type: mRNA  
 A:Residues: 1-165 <FTD>  
 A:Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:AAA96690.1; PI  
 R:Pollicastro, P.; Ovitc, C.E.; Hoshiba, M.; Fukunaka, H.; Boothby, M.R.; Bolme, I.  
 J. Biol. Chem. 258, 11492-11499, 1983  
 A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple gene  
 A:Reference number: 155224; PMID:84008141; PMID:6194155  
 A:Accession: 169972  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-165 <POL>  
 A:Cross-references: GB:X03189; NID:g180450; PIDN:AAA53288.1; PID:g180453  
 A:Note: clone CG-beta-e  
 A:Accession: 155224  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-23, 'W', 25-136, 'A', 138-165 <PO2>  
 A:Cross-references: GB:X03183; NID:g180442; PIDN:AAA53287.1; PID:g180444  
 A:Note: clone CG-beta-a  
 J. Biol. Chem. 261, 5907-5916, 1986  
 A:Title: A map of the hCG beta-LH beta gene cluster.  
 A:Reference number: 155250; PMID:86195987; PMID:2422163  
 A:Accession: 155250  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PO3>  
 A:Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088  
 A:Note: CG-beta-3 gene  
 A:Accession: 170007  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PO4>  
 A:Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089  
 A:Note: CG-beta-6 gene  
 A:Accession: 170008  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5 <RES>  
 A:Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090  
 A:Note: CG-beta-7 gene  
 R:Bitken, S.; Fetherston, J.; Canfield, R.; Bolme, I.  
 J. Biol. Chem. 256, 1816-1823, 1981  
 A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta  
 A:Reference number: A92303; PMID:81117260; PMID:7462224  
 A:Accession: A92303  
 A:Molecule type: protein  
 A:Residues: 1-20 <BR>  
 A:Note: The identity of the residue at position 19 could not be determined  
 R:Morgan, F.J.; Birken, S.; Canfield, R.E.  
 J. Biol. Chem. 250, 5247-5258, 1975  
 A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit a  
 A:Reference number: A92181; PMID:75211304; PMID:1150658  
 A:Accession: A92181  
 A:Molecule type: protein  
 A:Residues: 21-165 <WOR>  
 R:Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.  
 J. Biol. Chem. 248, 6810-6827, 1973  
 A:Reference number: A92142; PMID:74011267; PMID:4795659  
 A:Accession: A92142  
 A:Molecule type: protein  
 A:Residues: 21-22, 'Q', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SRP' <CAR>  
 R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.  
 Chinese Biochem. J. 6, 558-562, 1990  
 A:Title: The immunological characteristics of the enzymatic fragments of human chorio

A:Reference number: PC1016  
 A:Accession: PC1016  
 A:Molecule type: protein  
 A:Residues: 21-165 <SH1>  
 A:Note: article in Chinese with English abstract  
 R:Birken, S.; Armstrong, E.G.; Kolke, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichewsky, A.; Endocrinology 123, 572-583, 1988  
 A:Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregnancy  
 A:Reference number: A61097; MUID:88254680; PMID:2454811  
 A:Accession: A61097  
 A:Molecule type: protein  
 A:Residues: 26-32, 'X', 34-49, 'X', 51-60;75-112 <B12>  
 A:Note: this material from pregnancy urine lacks static acid in its carbohydrate and has R:Kardana, A.; Bagshaw, K.D.; Coles, B.; Read, D.; Taylor, M.  
 Br. J. Cancer 67, 686-692, 1993  
 A:Title: Characterisation of UGP and its relationship with beta-core fragment.  
 A:Reference number: A56873; MUID:93229246; PMID:8471426  
 A:Accession: B56873  
 A:Molecule type: protein  
 A:Residues: 26-28, 'X', 30-32, 'X', 34-42, 'X', 44-45, 'X', 47-48;75-76, 'X', 78-91, 'G', 93-102 <K>  
 A:Experimental source: urine  
 A:Note: sequence modified after extraction from NCBI backbone  
 A:Note: this material was designated urinary gonadotropin peptide (peak 2)  
 R:Laphorn, A.J.; Harris, D.C.; Littlejohn, A.; Lusthader, J.W.; Canfield, R.E.; Machin, Nature 369, 455-461, 1994  
 A:Title: Crystal structure of human chorionic gonadotropin.  
 A:Reference number: A44674; MUID:94261179; PMID:8202136  
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms; correction of disulfide bc R:Talnadge, K.; Vamvakopoulos, N.C.; Fildes, J.C.  
 Nature 307, 37-40, 1984  
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin and A:Reference number: I37231; MUID:84093590; PMID:6690982  
 A:Accession: I37412  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 21-165 <RES>  
 C:Genetics:  
 A:Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:g1335075  
 C:Genetics:  
 A:Gene: GDB:CGB  
 A:Cross-references: GDB:119055; OMIM:118860  
 A:Map position: 19q13.3-19q13.3  
 A:Introns: 5/3; 61/3  
 A:Note: the chorionadotropin beta chain locus contains six genes (or pseudogenes)  
 C:Superfamily: pituitary glycoprotein hormone beta chain  
 C:Keywords: glycoprotein, hormone, pituitary  
 F:1-20/Domains: signal sequence #status experimental <SIG>  
 F:21-165/Product: chorionadotropin beta chain #status experimental <MAT>  
 F:29-77,43-92,46-108,54-110,113-120/Disulfide bonds: #status experimental  
 F:33,50/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:138,150/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 3.3%; Score 8; DB 1; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GLLILL 22  
 Db 6 GLLILL 13

RESULT 10  
 T18321  
 hypothetical protein L7610.12 - Leishmania major  
 C:Species: Leishmania major  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2002  
 C:Accession: T18321  
 R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.; submitted to the EMBL Data Library, May 1999  
 A:Reference number: Z18876  
 A:Accession: T18321  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A:Residues: 1-169 <OLI>  
 A:Cross-references: EMBL:AL034356; NID:e1371878; PIDN:CAA22247.1  
 C:Genetics:  
 A:Note: L7610.12

Query Match 3.3%; Score 8; DB 2; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PAASPOL 13  
 Db 18 PAASPOL 25

RESULT 11  
 S37749  
 collagen alpha 2(XIV) chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 08-Dec-1995  
 C:Accession: S37749  
 R:Brown, J.C.; Goldik, R.; Mann, K.; Timpl, R.  
 submitted to the EMBL Data Library, October 1993  
 A:Description: Structure and stability of the triple helical domains of human collagen  
 A:Reference number: S37749  
 A:Accession: S37749  
 A:Molecule type: protein  
 A:Residues: 1-177 <BRO>  
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.  
 C:Genetics:  
 A:Gene: COL1A2  
 C:Complex: type XIV collagen may be a heterotrimer of alpha 1(XIV) chains and one alp C:Function:  
 A:Description: structural component of extracellular fibrous polymer associated with C:Superfamily: collagen alpha 1(XIV) chain; fibronectin type III repeat homology; von C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr F:1-24,39-45,59-62,74,80,86,92,98,106,109,116,118,122,137,140/Modified site: 4-hydrox F:12/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
 F:18,143/Modified site: 5-hydroxylysine (Lys) #status experimental  
 F:18,143/Binding site: carbohydrate (Lys) (covalent) #status experimental  
 F:27/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 3.3%; Score 8; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 PGKDSPPG 70  
 Db 86 PGKDSPPG 93

RESULT 12  
 T35724  
 cobalt transport integral membrane protein - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 17-Mar-2000  
 C:Accession: T35724  
 R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, January 1998  
 A:Reference number: Z21548  
 A:Accession: T35724  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-249 <MUR>  
 A:Cross-references: EMBL:AL021411; PIDN:CAA16216.1; GSPDB:GN00070; SCOPDB:SC7H1.29c  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: cbtQ; SCOPDB:SC7H1.29c  
 C:Superfamily: cobalt transport protein Q homolog

Query Match 3.3%; Score 8; DB 2; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 9.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 GPAGVPCR 65  
 |||||||  
 Db 54 GPAGVPCR 61

## RESULT 13

138427  
 4-1BB ligand - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
 C:Accession: 138427  
 R:Alfredson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; F  
 Eur. J. Immunol. 24, 2219-2227, 1994  
 A:Title: Molecular and biological characterization of human 4-1BB and its ligand.  
 A:Reference number: 138426; MUID:94374434; PMID:8088337  
 A:Accession: 138427  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-254 <RES>  
 A:Cross-references: EMBL:U03398; NID:g571322; PIDN:AAA53134.1; PID:g571323

Query Match 3.3%; Score 8; DB 2; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 9.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GLLLLLLL 22  
 |||||||  
 Db 34 GLLLLLLL 41

## RESULT 14

B60131  
 homeotic protein Xhox-7.1' - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 24-Sep-1999  
 C:Accession: B60131; S14514  
 R:Su, M.W.; Suzuki, H.R.; Solursh, M.; Ramirez, F.  
 Development 111, 1179-1187, 1991  
 A:Title: Progressively restricted expression of a new homeobox-containing gene during Xe  
 A:Reference number: A60131; MUID:91347929; PMID:1679007  
 A:Accession: B60131  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-9, 'P', 11-291 <SUA>  
 A:Cross-references: EMBL:X58772  
 R:Su, M.W.; Suzuki, H.R.; Solursh, M.; Ramirez, F.  
 submitted to the EMBL Data Library, December 1990  
 A:Reference number: S14513  
 A:Accession: S14514  
 A:Molecule type: mRNA  
 A:Residues: 1-291 <SUA>  
 A:Cross-references: EMBL:X58772; NID:g64784; PIDN:CAA41573.1; PID:g64785  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:161-217/Domain: homeobox homology <HOX>

## Query Match

Best Local Similarity 3.3%; Score 8; DB 2; Length 291;  
 Pred. No. 10;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLLQ 23  
 |||||||  
 Db 6 LLLLLLLQ 13

## RESULT 15

T24827  
 hypothetical protein T11B7.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1989 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T24827  
 R:Gardner, A.

submitted to the EMBL Data Library, September 1995  
 A:Reference number: T24827  
 A:Accession: T24827

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-296 <WIL>

A:Cross-references: EMBL:Z54237; PIDN:CAA90989.1; GSPDB:GN00022; CESP:T11B7.3

A:Experimental source: clone T11B7

C:Genetics:

A:Gene: CESP:T11B7.3

A:Map position: 4

A:Introns: 45/3; 111/1; 270/1

C:Superfamily: unassigned collagens

Search completed: August 13, 2003, 13:41:08

Job time : 40 secs

Query Match 3.3%; Score 8; DB 2; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 PGIPGRDG 85  
 |||||||  
 Db 266 PGIPGRDG 273

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:28:47 ; Search time 23 Seconds

(Without alignments)  
496.847 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MRPGPASPRLRGILL...GDASTGMSVSRITIELPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1289

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	3.7	120	GON2_HUMAN	O43555 homo sapien
2	9	3.7	133	XJ23_YEAST	P47004 saccharomyc
3	9	3.7	779	CA11_BOVIN	P02453 bos taurus
4	9	3.7	813	CADM_RAT	O63315 rattus norv
5	9	3.7	905	ATS8_MOUSE	P57110 mus musculu
6	9	3.7	1464	CA11_HUMAN	P02452 homo sapien
7	8	3.3	141	LSHB_HUMAN	P01229 homo sapien
8	8	3.3	165	CGHB_HUMAN	P01223 homo sapien
9	8	3.3	233	RS3_BUCAP	O8K956 buchiera ap
10	8	3.3	246	MOG_MOUSE	O61885 mus musculu
11	8	3.3	254	TNFP_HUMAN	P41273 homo sapien
12	8	3.3	291	HXP7_XENTLA	P35993 xenopus lae
13	8	3.3	365	WNT6_HUMAN	O9Y669 homo sapien
14	8	3.3	424	GSA_AQUAE	O66998 aquilex aeo
15	8	3.3	457	CD4_MOUSE	P06332 mus musculu
16	8	3.3	487	CP51_MOUSE	P03940 mus musculu
17	8	3.3	500	CAMA_MOUSE	P51942 mus musculu
18	8	3.3	636	CA13_RAT	P13941 rattus norv
19	8	3.3	652	CD93_HUMAN	O9NPJ3 homo sapien
20	8	3.3	674	CA1A_CHICK	O98125 gallus gall
21	8	3.3	787	NAH2_HUMAN	O98835 homo sapien
22	8	3.3	809	NAH2_RABIT	O50482 oryctolagus
23	8	3.3	832	SM4B_HUMAN	O9NP22 homo sapien
24	8	3.3	984	PK12_HUMAN	O16513 homo sapien
25	8	3.3	1019	CA26_HUMAN	P12110 homo sapien
26	8	3.3	1029	CA26_MOUSE	O02788 mus musculu
27	8	3.3	1103	CYGD_HUMAN	O02846 homo sapien
28	8	3.3	1108	CYGE_MOUSE	P52785 mus musculu
29	8	3.3	1108	CYGE_RAT	P51840 rattus norv
30	8	3.3	1266	NGCA_CHICK	O03696 gallus gall
31	8	3.3	1278	NPQ1_MOUSE	O35604 mus musculu
32	8	3.3	1355	CA21_RANCA	O42350 rana catesb
33	8	3.3	1388	CA1E_HUMAN	P39059 homo sapien

34	8	3.3	1460	CA11_CANFA	O9X577 canis famli1
35	8	3.3	1464	CA13_MOUSE	P08121 mus musculu
36	8	3.3	1466	CA13_HUMAN	P02461 homo sapien
37	8	3.3	1531	MRP1_HUMAN	P33527 homo sapien
38	8	3.3	1564	MRP2_RABIT	O28689 oryctolagus
39	7	2.9	31	LPL_BUCRP	O33017 buchiera ap
40	7	2.9	61	DNBI_BFDV	P13893 budgerigar
41	7	2.9	77	ENV_SMSAV	P03384 simlan sarc
42	7	2.9	77	YF78_ARCFU	O28694 archaeoglob
43	7	2.9	84	HEPC_HUMAN	P81172 homo sapien
44	7	2.9	100	MI2B_RAT	O10747 rattus norv
45	7	2.9	101	GRO_CRIGR	P09340 cricetus

## ALIGNMENTS

RESULT 1	ID	SEQUENCE	STANDARD	PRT	AA
GON2_HUMAN	GON2_HUMAN	043555; Q9BYN9; Q9BYP0;			
AC	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Progonadoliberin II precursor [Contains: Gonadoliberin II (LH-RH II) (Luteinizing hormone-releasing hormone II) (Gonadotropin-releasing hormone II) (GnRH II) (Luliberin II); GnRH-associated peptide II).				
GN	GNRH2				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE-98081869; PubMed-9419371.				
RA	White R.B., Eisen J.A., Kasten T.L., Fernald R.D.;				
RT	"Second gene for gonadotropin-releasing hormone in humans.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:305-309(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).				
RX	MEDLINE-21638749; PubMed-11780052;				
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,				
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.R., Bagguley C.L.,				
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,				
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,				
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,				
RA	Chapman J.C., Clamp W., Clark G., Clark L.N., Clark S.Y., Clee C.M.,				
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,				
RA	Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,				
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,				
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,				
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,				
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,				
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.R., Lawlor S.,				
RA	Lehvasaaho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,				
RA	Marsh V.L., Martin S.L., McConachle L.J., McRay K., McMurray A.A.,				
RA	Malne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nicolson T.,				
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.T.,				
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,				
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,				
RA	Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,				
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,				
RA	Tracey A., Tromans A.C., Taulin M., Wall M., Wallis J.M., Williams S.A.,				
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,				
RA	Willing L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,				
RA	Rogers J.;				
RT	"The DNA sequence and comparative analysis of human chromosome 20.";				
RL	Nature 414:865-871(2001).				
CC	-1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS. IT STIMULATES				
CC	THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING				
CC	HORMONES.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- ALTERNATIVE PRODUCTS:				

CC Event-Alternative splicing; Named isoforms-3;  
 CC Comment-Experimental confirmation may be lacking for some  
 CC Isoforms;  
 CC Name-1;  
 CC IsoId=043555-1; Sequence-Displayed;  
 CC Name-2;  
 CC IsoId=043555-2; Sequence-VSP\_001825;  
 CC Name-3;  
 CC IsoId=043555-3; Sequence-VSP\_001826;  
 CC TISSUE SPECIFICITY: MIDBRAIN; EXPRESSED AT SIGNIFICANTLY HIGHER  
 CC LEVELS OUTSIDE THE BRAIN (UP TO 30-FOLD), PARTICULARLY IN THE  
 CC KIDNEY, BONE MARROW, AND PROSTATE.  
 CC -1 SIMILARITY: Belongs to the GNRH family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF036329; AAC02980.1; -  
 CC EMBL; AF036330; AAC02981.1; -  
 CC EMBL; AL121905; CAC10338.1; -  
 CC EMBL; AL121905; CAC29100.1; -  
 CC EMBL; AL121905; CAC29101.1; -  
 CC Genew; HGNC:4420; GNRH2.  
 CC MIM; 602352; -  
 CC DR GO; 0005625; C:soluble fraction; TAS.  
 CC DR GO; 0005179; P:hormone activity; TAS.  
 CC DR GO; 0007165; P:signal transduction; TAS.  
 CC InterPro; IPR02012; GNRH.  
 CC DR Pfam; PF00446; GNRH; 1.  
 CC DR PROSITE; PS00473; GNRH; 1.  
 CC KM Cleavage on pair of basic residues; Hormone; Amidation; Signal;  
 CC Alternative splicing; Pyrrolidone carboxylic acid.  
 CC FT SIGNAL 1 23  
 CC FT CHAIN 24 120  
 CC FT PEPTIDE 24 33  
 CC FT PEPTIDE 39 120  
 CC FT MOD\_RES 24 24  
 CC FT MOD\_RES 33 33  
 CC FT VARSPPLIC 52 59  
 CC FT VARSPPLIC 52 58  
 CC FT VARSPPLIC 52 58  
 CC SEQUENCE 120 AA; 12917 MW; D58CDA14B6D6FB8D CRC64;  
 CC  
 CC Query Match 3.7%; Score 9; DB 1; Length 120;  
 CC Best Local Similarity 100.0%; Pred. No. 0.34;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC DB 14 RGLILLLL 22  
 CC 6 RGLILLLL 14  
 CC  
 CC RESULT 2  
 CC ID YJ23 YEAST STANDARD; PRT: 133 AA.  
 CC AC P47094;  
 CC DT 01-FEB-1996 (Rel. 33, Created)  
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 CC DE Hypothetical 15.3 kDa protein in MER2-BN1 intergenic region.  
 CC GN YJ0823C OR J1470 OR YJ083.19.  
 CC OS Saccharomyces cerevisiae (Paker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CC OX NCBI\_TaxID=4932;  
 CC RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-S288c / FY1679;  
 RA de Haan M., Smits P.H.M., Grievell L.A.;  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 13-93 FROM N.A.  
 RX MEDLINE=9610930; PubMed=8619316;  
 RA Zagulski M., Babinska B., Gromadka R., Migdalski A., Rytko J.,  
 RA Sulicka J., Herbert C.J.;  
 RT The sequence of 24.3 kb from chromosome X reveals five complete open  
 RT reading frames, all of which correspond to new genes, and a tandem  
 RT insertion of a Ty1 transposon.  
 RL Yeast 11:1179-1186(1995).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X87611; CAA60946.1; -  
 CC EMBL; Z49522; CAA89548.1; -  
 CC PIR; S57038; S57038.  
 CC DR SCD; S0003784; YJ023C.  
 CC KW Hypothetical protein; Transmembrane.  
 CC FT TRANSMEM 8 28  
 CC FT TRANSMEM 46 66  
 CC FT DOMAIN 10 30  
 CC FT DOMAIN 28 28  
 CC FT CONFLICT 133 AA; 15282 MW; 4303172FF250008 CRC64;  
 CC SEQUENCE  
 CC  
 CC Query Match 3.7%; Score 9; DB 1; Length 133;  
 CC Best Local Similarity 100.0%; Pred. No. 0.37;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC DB 16 LILLILL 24  
 CC 22 LILLILL 30  
 CC  
 CC RESULT 3  
 CC ID CALL BOVIN STANDARD; PRT: 779 AA.  
 CC AC P02453;  
 CC DT 21-JUL-1986 (Rel. 01, Created)  
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Collagen alpha 1(I) chain (fragments).  
 CC GN COL1A1.  
 CC OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC OX NCBI\_TaxID=9913;  
 CC RN [1]  
 CC SEQUENCE OF 1-19.  
 CC RX MEDLINE=7225334; PubMed=4115172;  
 CC RA Rautenberg J., Timpl R., Furtmayr H.;  
 CC RT "Structural characterization of N-terminal antigenic determinants in  
 CC RT calf and human collagen."  
 CC RL Eur. J. Biochem. 27:231-237(1972).  
 CC RN [2]  
 CC SEQUENCE OF 20-145.  
 CC RX MEDLINE=7602320; PubMed=1164916;  
 CC RA Fietzek P.P., Kuehn K.;  
 CC RT "The covalent structure of collagen: amino-acid sequence of the  
 CC RT cyanoogen-bromide peptides alpha-1-CB2, alpha-1-CB4 and alpha-1-CB5  
 CC RT from calf-skin collagen."  
 CC RL Eur. J. Biochem. 52:77-82(1975).  
 CC RN [3]  
 CC SEQUENCE OF 146-294.

RA MEDLINE-73049499; PubMed-4673951.  
 RA Fietzek P.P., Wendt P., Kell I., Kuehn K.;  
 RT "The covalent structure of collagen: amino acid sequence of alpha-1-  
 RT C3 from calf skin collagen.";  
 RL FEBS Lett. 26:74-76(1972).  
 RN [4]  
 RP SEQUENCE OF 295-562.  
 RX MEDLINE-74086118; PubMed-4359390;  
 RA Fietzek P.P., Rexrodt F.W., Hopper K.E., Kuehn K.;  
 RT "The covalent structure of collagen. 2. The amino-acid sequence of  
 RT alpha-1-CB7 from calf-skin collagen.";  
 RL Eur. J. Biochem. 38:396-400(1973).  
 RN [5]  
 RP SEQUENCE OF 563-675.  
 RX MEDLINE-73042276; PubMed-4343808;  
 RA Wendt P., Mark K.V.D., Rexrodt F., Kuehn K.;  
 RT "The covalent structure of collagen. The amino-acid sequence of the  
 RT 112-residues. Amino-terminal part of peptide alpha-1-CB6 from calf-  
 RT skin collagen.";  
 RL Eur. J. Biochem. 30:169-183(1972).  
 RN [6]  
 RP SEQUENCE OF 676-751.  
 RX MEDLINE-73042275; PubMed-4343807;  
 RA Fietzek P.P., Rexrodt F.W., Wendt P., Stark M., Kuehn K.;  
 RT "The covalent structure of collagen. Amino-acid sequence of peptide  
 RT alpha-1-CB6-C2.";  
 RL Eur. J. Biochem. 30:163-168(1972).  
 CC -1- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN  
 CC (FIBRILLAR FORMING COLLAGEN).  
 CC -1- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.  
 CC -1- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND  
 CC BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM  
 CC HYDROXYAPATITE.  
 CC -1- PPM: Proline residues at the third position of the tripeptide  
 CC repeating unit (G-X-Y) are hydroxylated in some or all of the  
 CC chains. Pro-726 is the only 3-hydroxypro and the only hydroxylated  
 CC proline in position X.  
 CC -1- PPM: O-linked glycan consists of a Glc-Gal disaccharide bound to  
 CC the oxygen atom of a post-translationally added hydroxyl group.  
 CC -1- MISCELLANEOUS: THE COMPLETE CHAIN CONTAINS 1052 RESIDUES.  
 CC PIR: A91193; CGB015.  
 DR InterPro: IPR000087; Collagen.  
 DR InterPro: IPR001007; WFC\_C.  
 DR PRODOM: PD000007; C1g\_helix; 1.  
 DR PROSITE: PS01208; WFC\_1; PARTIAL.  
 KM Extracellular matrix; Connective tissue; Repeat; Hydroxylation;  
 KM Glycoprotein; Collagen; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 9 9  
 FT MOD\_RES 9 9  
 FT MOD\_RES 103 103  
 FT CARBOHYD 103 103  
 FT MOD\_RES 115 115  
 FT MOD\_RES 124 124  
 FT MOD\_RES 145 146  
 FT MOD\_CONS 274 274  
 FT MOD\_RES 346 346  
 FT MOD\_RES 424 424  
 FT MOD\_RES 496 496  
 FT MOD\_RES 658 658  
 FT MOD\_RES 670 670  
 FT MOD\_RES 726 726  
 FT MOD\_RES 726 726  
 SQ SEQUENCE 779 AA; 70346 MW; E554A7FF084283D1 CRC64;

Query Match 3.7%; Score 9; DB 1; Length 779;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 PGRDSPA 71  
 |||||  
 DB 586 PGRDSPA 594

RESULT 4  
 ID CADM\_RAT STANDARD; PRT; 813 AA.  
 AC 063315; 063561;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cadherin-22 precursor (PB-cadherin).  
 OS CDH22.  
 GN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.  
 RC STRAIN=Wistar; TISSUE=Brain, and Pituitary;  
 RX MEDLINE-9621232; PubMed-8626716;  
 RA Sugimoto K., Honda S., Yamamoto T., Ueki T., Monden M., Kajl A.,  
 RA Matsumoto K., Nakamura T.;  
 RT "Molecular cloning and characterization of a newly identified member  
 RT of the cadherin family, PB-cadherin.";  
 RL J. Biol. Chem. 271:11548-11556(1996).  
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.  
 CC They preferentially interact with themselves in a homophilic  
 CC manner in connecting cells; cadherins may thus contribute to the  
 CC sorting of heterogeneous cell types. PB-cadherins may have a role  
 CC in the morphological organization of pituitary gland and brain  
 CC tissues.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=063315-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=063315-2; Sequence=VSP\_000643, VSP\_000644;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Strongly expressed in the pituitary gland and  
 CC the brain (in the inner granular and glomerular layers of the  
 CC olfactory bulb, anterior olfactory nucleus, primary olfactory  
 CC cortex, Purkinje cell layer of cerebellum, and pineal gland). Low  
 CC expression in lung and heart. No expression in submandibular  
 CC gland, thymus, liver, spleen, adrenal, and kidney.  
 CC -1- DEVELOPMENTAL STAGE: Expressed strongly in fetal brain.  
 CC -1- SIMILARITY: Contains 5 cadherin domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; D83348; BA011894.1; -;  
 DR EMBL; D83349; BA011895.1; -;  
 DR HSSP; P15116; INCU.  
 DR InterPro: IPR002126; Cadherin.  
 DR InterPro: IPR000233; Cadherin\_C\_term.  
 DR Pfam; PF00028; cadherin\_5.  
 DR Pfam; PF01043; Cadherin\_C\_term; 1.  
 DR PRINTS; PR0205; CADHERIN.  
 DR SMART; SM00112; CA; 5.  
 DR PROSITE; PS00232; CADHERIN\_1; 2.  
 DR PROSITE; PS0268; CADHERIN\_2; 5.  
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;  
 KW Signal; Alternative splicing.  
 FT SIGNAL 1 33  
 FT CHAIN 34 813  
 FT DOMAIN 33 621  
 FT TRANSMEM 622 642  
 FT DOMAIN 643 813  
 FT DOMAIN 61 165  
 FT DOMAIN 166 274  
 FT DOMAIN CADHERIN 2.  
 FT DOMAIN CADHERIN 2.

**Query Match**

Best Local Similarity    3.7%    Score 9; DB 1; Length 905;  
Matches    9; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

DQ         17 LLLLIIQLP 25  
            |  
Db         13 LLLLIIQLP 21

**RESULT 6**

CALL\_HUMAN STANDARD; PRT; 1464 AA.

ID CALL\_HUMAN STANDARD; PRT; 1464 AA.  
AC P02452; Q14037; Q15176;  
DT 21-JUL-1986 (Rel. 01, Created)  
DI 01-MAR-1989 (Rel. 10, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DR Collagen alpha 1(I) chain precursor.  
DS COL1A1.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 1-472 FROM N.A.  
RX MEDLINE=89025644; PubMed=3178743;  
RA Tromp G., Kuliyanti H., Stacey A., Shikata H., Baldwin C.T.,  
R Jaenisch R., Prockup D.J.;  
RT "Structure of a full-length cDNA clone for the prepro alpha 1(I)  
chain of human type I procollagen.",  
RL Biochem. J. 253:919-922(1988).  
RN [2]  
RP SEQUENCE OF 1-181 FROM N.A.  
RX MEDLINE=84270697; PubMed=6462220;  
RA Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,  
R Myers J., Williams C., Ramirez F.;  
RT "Human pro alpha 1(I) collagen gene structure reveals evolutionary  
conservation of a pattern of introns and exons.",  
RL Nature 310:337-340(1984).  
RN [3]

SEQUENCE OF 162-301.  
FP TISSUE-Skin;  
RX MEDLINE=71038625; PubMed=5529814;  
RA Click E.M., Bornstein P.;  
RT "Isolation and characterization of complementary DNA clones encoding  
the rat alpha 1(I) procollagen chain."

RT the alpha 1 and alpha 2 chains of human skin collagen.";  
 RL Biochemistry 9:4659-4706(1970).  
 [4]  
 RP SEQUENCE OF 263-268.  
 RC TISSUE-Skin;  
 RX MEDLINE-71001508; PubMed-4319110;  
 RA Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;  
 RT "A comparative study of glycopeptides derived from selected  
 RT vertebrate collagens. A possible role of the carbohydrate in fibril  
 RT formation.";  
 RL J. Biol. Chem. 245:5042-5048(1970).  
 [5]  
 RP SEQUENCE OF 425-1464 FROM N.A.  
 RX MEDLINE-84080385; PubMed-6689127;  
 RA Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Elkenberry E.F.,  
 RT Prockop D.J.;  
 RT "Nucleotide sequences of complementary deoxyribonucleic acids for the  
 RT pro alpha 1 chain of human type I procollagen. Statistical evaluation  
 RT of structures that are conserved during evolution.";  
 RL Biochemistry 22:5213-5223(1983).  
 [6]  
 RP SEQUENCE OF 1229-1454 FROM N.A.  
 RC TISSUE-Bone;  
 RX MEDLINE-88124208; PubMed-3340531;  
 RA Mackelae J.K., Raassina M., Virta A., Vuorio E.;  
 RT "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide  
 RT domain.";  
 RL Nucleic Acids Res. 16:349-349(1988).  
 [7]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE-88097389; PubMed-3480516;  
 RA Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gellinas R.E.;  
 RT "Regulatory elements in the first intron contribute to  
 RT transcriptional control of the human alpha 1(I) collagen gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).  
 [8]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE-85130970; PubMed-2857713;  
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;  
 RT "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.  
 RT Promoter structure, Alu repeats, and polymorphic transcripts.";  
 RL J. Biol. Chem. 260:2315-2320(1985).  
 [9]  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE-88033098; PubMed-2822714;  
 RA Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,  
 RT de Wet W.J.;  
 RT "DNA sequences in the first intron of the human pro-alpha 1(I)  
 RT collagen gene enhance transcription.";  
 RL J. Biol. Chem. 262:15151-15157(1987).  
 [10]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-91184577; PubMed-2010058;  
 RA Kuivanen H., Tromp G., Prockop D.J.;  
 RT "Mutations in collagen genes: causes of rare and some common diseases  
 RT in humans.";  
 RL FASEB J. 5:2052-2060(1991).  
 [11]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-97255959; PubMed-9101290;  
 RA Kuivanen H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 RT associated collagen (type IX), and network-forming collagen (type X)  
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 [12]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-91374476; PubMed-1895312;  
 RA Byers P.H., Wallis G.A., Willing M.C.;  
 RT "Osteogenesis imperfecta: translation of mutation to phenotype.";  
 RL J. Med. Genet. 28:433-442(1991).  
 [13]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-97169389; PubMed-9016532;  
 RA Daigleish R.;  
 RT "The human type I collagen mutation database.";  
 RL Nucleic Acids Res. 25:181-187(1997).  
 [14]  
 RP VARIANT OF-II CYS-1166.  
 RX MEDLINE-86287390; PubMed-3016737;  
 RA Cohn D.H., Byers P.H., Steinmann B., Gellinas R.E.;  
 RT "Lethal osteogenesis imperfecta resulting from a single nucleotide  
 RT change in one human pro alpha 1(I) collagen allele.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).  
 [15]  
 RP VARIANT OF-II ARG-569.  
 RX MEDLINE-87222295; PubMed-3108247;  
 RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;  
 RT "Lethal perinatal osteogenesis imperfecta due to the substitution of  
 RT arginine for glycine at residue 391 of the alpha 1(I) chain of type I  
 RT collagen.";  
 RL J. Biol. Chem. 262:7021-7027(1987).  
 [16]  
 RP VARIANT OF-II CYS-926.  
 RX MEDLINE-88033031; PubMed-3667599;  
 RA Vogel B.E., Minor R.R., Freund M., Prockop D.J.;  
 RT "A point mutation in a type I procollagen gene converts glycine 748  
 RT of the alpha 1 chain to cysteine and destabilizes the triple helix in  
 RT a lethal variant of osteogenesis imperfecta.";  
 RL J. Biol. Chem. 262:14737-14744(1987).  
 [17]  
 RP VARIANT OF-II ARG-842.  
 RX MEDLINE-88298828; PubMed-3403550;  
 RA Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;  
 RT "Substitution of arginine for glycine 664 in the collagen alpha 1(I)  
 RT chain in lethal perinatal osteogenesis imperfecta. Demonstration of  
 RT the peptide defect by in vitro expression of the mutant cDNA.";  
 RL J. Biol. Chem. 263:11627-11630(1988).  
 [18]  
 RP VARIANT OF CYS-1195.  
 RX MEDLINE-89218628; PubMed-3244312;  
 RA Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;  
 RT "A cysteine for glycine substitution at position 1017 in an alpha  
 RT 1(I) chain of type I collagen in a patient with mild dominantly  
 RT inherited osteogenesis imperfecta.";  
 RL Mol. Biol. Med. 5:197-207(1988).  
 [19]  
 RP VARIANT OF-II VAL-434.  
 RX MEDLINE-89255493; PubMed-2470760;  
 RA Patterson E., Smiley E., Bonadio J.;  
 RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta  
 RT mutation.";  
 RL J. Biol. Chem. 264:10083-10087(1989).  
 [20]  
 RP VARIANT OF-IV SER-1010.  
 RX MEDLINE-89308591; PubMed-2745420;  
 RA Martin J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koepf D.A.;  
 RT "Osteogenesis imperfecta type IV. Detection of a point mutation in  
 RT one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";  
 RL J. Biol. Chem. 264:11893-11900(1989).  
 [21]  
 RP VARIANTS OF-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.  
 RX MEDLINE-89380165; PubMed-277764;  
 RA Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;  
 RT "Characterization of point mutations in the collagen COL1A1 and  
 RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";  
 RL J. Biol. Chem. 264:15809-15812(1989).  
 [22]  
 RP VARIANT OF SER-1022.  
 RX MEDLINE-90062068; PubMed-2511192;  
 RA Pack M., Constantino C.D., Kalia K., Nielsen K.B., Prockop D.J.;  
 RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe  
 RT variant of osteogenesis imperfecta minimally destabilizes the triple  
 RT helix of type I procollagen. The effects of glycine substitutions on  
 RT thermal stability are either position of amino acid specific.";  
 RL J. Biol. Chem. 264:19694-19699(1989).

RN [23]  
 RP VARIANT OI-II CYS-1082.  
 RX MEDLINE-89109573; PubMed-2913053;  
 RA Constantinou C.D., Nielsen K.B., Prockop D.J.;  
 RT "A lethal variant of osteogenesis imperfecta has a single base  
 RT mutation that substitutes cysteine for glycine 904 of the alpha 1(I)  
 RT chain of type I procollagen. The asymptomatic mother has an  
 RT unidentified mutation producing an overmodified and unstable type I  
 RT procollagen.";  
 RL J. Clin. Invest. 83:574-584(1989).  
 RN [24]  
 RP VARIANTS OI CYS-272; CYS-704 AND CYS-896.  
 RX MEDLINE-90009313; PubMed-2794057;  
 RA Starman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,  
 RA Weiss L., Graham J.M., Byers P.H.;  
 RT "Osteogenesis imperfecta. The position of substitution for glycine by  
 RT cysteine in the triple helical domain of the pro alpha 1(I) chains of  
 RT type I collagen determines the clinical phenotype.";  
 RL J. Clin. Invest. 84:1206-1214(1989).  
 RN [25]  
 RP VARIANT OI-II CYS-422.

Query Match 3.7%; Score 9; DB 1; Length 1464;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 PGDGSFGA 71  
 Db 1024 PGDGSFGA 1032

RESULT 7  
 LSHB\_HUMAN  
 ID LSHB\_HUMAN STANDARD; PRT; 141 AA.  
 AC P01229;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-  
 DE beta) (LSH-B) (LH-B).  
 GN LHB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-84093590; PubMed-6690982;  
 RA Talmadge R., Vamvakopoulos N.C., Fiddes J.C.;  
 RT "Evolution of the genes for the beta subunits of human chorionic  
 RT gonadotropin and luteinizing hormone.";  
 RL Nature 307:37-40(1984).  
 RN [2]  
 RP SEQUENCE OF 21-141.  
 RX MEDLINE-76062547; PubMed-1191677;  
 RA Saitam M.R., Li C.H.;  
 RT "Human pituitary lutropin. Isolation, properties, and the complete  
 RT amino acid sequence of the beta-subunit.";  
 RL Biochim. Biophys. Acta 412:70-81(1975).  
 RN [3]  
 RP PRELIMINARY SEQUENCE OF 21-141.  
 RX MEDLINE-73090987; PubMed-4685398;  
 RA Shome B., Parlow A.F.;  
 RT "The primary structure of the hormone-specific, beta subunit of human  
 RT pituitary luteinizing hormone (hLH).";  
 RL J. Clin. Endocrinol. Metab. 36:618-621(1973).  
 RN [4]  
 RP PRELIMINARY PARTIAL SEQUENCE.  
 RX MEDLINE-73221227; PubMed-4719207;  
 RA Closset J., Heenen G., Leguin R.M.;  
 RT "Human luteinizing hormone. The amino acid sequence of the  
 RT subunit.";  
 RL FEBS Lett. 29:97-100(1973).

RN [5]  
 RP STRUCTURE OF CARBOHYDRATE.  
 RX MEDLINE-91122088; PubMed-1991473;  
 RA Weishaar G., Hiyma J., Renwick A.G.C., Nintz M.;  
 RT "NMR investigations of the N-linked oligosaccharides at individual  
 RT glycosylation sites of human lutropin.";  
 RL Eur. J. Biochem. 195:257-268(1991).  
 RN [6]  
 RP STRUCTURE BY NMR OF 58-77.  
 RX MEDLINE-92357029; PubMed-1495492;  
 RA Keutmann H.T., Hua O.-X., Weiss M.A.;  
 RT "Structure of a receptor-binding fragment from human luteinizing  
 RT hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic  
 RT resonance spectroscopy.";  
 RL Mol. Endocrinol. 6:904-913(1992).  
 RN [7]  
 RP VARIANT HYPOGONADISM ARG-74.  
 RX MEDLINE-92085985; PubMed-1727547;  
 RA Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,  
 RA Jameson J.L.;  
 RT "Hypogonadism caused by a single amino acid substitution in the beta  
 RT subunit of luteinizing hormone.";  
 RL New Engl. J. Med. 326:179-183(1992).  
 RN [8]  
 RP VARIANT SER-122.  
 RX PubMed-9457942;  
 RA Liao W.X., Roy A.C., Chan C., Arulkumaran S., Ratnam S.S.;  
 RT "A new molecular variant of luteinizing hormone associated with female  
 RT infertility.";  
 RL Fertil. Steril. 69:102-106(1998).  
 RN [9]  
 RP VARIANTS ARG-28 AND THR-35.  
 RX PubMed-9886510;  
 RA Takahashi K., Kurioka H., Ozaki T., Kanasaki H., Kohsaka M.,  
 RA Miyazaki K., Karino K.;  
 RT "Increased prevalence of luteinizing hormone beta-subunit variant in  
 RT Japanese infertile patients.";  
 RL Hum. Reprod. 13:338-344(1998).  
 RN [10]  
 RP VARIANT THR-18.  
 RX PubMed-11870227;  
 RA Jiang M., Lamminen T., Pakarinen P., Hellman J., Manna P.,  
 RA Herrera R.J., Huhnamemi I.;  
 RT "A novel Ala(-3)Thr mutation in the signal peptide of human  
 RT luteinizing hormone beta-subunit: potentiation of the inositol  
 RT phosphate signalling pathway and attenuation of the adenylate cyclase  
 RT pathway by recombinant variant hormone.";  
 RL Mol. Hum. Reprod. 8:201-212(2002).  
 RN [11]  
 RP FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC [1] TISSUE SPECIFICITY: PITUITARY.  
 CC [1] DISEASE: Defects in LHB are a cause of hypogonadism [MIM:152780]  
 CC which is characterized by infertility and pseudohypoparathyroidism.  
 CC [1] SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
 CC FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X00264; CA425067.1;  
 CC EMBL: S71273; AAD14960.1; ALT\_SEQ.  
 CC PIR: I37994; UTHUB.  
 CC HSSP: P01233; 1XU.  
 CC GlycoSuiteDB: P01229;  
 CC Genew: HGNC:6584; LHB.





RL J. Biol. Chem. 261:5907-5916(1986).  
 RN [10]  
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
 RX MEDLINE-81215630; PubMed-7240231;  
 RA Mise T., Bahl O.P.;  
 RT "Assignment of disulfide bonds in the beta subunit of human chorionic  
 RL gonadotropin.";  
 RN J. Biol. Chem. 256:6587-6592(1981).  
 RP DISULFIDE BONDS.  
 RX MEDLINE-90094415; PubMed-1688430;  
 RA Saccuzzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,  
 RT "Role of disulfide bond formation in the folding of human chorionic  
 RL gonadotropin beta subunit into an alpha beta dimer assembly-competent  
 RT form.";  
 RN J. Biol. Chem. 265:312-317(1990).  
 RP STRUCTURE OF CARBOHYDRATES.  
 RX MEDLINE-92314469; PubMed-1820200;  
 RA Weisshaar G., Hiyama J., Renwick A.G.C.;  
 RT "Site-specific N-glycosylation of human chorionic gonadotropin --  
 RL structural analysis of glycopeptides by one- and two-dimensional 1H  
 RT NMR spectroscopy.";  
 RN Glycobiology 1:393-404(1991).  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE-94261179; PubMed-8202136;  
 RA Lathhorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,  
 RT Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;  
 RL "Crystal structure of human chorionic gonadotropin.";  
 RN Nature 369:455-461(1994).  
 RP -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT  
 CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.  
 CC -1- SUBUNIT: HETEROIDIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTRONIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC -1- TISSUE SPECIFICITY: PLACENTA.  
 CC -1- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.  
 CC -1- PHARMACEUTICAL: Available under the names Novarel (Ferring) and  
 CC Profasi (Serono).  
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
 CC or send an email to [license@sib.ch](mailto:license@sib.ch)).  
 CC -----  
 DR EMBL; J00117; AAA96690.1; -  
 DR EMBL; X00265; CAA25068.1; ALT\_INIT.  
 DR EMBL; X00266; CAA25069.1; ALT\_INIT.  
 DR EMBL; M13504; AAA52005.1; -  
 DR EMBL; M13505; AAA52008.1; -  
 DR EMBL; M13503; AAA52009.1; -  
 DR EMBL; K03189; AAA53288.1; -  
 DR EMBL; K03187; AAA53288.1; JOINED.  
 DR EMBL; K03188; AAA53288.1; JOINED.  
 DR EMBL; K03183; AAA53287.1; -  
 DR EMBL; K00092; AAA53287.1; JOINED.  
 DR EMBL; BC006290; AAH06990.1; JOINED.  
 DR EMBL; BC022796; AAH22796.1; -  
 DR EMBL; BC030994; AAH30994.1; -  
 DR EMBL; AF397576; AAL69704.1; -  
 DR EMBL; AF397577; AAL69705.1; -  
 DR EMBL; AF397578; AAL69706.1; -  
 DR EMBL; AF397579; AAL69707.1; -  
 DR EMBL; AF397580; AAL69708.1; -  
 DR PIR; A93230; KTHOB.

DR PDB; 1HCN; 30-SEP-94.  
 DR PDB; 1HRP; 01-NOV-94.  
 DR PDB; 1OFW; 26-APR-00.  
 DR PDB; 1XUL; 15-MAY-97.  
 DR GlycoSuiteDB; P01233; -  
 DR Genew; HGNC:1866; CGB.  
 DR Genew; HGNC:16451; CGB7.  
 DR Genew; HGNC:16452; CGB5.  
 DR MIM; 118860; -  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005179; F:hormone activity; TAS.  
 DR GO; GO:0006915; P:apoptosis; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007292; P:ogenesis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR006208; Cys\_knot.  
 DR InterPro; IPR002400; GF\_cys\_knot.  
 DR InterPro; IPR001545; Gly\_hormoneb.  
 DR Pfam; PF00007; Cys\_knot; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR SMART; SM00068; GHB; 1.  
 DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE; PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 DR Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure;  
 DR Polymorphism.  
 FT SIGNAL 1 20  
 FT CHAIN 29 165 CHORIONGONADOTROPIN BETA CHAIN.  
 FT DISULFID 29 77  
 FT DISULFID 43 92  
 FT DISULFID 46 130  
 FT DISULFID 54 108  
 FT DISULFID 58 110  
 FT DISULFID 113 120  
 FT CARBOHYD 33 33  
 FT  
 Query Match 33%; Score 8; DB 1; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 GLLILL 22  
 DB 6 GLLILL 13  
 RESULT 9  
 RS3\_BUCAP STANDARD; PRT; 233 AA.  
 AC Q8K956;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 30S ribosomal protein S3.  
 GN RPS3 OR BSG499.  
 OS Buchnera aphidicola (subsp. Schizaphis graminum).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_Taxid=98794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-22084549; PubMed-12089438;  
 RA Tamas I., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,  
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";  
 RL Science 296:2376-2379(2002).  
 CC -1- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA  
 CC in the 70S ribosome, positioning it for translation (By  
 CC similarity).  
 CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex  
 CC with proteins S10 and S14 (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -1- SIMILARITY: Contains 1 KH type-2 domain.



This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL; AE014125; AAM68042.1; -  
CC HAMAP; MF\_01309; -; 1.  
DR InterPro: IPR004087; KH\_dom.  
DR InterPro: IPR004044; KH\_TYPE\_2.  
DR InterPro: IPR001351; Ribosomal\_S3.  
DR InterPro: IPR005704; S3\_bact.  
DR Pfam; PF00013; KH; 1.  
DR Pfam; PF00189; Ribosomal\_S3\_C; 1.  
DR Pfam; PF00417; Ribosomal\_S3\_N; 1.  
DR SMART; SM00332; KH; 1.  
DR TIGRfams; TIGR01009; rpsc\_bact; 1.  
DR PROSITE; PS50823; KH\_TYPE\_2; 1.  
DR PROSITE; PS00548; RIBOSOMAL\_S3; 1.  
DR Ribosomal protein; RNA-binding; RNA-binding; Complete proteome.  
FT DOMAIN 39 107 KH TYPE-2.  
SQ SEQUENCE 233 AA; 26530 MW; 60C476BEA7081BA5 CRC64;

Query Match 3.3%; Score 8; DB 1; Length 233;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 SVSRITTE 239  
DB 51 SVSRITTE 58

RESULT 10  
MOG\_MOUSE STANDARD; PRT; 246 AA.  
ID MOG\_MOUSE  
AC Q61885; F70364; Q62003;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Myelin-oligodendrocyte glycoprotein precursor.  
GN MOG.  
OS Mus musculus (Mouse).  
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-129;  
RX MEDLINE=95130110; PubMed=7829100;  
RA Daubas P., Pham-Dinh D., Dautigny A.;  
RT "Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein gene";  
RL Genomics 23:36-41(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gardiner M.V., Matthieu J.M.;  
RT "Murine and human MOG are highly conserved: cDNA analysis";  
RL Trans. Am. Soc. Neurochem. 24:234-234(1993).  
RN [3]  
RP SEQUENCE OF 29-246 FROM N.A.  
RC STRAIN-BALB/c; TISSUE=Brain;  
RX MEDLINE=93376728; PubMed=8367453;  
RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,  
RA Pontarotti P., Roedel N., Mather I.H., Artzt K., Lindahl K.F.,  
RA Dautigny A.;  
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin superfamily encoded within the major histocompatibility complex";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).  
RN [4]  
RP SEQUENCE OF 29-54.

RC STRAIN-BALB/c; TISSUE=Brain;  
RX MEDLINE=92218912; PubMed=1373175;  
RA Amiguet P., Gardiner M.V., Zanetta J.-P., Matthieu J.-M.;  
RT "Purification and partial structural and functional characterization of mouse myelin/oligodendrocyte glycoprotein";  
RL J. Neurochem. 58:1676-1682(1992).  
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-CELL COMMUNICATION.  
CC -1- SUBUNIT: MAY FORM HOMODIMERS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC MEMBRANES.  
CC -1- DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN JIMPY AND QUACKING DYSMYELINATING MUTANT MICE.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG SUBFAMILY.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG) WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL; L29503; AAC42023.1; -  
DR EMBL; L29498; AAC42023.1; JOINED.  
DR EMBL; L29500; AAC42023.1; JOINED.  
DR EMBL; L29501; AAC42023.1; JOINED.  
DR EMBL; L29499; AAC42023.1; JOINED.  
DR EMBL; L29502; AAC42023.1; JOINED.  
DR EMBL; U64572; AAB08096.1; -  
DR EMBL; L20942; AAA03180.1; -  
DR PIR; A55717; A55717.  
DR MGD; MGI:97435; Mog.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.  
FT SIGNAL 1 28  
FT CHAIN 1 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.  
FT DOMAIN 29 156 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 157 177 POTENTIAL.  
FT DOMAIN 178 209 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 210 230 POTENTIAL.  
FT DOMAIN 231 246 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 31 144 IG-LIKE V-TYPE.  
FT DISULFID 52 126 POTENTIAL.  
FT CARBOHYD 59 126 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 21 21 L -> LL (IN REF. 2).  
FT CONFLICT 32 32 G -> G (IN REF. 4).  
FT CONFLICT 95 95 G -> E (IN REF. 3).  
FT CONFLICT 169 169 P -> S (IN REF. 2).  
SQ SEQUENCE 246 AA; 28271 MW; 1F1A8A4A0D5CFB89 CRC64;

Query Match 3.3%; Score 8; DB 1; Length 246;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLQL 24  
DB 16 LLLLLQL 23

RESULT 11

TNF9\_HUMAN  
ID TNF9\_HUMAN STANDARD; PRT; 254 AA.  
AC P41273;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 9 (4-1BB ligand) (4-1BBL).  
GN TNFSP9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-94374434; PubMed-8088337;  
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G., "Molecular and biological characterization of human 4-1BB and its ligand."  
RT Eur. J. Immunol. 24:2219-2227(1994).  
RL -1- FUNCTION: Cytokine that binds to TNFRSP9. Induces the proliferation of activated peripheral blood T cells. May have a role in activation-induced cell death (AICD). May play a role in cognate interactions between T cells and B cells/macrophages.  
CC -1- SUBUNIT: Homotrimer (potential).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LONG, SKELETAL MUSCLE AND KIDNEY.  
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL: U03398; AAA53134.1; -  
DR PIR: I38427; I38427.  
DR Gene: HGNC:11939; TNFSF9.  
DR MIM: 606182; -  
DR GO: GO:0006915; P:apoptosis; TAS.  
DR GO: GO:0008283; P:cell proliferation; TAS.  
DR GO: GO:0007267; P:cell-cell signaling; TAS.  
DR GO: GO:0007165; P:signal transduction; TAS.  
DR InterPro: IPR006052; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR SMART: SM00207; TNF\_1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Polymorphism.  
FT DOMAIN 1 28 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 29 49 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
FT DOMAIN 50 254 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 35 41 POLY-LEU.  
FT VARIANT 17 17 P -> A (IN DBSNP:442511).  
SQ SEQUENCE 254 AA; 26624 MW; 827551F34563E508 CRC64;  
Query Match 3.3%; Score 8; DB 1; Length 254;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
HX7P\_XENLA

DB 34 GLLLLLLL 41  
OY 15 GLLLLLLL 22  
OY 34 GLLLLLLL 41

ID HX7P\_XENLA STANDARD; PRT; 291 AA.  
AC P35993;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Homeobox protein XHOX-7.1' (Fragment).  
GN XHOX-7.1'.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OX NCBI\_Taxid=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91347929; PubMed-1679007;  
RA Su M.-W., Suzuki H.R., Solursh M., Ramirez F., "Progressively restricted expression of a new homeobox-containing gene during Xenopus laevis embryogenesis."  
RT Development 111:1179-1187(1991).  
RL -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -1- SIMILARITY: BELONGS TO THE MSH HOMEBOX FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL: X58772; CAA41573.1; -  
DR PIR: B60131; B60131.  
DR HSSP: P22808; INK3.  
DR InterPro: IPR001356; Homeobox.  
DR InterPro: IPR000047; HTH\_1andrepressr.  
DR Pfam: PF00046; homeobox; 1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
FT DNA\_BIND 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 291 AA; 32293 MW; 9D3D45FBEF9CB50 CRC64;  
Query Match 3.3%; Score 8; DB 1; Length 291;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

WNT6\_HUMAN  
ID WNT6\_HUMAN STANDARD; PRT; 365 AA.  
AC Q9Y6F9; Q9Y1J6; Q9H238;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Wnt-6 protein precursor.  
GN WNT6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tesse T.T., Mossakowska D.E., Carter P.S., Hu E., Zhu Y., Kelsell D.P., Murdoch P.R., Herrity N.C., Lewis C.J., Cross D.A.,

DB 16 LLLLLLLQ 23  
OY 16 LLLLLLLQ 23  
OY 6 LLLLLLLQ 13

RA Culbert A.A., Reith A.D., Barnes M.R.;  
 RT "Molecular cloning and characterization of six novel human WNT  
 genes.";  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21248387; PubMed-11350055;  
 RA Kirikoshi H., Sekihara H., Katoh M.;  
 RT "WNT10A and WNT6, clustered in human chromosome 2q35 region with  
 head-to-tail manner, are strongly co-expressed in SK480 cells.";  
 RL Biochem. Biophys. Res. Commun. 283:798-805(2001).  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-Placenta;  
 RC MEDLINE-22388257; PubMed-12477932;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Zeeberg B., Buélow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Scheetz T.E.,  
 RA Brownstein M.J., Uslin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 28-365 FROM N.A.  
 RA Rump A., Hayes C., Brown S.D.M., Rosenthal A.;  
 RT "Genomic sequence of the Wnt6 gene and the Wnt10a gene from human  
 2q35.";  
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 295-337 FROM N.A.  
 RX MEDLINE-99276447; PubMed-10343101;  
 RA Rankin J., Strachan T., Lako M., Lindsay S.;  
 RT "Partial cloning and assignment of WNT6 to human chromosome band 2q35  
 by in situ hybridization.";  
 RL Cytogenet. Cell Genet. 84:50-52(1999).  
 CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN  
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A  
 CC SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE  
 CC REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL  
 CC DIAMETERS.  
 CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the  
 CC extracellular matrix.  
 CC -1- SIMILARITY: Belongs to the Wnt family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AY009401; AAC38661.1; -  
 DR EMBL: AB059570; BAB35603.1; -  
 DR EMBL: BC004329; AA04329.1; -  
 DR EMBL: AF315943; AAG45154.1; -  
 DR EMBL: AF079522; AAD41674.1; -  
 DR PIR: JC7694; JC7694.  
 DR Genew: HGNC:12785; WNT6.  
 DR MIM: 604663; -

DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0005201; F:extracellular matrix structural constituent; NAS.  
 DR GO: GO:0007267; P:cell-cell signaling; NAS.  
 DR GO: GO:0007275; P:development; NAS.  
 DR InterPro: IPR005817; Wnt.  
 DR InterPro: IPR005816; Wnt\_grtfactor.  
 DR Pfam: PF00110; Wnt; 1.  
 DR PRINTS: PR01349; WNTPROTEIN.  
 DR SMART: SM00097; WNT1; 1.  
 DR PROSITE: PS00246; WNT1; 1.  
 KM Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 365 WNT-6 PROTEIN.  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 311 311 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 365 AA; 39720 MW; 928DE396C58E255B CRC64;  
 Query Match 3.3%; Score 8; DB 1; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 15 GILLILL 22  
 Db 10 GILLILL 17  
 RESULT 14  
 ID GSA:AQ0AE STANDARD; PRT; 424 AA.  
 AC 066998;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA)  
 DE (Glutamate-1-semialdehyde aminotransferase) (GSA-AT).  
 GN HEML OR GSA OR AQ\_816.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_Taxid-63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VF5;  
 RX MEDLINE-98196666; PubMed-9537320;  
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 aeolicus.";  
 RL Nature 392:353-358(1998).  
 CC -1- CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate - 5-  
 CC aminolevulinate.  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; second step.  
 CC -1- SUBUNIT: Homodimer (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent  
 CC aminotransferases.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AE000709; AAC06964.1; -  
 DR PIR: C70371; C70371.  
 DR HSSP: P24630; 2GSA.  
 DR HAMAP: MF\_00375; - 1.  
 DR InterPro: IPR005814; Aminotrans\_3.  
 DR InterPro: IPR004639; HemL.  
 DR Pfam: PF00202; aminotran\_3; 1.

DR TIGR00713; hemL; 1.  
 DR PROSITE; PS00600; AA TRANSFER CLASS\_3; 1.  
 KW Porphyrin biosynthesis; Isomerase; Pyridoxal phosphate;  
 FT Complete proteome. 264  
 FT BINDING 264  
 SQ SEQUENCE 424 AA; 46393 MW; 114DEF64E05E1EA CMC64; PYRIDOXAL PHOSPHATE (BY SIMILARITY).

Query Match 3.3%; Score 8; DB 1; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 IPGTGP 81  
 Db 161 IPGTGP 168

RESULT 15  
 CD4\_MOUSE STANDARD; PRT; 457 AA.

AC P06332;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen  
 T4/Leu-3) (T-cell differentiation antigen L3T4).  
 GN CD4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-87018845; PubMed-3094146;  
 RX Tourville B., Gorman S.D., Field E.H., Hunkapiller T., Parnes J.R.;  
 RT "Isolation and sequence of L3T4 complementary DNA clones: expression  
 in T cells and brain.";  
 RL Science 234:610-614(1986).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-87115821; PubMed-3027575;  
 RX Littman D.R., Gettner S.N.;  
 RT "Unusual function in the immunoglobulin domain of the newly isolated  
 murine CD4 (L3T4) gene.";  
 RL Nature 325:453-455(1987).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-88152875; PubMed-3326818;  
 RA Parnes J.R., Hunkapiller T.;  
 RT "L3T4 and the immunoglobulin gene superfamily: new relationships  
 between the immune system and the nervous system.";  
 RL Immunol. Rev. 100:109-127(1987).  
 RN (4)  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE-Brain;  
 RX MEDLINE-88041159; PubMed-2823269;  
 RA Gorman S.D., Tourville B., Parnes J.R.;  
 RT "Structure of the mouse gene encoding CD4 and an unusual transcript  
 in brain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).  
 RN (5)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98112780; PubMed-9445485;  
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,  
 RA Gibbs R.A.;  
 RT "Comparative sequence analysis of a gene-rich cluster at human  
 chromosome 12p13 and its syntenic region in mouse chromosome 6.";  
 RL Genome Res. 8:23-40(1998).  
 RN (6)  
 RP SEQUENCE OF 27-43.  
 RX MEDLINE-86166694; PubMed-3082751;  
 RA Classon B.J., Tsagaratos J., Kirschbaum L., Maddox J., McKay C.R.,

RA Brandon M., McKenzie I.F.C., Walker I.D.;  
 RT "The L3T4 antigen in mouse and the sheep equivalent are  
 immunoglobulin-like.";  
 RL Immunogenetics 23:129-132(1986).  
 RN (7)  
 RP DISULFIDE BONDS.  
 RX MEDLINE-86233454; PubMed-3086886;  
 RA Classon B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;  
 RT "Partial primary structure of the T4 antigens of mouse and sheep:  
 assignment of intrachain disulfide bonds.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).  
 CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL  
 RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.  
 CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=2;  
 Name=1;  
 IsoId=P06332-1; Sequence-Displayed;  
 Name=2; Synonyms-Brain-specific;  
 IsoId=P06332-2; Sequence-VSP\_002489;  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M36850; AAA39401.1; -  
 DR EMBL; M13816; AAA37267.1; -  
 DR EMBL; X04836; CA28539.1; -  
 DR EMBL; M36851; AAA39402.1; -  
 DR EMBL; M17080; AAA37403.1; -  
 DR EMBL; M17078; AAA37403.1; JOINED.  
 DR EMBL; M17079; AAA37403.1; JOINED.  
 DR EMBL; AC002397; AAC36010.1; -  
 DR PIR; A02110; RNMST4.  
 DR HSSP; P01730; IWBK.  
 DR MGD; MGI:86335; CD4.  
 DR GO; GO:0042101; C:T-cell receptor complex; ISS.  
 DR GO; GO:0015026; F:coreceptor activity; ISS.  
 DR GO; GO:0042289; F:MHC class II protein binding activity; ISS.  
 DR GO; GO:0006955; P:immune response; ISS.  
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.  
 DR GO; GO:0030217; P:T-cell differentiation; ISS.  
 DR GO; GO:0045058; P:T-cell selection; ISS.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.  
 DR InterPro: IPR00973; CD4\_TcRg.  
 DR InterPro: IPR007110; I9-1like.  
 DR InterPro: IPR003006; I9\_MHC.  
 DR InterPro: IPR003596; I9\_V.  
 DR Pfam: PF00047; I9; 1.  
 DR PRINTS: PR00692; CD4TCANTIGEN.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG-LIKE; 1.  
 DR Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;  
 KW Immune response; Repeat; Signal; Lipoprotein; Palmitate;  
 Alternative splicing.  
 FT FT SIGNAL 1 26  
 FT CHAIN 27 457  
 FT DOMAIN 27 394  
 FT TRANSMEM 395 417  
 FT DOMAIN 418 457  
 FT DOMAIN 27 128  
 FT DOMAIN 129 207  
 FT DOMAIN 208 317  
 FT DOMAIN 318 374  
 FT CARBOHYD 187 187  
 FT CARBOHYD 298 298  
 FT  
 T-CELL SURFACE GLYCOPROTEIN CD4.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 IG-LIKE V-TYPE.  
 IG-LIKE C2-TYPE 1.  
 IG-LIKE C2-TYPE 2.  
 IG-LIKE C2-TYPE 3.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	323	323	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	42	112	
FT	DISULFID	159	188	
FT	DISULFID	328	370	
FT	LIPID	418	418	PALMITATE (BY SIMILARITY).
FT	LIPID	421	421	PALMITATE (BY SIMILARITY).
FT	VARSPIC	1	240	Missing (in isoform 2).
FT	VARSPIC	1	240	/FTId-VSP_002489.
SQ	SEQUENCE	457 AA;	51296 MW;	IBIDA7527CB00F33 CRC64;

Query Match 3.3%: Score 8; DB 1; Length 457;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLLQL 24  
11111111  
Db 10 LLLLLLQL 17

Search completed: August 13, 2003, 13:38:39  
Job time : 25 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 13, 2003, 13:35:12 ; Search time 96 Seconds

(without alignments)  
653.196 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MRQGPASPORLGLLL.....GDASTGMSVSRILIELPK 243

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 6

Total number of hits satisfying chosen parameters: 5107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTRMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	70.0	243	4	096CG8
2	169	69.5	232	4	081X63
3	111	45.7	245	11	09D1D6
4	111	45.7	245	11	08CG08
5	9	3.7	41	4	09DMW7
6	9	3.7	144	5	P90741
7	9	3.7	501	10	09AVM0
8	9	3.7	558	10	09ASN8
9	9	3.7	870	11	0921B6
10	9	3.7	996	11	0924X6
11	9	3.7	1461	4	076045
12	9	3.7	1464	4	08N473
13	8	3.3	59	11	08K312
14	8	3.3	65	11	0912H3
15	8	3.3	108	11	09D9P8
16	8	3.3	111	5	09W2P6

17	8	3.3	113	11	060810	Q60810 mus musculu
18	8	3.3	116	5	08T3M4	Q8T3M4 drosophila
19	8	3.3	125	5	08IR67	Q8IR67 drosophila
20	8	3.3	136	4	08WXL0	Q8WXL0 homo sapien
21	8	3.3	141	6	09XSF0	Q9XSF0 bos taurus
22	8	3.3	159	4	08WXL1	Q8WXL1 homo sapien
23	8	3.3	181	16	Q8D4M9	Q8D4M9 vibrio vuln
24	8	3.3	185	11	Q9JL41	Q9JL41 mus musculu
25	8	3.3	204	11	08CGL2	Q8CGL2 rattus norv
26	8	3.3	228	4	08IXU9	Q8IXU9 homo sapien
27	8	3.3	230	11	09RI49	Q9RI49 cavia porce
28	8	3.3	249	16	054188	Q54188 streptomyce
29	8	3.3	249	17	08U2U7	Q8U2U7 pyrococcus
30	8	3.3	251	4	08WY22	Q8WY22 homo sapien
31	8	3.3	259	4	08NBH9	Q8NBH9 homo sapien
32	8	3.3	272	16	08D1L1	Q8D1L1 yersinia pe
33	8	3.3	284	4	09UC14	Q9UC14 homo sapien
34	8	3.3	289	4	096A28	Q96A28 homo sapien
35	8	3.3	290	10	09XH03	Q9XH03 arabidopsis
36	8	3.3	296	5	022389	Q22389 caenorhabd1
37	8	3.3	296	5	019725	Q19725 caenorhabd1
38	8	3.3	302	5	019725	Q19725 caenorhabd1
39	8	3.3	305	4	09UDP6	Q9UDP6 homo sapien
40	8	3.3	307	11	063742	Q63742 rattus sp.
41	8	3.3	316	4	09BV39	Q9BV39 mus musculu
42	8	3.3	322	4	09UHS4	Q9UHS4 homo sapien
43	8	3.3	332	5	019050	Q19050 caenorhabd1
44	8	3.3	337	11	08C972	Q8C972 mus musculu
45	8	3.3	349	4	099018	Q99018 homo sapien

## ALIGNMENTS

## RESULT 1

Q96CG8 PRELIMINARY; PRT; 243 AA.  
ID Q96CG8  
AC Q96CG8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Similar to RIKEN cDNA 1110014B07 gene (Collagen triple helix repeat-containing protein 1).  
GN CTRHCL.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC TISSUE=Kidney;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aortic smooth muscle;  
RA Lehnert W., Moore D.P., Harmon R.J., Mancini M.L., Lindner V.;  
RT "Expression of the novel collagen triple helix repeat-containing gene  
(Chrcel) suggests functions in multiple organ systems.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC014245; A0114245.1; -  
DR EMBL; AY136825; A0115749.1; -  
DR InterPro: IPR000087; Collagen.  
DR Pfam: PF01391; Collagen.1.  
SQ SEQUENCE 243 AA; 26224 MW; A11FE61C6867F9 CRC64;

Query Match 70.0%; Score 170; DB 4; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.8e-167;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPPTGIPGKDGKGEKCECLRESFESWTPNKKCSWSLNGIDGKIAECTFTKMS 133  
DB 74 IPCTPGIPGKDGKGEKCECLRESFESWTPNKKCSWSLNGIDGKIAECTFTKMS 133

QY 134 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPENNSTNIHR 193  
 DB 134 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPENNSTNIHR 193  
 QY 194 TSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGWNVSRIIEELPR 243  
 DB 194 TSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGWNVSRIIEELPR 243

## RESULT 2

Q81X63 PRELIMINARY; PRT; 232 AA.  
 AC Q81X63;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE NMCI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sasaki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;  
 RT "Novel polypeptide found in human cornea cDNA library";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB395488; AAO17919.1; -  
 SQ SEQUENCE 232 AA; 25163 MW; E9D4BC30304837ED CRC64;

Query Match 69.5%; Score 169; DB 4; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-166;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFKEGKGECLRESEFESWTPTNYKQCSWSLNYGIDLGKIAECTFTKMS 133  
 DB 60 IPGTGPIGRDGFKEGKGECLRESEFESWTPTNYKQCSWSLNYGIDLGKIAECTFTKMS 119  
 QY 134 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPENNSTNIHR 193  
 DB 120 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPENNSTNIHR 179  
 QY 194 TSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGWNVSRIIEELPR 242  
 DB 180 TSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGWNVSRIIEELPR 228

## RESULT 3

Q9DID6 PRELIMINARY; PRT; 245 AA.  
 AC Q9DID6;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE 1110014B07RIK protein.  
 GN CTRHC1 OR 1110014B07RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochava H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,  
 RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyono K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Yushan-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK003674; BAB22930.1; -  
 DR MGD: MGI:1915838; Ctrhl.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF01391; Collagen; 1.  
 SQ SEQUENCE 245 AA; 26460 MW; 14951B87D8181A0E CRC64;

Query Match 45.7%; Score 111; DB 11; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-106;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFKEGKGECLRESEFESWTPTNYKQCSWSLNYGIDLGKIAECTFTKMS 133  
 DB 76 IPGTGPIGRDGFKEGKGECLRESEFESWTPTNYKQCSWSLNYGIDLGKIAECTFTKMS 135  
 QY 134 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPE 184  
 DB 136 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPE 186

## RESULT 4

Q8CG08 PRELIMINARY; PRT; 245 AA.  
 AC Q8CG08;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Collagen triple helix repeat-containing protein 1.  
 GN CTRHC1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;  
 RT "Expression of the novel collagen triple helix repeat-containing gene  
 (Ctrhl) suggests functions in multiple organ systems.";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY136824; AAN15748.1; -  
 SQ SEQUENCE 245 AA; 26424 MW; 2296FD6DCDBA21F2 CRC64;

Query Match 45.7%; Score 111; DB 11; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-106;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFKEGKGECLRESEFESWTPTNYKQCSWSLNYGIDLGKIAECTFTKMS 133  
 DB 76 IPGTGPIGRDGFKEGKGECLRESEFESWTPTNYKQCSWSLNYGIDLGKIAECTFTKMS 135  
 QY 134 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPE 184  
 DB 136 NSALRVLFSGSLRLKCRNACCORWYFTFNAGACSGPLPIEATIIYLDQSGPE 186

## RESULT 5

Q9DMM7 PRELIMINARY; PRT; 41 AA.  
 AC Q9DMM7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)



```

DE Alpha-1 type I collagen (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064528; PubMed=6183642;
RA Chu M.L., Myers J.C., Bernard M.P., Ding J.F., Ramirez F.;
RT "Cloning and characterization of five overlapping cDNAs specific for
RT the human pro alpha 1(I) collagen chain.";
RL Nucleic Acids Res. 10:5925-5934(1982).
DR EMBL; J00111; AAA52290.1; -.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF01391; Collagen; 1.
KM Collagen.
FT NON_TER.
FT SEQUENCE 41 AA; 3771 MW; 1B9D591B06A6C800 CRC64;
SQ
Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PGRDGSFGA 71
DB 26 PGRDGSFGA 34
|||||
P90741 PRELIMINARY; PRT; 144 AA.
ID P90741
AC P90741;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE C02F4.3 protein.
GN C02F4.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Cummings P.N.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z61032; CAB02722.1; -.
DR WormPep; C02F4.3; CE07854.
SQ SQUINCE 144 AA; 16112 MW; 907F9DB1AC1762 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 5; Length 144;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
DB 67 LLLLLLQL 75
|||||
P9AVM0 PRELIMINARY; PRT; 501 AA.
ID P9AVM0
AC P9AVM0;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

```

```

DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Cytochrome P450.
GN Asp1-2.
OS Asparagus officinalis (Garden asparagus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
OC Asparagus.
OX NCBI_TaxID=4686;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Shoot;
RA Imishi H., Iwai C., Ohkawa H.;
RT "Molecular cloning of cytochrome P450 cDNA involved in the seedling of
RT Asparagus.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AB037245; BAB40324.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 501 AA; 56336 MW; 8593A426B5C21D5A CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 10; Length 501;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
DB 13 LLLLLLQL 21
|||||
P9ASNB PRELIMINARY; PRT; 558 AA.
ID P9ASNB
AC P9ASNB;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE P0554D10.9 protein.
GN P0554D10.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0554D10.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002869; BAB39225.1; -.
DR Gramene; P9ASNB; -.
DR InterPro; IPR002123; Acyltransferase.
DR SMART; SM00563; Plsc; 1.
SQ SEQUENCE 558 AA; 60411 MW; 7893EDF390B716B9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 10; Length 558;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LRGILLLL 21
DB 93 LRGILLLL 101
|||||
P921B6 PRELIMINARY; PRT; 870 AA.
ID P921B6
AC P921B6;

```

```

DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apoe receptor-2.
GN LRP8 OR APOER2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21303597; PubMed=11294845;
RA Brandes C., Kahr L., Stockinger W., Hiesberger T., Schneider W.J.,
RA Nimpf J.;
RT *Alternative splicing in the ligand binding domain of mouse Apoe
RT receptor-2 produces receptor variants binding reelin but not alpha2-
RT macroglobulin.*
RL J. Biol. Chem. 276:22160-22169(2001).
DR MGD; MGI:1340044; Lrp8.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR002172; Ldl_receptor_A.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00057; ldl_recept_a; 5.
DR Pfam; PF00058; ldl_recept_b; 5.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00192; LDLA; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01209; LDLRA_1; 5.
DR PROSITE; PS00068; LDLRA_2; 5.
DR EGF-like domain; Receptor.
SQ SEQUENCE 870 AA; 96268 MW; FCD3982FDE18E3E0 CRC64;

Query Match 3.7%; Score 9; DB 11; Length 870;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLQL 24
DB 14 LLLLLLQL 22

RESULT 10
O924X6 PRELIMINARY; PRT; 996 AA.
AC O924X6.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein E receptor 2 precursor.
GN LRP8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98352008; PubMed=9685741;
RA Kim H.-J., Kim D.-H., Magoori K., Saeki S., Yamamoto T.;
RT *Evolution of the Apolipoprotein E Receptor 2 Gene by Exon Loss.*;
RL J. Biochem. 124:451-456(1998).
DR EMBL; D85633; BAB46965.1; -.
DR MGD; MGI:1340044; Lrp8.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001881; EGF_CA.

```

```

DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR002172; Ldl_receptor_A.
DR InterPro: IPR000033; Ldl_receptor_rep.
DR Pfam; PF00057; ldl_recept_a; 8.
DR Pfam; PF00058; ldl_recept_b; 5.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00192; LDLA; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS00068; LDLRA_2; 8.
DR EGF-like domain; Lipoprotein; Receptor; Signal.
FT SIGNAL 1 35
FT CHAIN 36 996
SQ SEQUENCE 996 AA; 109833 MW; 51DDA30ACE572529 CRC64;

Query Match 3.7%; Score 9; DB 11; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLQL 24
DB 14 LLLLLLQL 22

RESULT 11
O76045 PRELIMINARY; PRT; 1461 AA.
AC O76045.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Pro alpha 1(I) collagen.
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85130970; PubMed=2857713;
RA Chu M.-L., de Wet W., Bernard M., Ramirez F.;
RT *Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
RT Promoter structure, Alu repeats, and polymorphic transcripts.*;
RL J. Biol. Chem. 260:2315-2320(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329734; PubMed=2843432;
RA D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.;
RT *Complete nucleotide sequence of the region encompassing the first
RT twenty-five exons of the human pro alpha 1(I) collagen gene.*;
RL Gene 67:105-115(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89025644; PubMed=3178743;
RA Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
RA Jaenisch R., Prockop D.J.;
RT *Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
RT of human type I procollagen.*;
RL Biochem. J. 253:919-922(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91138770; PubMed=1995349;
RA Maatta A., Bornstein P., Penttinen R.P.;
RT *Highly conserved sequences in the 3'-untranslated region of the
RT COL1A1 gene bind cell-specific nuclear proteins.*;
RL FEBS Lett. 279:9-13(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92157916; PubMed=1787829;

```

RA Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning C.,  
 RA Olsen A.S., Prockop D.J.;  
 RT "Completion of the last half of the structure of the human gene for  
 RT the Pro alpha 1 (I) chain of type I procollagen (COL1A1).";  
 RL Matrix 11:375-379(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98107942; PubMed-9443882;  
 RA Korkko J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J.,  
 RA Prockop D.J.;  
 RT "Analysis of the COL1A1 and COL1A2 genes by PCR amplification and  
 RT scanning by conformation-sensitive gel electrophoresis identifies only  
 RT COL1A1 mutations in 15 patients with osteogenesis imperfecta type I;  
 RT identification of common sequences of null-allele mutations.";  
 RL Am. J. Hum. Genet. 62:98-110(1998).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Korkko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,  
 RA Ala-Kokko L.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF017178; AAB94054.2;  
 DR InterPro: IPR000087; Collagen.  
 DR InterPro: IPR000885; Fib.collagen\_C.  
 DR Pfam: PF01410; COLFI; 1.  
 DR Pfam: PF01391; Collagen; 18.  
 DR Pfam: PF00093; VWC; 1.  
 DR ProDom: PD000007; Collagen; 2.  
 DR ProDom: PD002078; Fib.collagen\_C; 1.  
 DR SMART: SM00038; COLFI; 1.  
 DR SMART: SM00214; VWC; 1.  
 DR PROSITE: PS01208; VWC; 1.  
 KW Collagen.  
 SQ SEQUENCE 1461 AA; 138630 MW; 9ACF6DE30EA78E21 CRC64;  
 Query Match 3.7%; Score 9; DB 4; Length 1461;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 63 PGRDGPFGA 71  
 Db 1021 PGRDGPFGA 1029

RESULT 12

08N473 PRELIMINARY; PRT; 1464 AA.  
 ID 08N473;  
 AC 08N473;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC036531; AAB36531.1;  
 DR InterPro: IPR000087; Collagen.  
 DR InterPro: IPR001007; VWC\_C.  
 DR Pfam: PF01391; COLFI; 1.  
 DR Pfam: PF01391; Collagen; 18.  
 DR ProDom: PD000007; Collagen; 2.  
 DR ProDom: PD002078; Fib.collagen\_C; 1.  
 DR SMART: SM00038; COLFI; 1.  
 DR SMART: SM00214; VWC; 1.  
 DR PROSITE: PS01208; VWC; 1.  
 KW Hypothetical protein; Collagen.

SQ SEQUENCE 1464 AA; 139011 MW; B0581F8D1C89DDE8 CRC64;  
 Query Match 3.7%; Score 9; DB 4; Length 1464;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 63 PGRDGPFGA 71  
 Db 1024 PGRDGPFGA 1032

RESULT 13

08K312 PRELIMINARY; PRT; 59 AA.  
 ID 08K312;  
 AC 08K312;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
 DE Novel secreted protein precursor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1;  
 RA Moffatt P., Salois P., Lanctot C., Gaumond M.-H., St-Amant N.,  
 RA Godin E.;  
 RT "Engineered viruses to select genes encoding secreted and membrane-  
 RT bound proteins in mammalian cells.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY100450; AAM47508.1;  
 KW Signal.  
 FT SIGNAL.  
 FT NON\_TER  
 SQ SEQUENCE 59 AA; 6775 MW; E88594100AF0C8B0 CRC64;  
 Query Match 3.3%; Score 8; DB 11; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 15 GLILLILL 22  
 Db 14 GLILLILL 21

RESULT 14

0912H3 PRELIMINARY; PRT; 65 AA.  
 ID 0912H3;  
 AC 0912H3;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Endothelial and smooth muscle cell-derived neuropilin-like protein  
 DE (Fragment).  
 GN ESDN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ;  
 RX PubMed=11447234;  
 RA Kobuke K., Furukawa Y., Sugai M., Tanigaki K., Ohashi N.,  
 RA Matsumori A., Sasayama S., Honjo T., Tashiro K.;  
 RT "ESDN, A Novel Neuropilin-like Membrane Protein Cloned from Vascular  
 RT Cells with the Longest Secretory Signal Sequence among Eukaryotes, Is  
 RT Up-regulated after Vascular Injury.";  
 RL J. Biol. Chem. 276:34105-34114(2001).  
 DR EMBL; AF442820; AAL30434.1;  
 FT NON\_TER  
 SQ SEQUENCE 65 AA; 6452 MW; 278864A1DE2E8D50 CRC64;

Query Match 3.3%; Score 8; DB 11; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 3.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLLQ 23  
 |||||  
 DB 52 LLLLLLLQ 59

RESULT 15  
 Q9D9P8

PRELIMINARY; PRT; 108 AA.

ID Q9D9P8  
 AC Q9D9P8  
 DT 01-JUN-2001 (TRMBLrel. 17, Created)  
 DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
 DE 1700034015RIK  
 GN 1700034015RIK  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK006606; BAB24671.1; -  
 DR MGD; MGI:1923856; 1700034015RIK.  
 SQ SEQUENCE 108 AA; 12138 MW; 154E27F37C5B6101 CRC64;

Query Match 3.3%; Score 8; DB 11; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLLLLQ 23  
 |||||  
 DB 17 LLLLLLLQ 24

Search completed: August 13, 2003, 13:40:22  
 Job time : 97 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:36:43 ; Search time 30 Seconds  
(without alignments)  
342.718 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MKPGPASPRLRGILLTL.....GPASTGMSVSRHIEELPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1566

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/ECTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Dackfiltest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	70.0	276	4	US-09-205-258-958 Sequence 958, App
2	88	36.2	243	4	US-09-489-847-205 Sequence 205, App
3	66	27.2	66	4	US-09-205-258-962 Sequence 962, App
4	52	21.4	52	4	US-09-205-258-961 Sequence 961, App
5	51	21.0	51	4	US-09-205-258-963 Sequence 963, App
6	40	16.5	93	4	US-09-489-847-240 Sequence 240, App
7	40	16.5	93	4	US-09-489-847-362 Sequence 362, App
8	30	12.3	52	4	US-09-205-258-960 Sequence 960, App
9	9	3.7	654	4	US-09-252-991A-25801 Sequence 25801, A
10	9	3.7	905	4	US-09-369-364A-9 Sequence 9, Appl
11	9	3.7	1057	3	US-08-931-820-1 Sequence 1, Appl
12	9	3.7	1341	3	US-08-963-825-18 Sequence 18, Appl
13	9	3.7	1341	4	US-09-500-811-18 Sequence 18, Appl
14	9	3.7	1341	4	US-09-570-573-18 Sequence 18, Appl
15	9	3.7	1441	4	US-09-548-608-18 Sequence 18, Appl
16	9	3.7	1461	4	US-09-585-887-9 Sequence 9, Appl
17	9	3.7	1461	4	US-09-289-578-9 Sequence 9, Appl
18	8	3.3	20	3	US-08-918-288-51 Sequence 51, Appl
19	8	3.3	20	3	US-08-918-288-56 Sequence 56, Appl
20	8	3.3	20	3	US-09-282-357-51 Sequence 51, Appl
21	8	3.3	20	3	US-09-282-357-56 Sequence 56, Appl
22	8	3.3	20	3	US-09-059-625-38 Sequence 38, Appl
23	8	3.3	71	4	US-09-059-625-7 Sequence 7, Appl
24	8	3.3	72	4	US-09-059-625-4 Sequence 4, Appl
25	8	3.3	143	4	US-09-227-357-192 Sequence 192, App
26	8	3.3	151	4	US-09-059-625-32 Sequence 32, Appl
27	8	3.3	151	4	US-09-059-625-43 Sequence 43, Appl

28	8	3.3	151	4	US-09-059-625-46 Sequence 46, Appl
29	8	3.3	151	4	US-09-059-625-59 Sequence 59, Appl
30	8	3.3	155	4	US-09-059-625-62 Sequence 62, Appl
31	8	3.3	158	4	US-09-059-625-1 Sequence 1, Appl
32	8	3.3	159	4	US-09-059-625-164 Sequence 64, Appl
33	8	3.3	165	2	US-08-709-924-2 Sequence 2, Appl
34	8	3.3	165	2	US-08-709-925-2 Sequence 2, Appl
35	8	3.3	165	4	US-08-709-948-2 Sequence 2, Appl
36	8	3.3	165	4	US-09-220-415-2 Sequence 2, Appl
37	8	3.3	181	3	US-08-918-288-36 Sequence 36, Appl
38	8	3.3	181	3	US-09-282-357-36 Sequence 36, Appl
39	8	3.3	181	4	US-09-059-625-66 Sequence 66, Appl
40	8	3.3	184	4	US-09-059-625-67 Sequence 67, Appl
41	8	3.3	186	4	US-09-059-625-68 Sequence 68, Appl
42	8	3.3	203	4	US-09-059-625-85 Sequence 85, Appl
43	8	3.3	203	4	US-09-059-625-88 Sequence 88, Appl
44	8	3.3	204	4	US-09-059-625-35 Sequence 35, Appl
45	8	3.3	204	4	US-09-059-625-49 Sequence 49, Appl

ALIGNMENTS

RESULT 1  
US-09-205-258-958  
; Sequence 958, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06



EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070, 923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092, 921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094, 657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 962  
LENGTH: 66  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-962

Query Match 27.2% Score 66; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 1.3e-56;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 FTMRSSALRVLFSSGLRLKCRNACQRYFTFNAGCSGPLYEATITLIDGSPPMNS 187  
DB 1 FTMRSSALRVLFSSGLRLKCRNACQRYFTFNAGCSGPLYEATITLIDGSPPMNS 60  
QY 188 TINHR 193

Db 61 TINHR 66  
RESULT 4  
US-09-205-258-961  
Sequence 961, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048, 885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 974

```

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 961
; LENGTH: 52
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-205-258-961

Query Match          21.4%; Score 52; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,9e-43;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 TPGIDRGDFGKGEKCELRSEFESWTPNYKQCSNINYGIDLKIACCTF 128
Db 1 TPGIDRGDFGKGEKCELRSEFESWTPNYKQCSNINYGIDLKIACCTF 52

RESULT 5
US-09-205-258-963
; Sequence 963, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
```

```

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 963
; LENGTH: 51
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-205-258-963

Query Match          21.0%; Score 51; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.6e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 RTSSVEGICBGIAGLDVVAIWGTGSDYPRGDASTGNSVSRIITEELPK 243
Db 1 RTSSVEGICBGIAGLDVVAIWGTGSDYPRGDASTGNSVSRIITEELPK 51

RESULT 6
```



```

US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-240

```

```

Query Match 16.5%; Score 40; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.9e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MRPOGPASPORLGLLLILLQLPAPSSASEIPKGRKA 40
    |||||
DB 1 MRPOGPASPORLGLLLILLQLPAPSSASEIPKGRKA 40

```

```

RESULT 7
US-09-489-847-362
; Sequence 362, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 362
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-362

```

```

Query Match 16.5%; Score 40; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.9e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPOGPASPORLGLLLILLQLPAPSSASEIPKGRKA 40

```

```

Db 1 MRPOGPASPORLGLLLILLQLPAPSSASEIPKGRKA 40
|||||
RESULT 8
US-09-205-258-960
; Sequence 960, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974

```

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 960  
LENGTH: 52  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-960

Query Match 12.3%: Score 30; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 8,4e-22;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ROREVVDLYNMGKLOGPAGVPGRDSPGAN 72  
DB 15 ROREVVDLYNMGKLOGPAGVPGRDSPGAN 44

RESULT 9  
US-09-252-991A-25801  
Sequence 25801, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25801  
LENGTH: 654  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-25801

Query Match 3.7%: Score 9; DB 4; Length 654;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RPOGPAASP 10  
DB 453 RPOGPAASP 461

RESULT 10  
US-09-369-364A-9  
Sequence 9, Application US/09369364A  
Patent No. 6391610

GENERAL INFORMATION:  
APPLICANT: Apte, Suneel  
APPLICANT: Hurskaenen, Taina L.  
APPLICANT: Hirohata, Satoshi  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
FILE REFERENCE: 26473/4007/10-30-00  
CURRENT APPLICATION NUMBER: US/09/369,364A  
CURRENT FILING DATE: 1999-08-06  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 905  
TYPE: PRT  
ORGANISM: Mus musculus ADAMTS-8  
US-09-369-364A-9

Query Match 3.7%: Score 9; DB 4; Length 905;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LLLLLQLP 25  
DB 13 LLLLLQLP 21

RESULT 11  
US-08-931-820-1  
Sequence 1, Application US/08931820  
Patent No. 6010863  
GENERAL INFORMATION:  
APPLICANT: Assay for collagen degradation  
TITLE OF INVENTION: Assay for collagen degradation  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,820  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 96202596.1  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Collagen type I  
US-08-931-820-1

Query Match 3.7%: Score 9; DB 3; Length 1057;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 PGRDSPGA 71  
DB 863 PGRDSPGA 871

RESULT 12  
US-08-963-825-18  
Sequence 18, Application US/08963825  
Patent No. 6110689  
GENERAL INFORMATION:

APPLICANT: Ovist, Per  
TITLE OF INVENTION: A Method for Assaying Collagen Fragments  
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the  
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of  
TITLE OF INVENTION: Disorders Associated with the Metabolism of  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/963,825  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/187,319  
FILING DATE: 21-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda C  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 4305/08701  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ. ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1341 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: COLLAGEN ALPHA 1 (I)  
US-08-963-825-18  
Query Match 3.7%; Score 9; DB 3; Length 1341;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 63 PGRDGSFGA 71  
Db 900 PGRDGSFGA 908  
RESULT 13  
US-09-500-811-18  
Sequence 18, Application US/09500811  
Patent No. 6323314  
GENERAL INFORMATION:  
APPLICANT: Ovist, Per  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/570,573  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/187,319

ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,811  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/187,319  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda C  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 4305/08701  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ. ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1341 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: COLLAGEN ALPHA 1 (I)  
US-09-500-811-18  
Query Match 3.7%; Score 9; DB 4; Length 1341;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 63 PGRDGSFGA 71  
Db 900 PGRDGSFGA 908  
RESULT 14  
US-09-570-573-18  
Sequence 18, Application US/09570573  
Patent No. 6342361  
GENERAL INFORMATION:  
APPLICANT: Ovist, Per  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/570,573  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/187,319

ATTORNEY/AGENT INFORMATION:  
NAME: GOGOTIS, Adda C  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 4305/08701  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1341 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: COLLAGEN ALPHA 1 (I)  
US-09-570-573-18

Query Match 3.7%; Score 9; DB 4; Length 1341;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PERDSSPA 71  
Db 900 PERDSSPA 908

RESULT 15  
US-09-548-608-18  
Sequence 18, Application US/09548608  
Patent No. 6355442  
GENERAL INFORMATION:  
APPLICANT: Qvist, Per  
APPLICANT: Bonde, Martin  
TITLE OF INVENTION: A Method for Assaying Collagen Fragments  
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the  
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of  
TITLE OF INVENTION: Disorders Associated with the Metabolism of  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/548,608  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/187,319  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GOGOTIS, Adda C  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 4305/08701  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1341 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: COLLAGEN ALPHA 1 (I)  
US-09-548-608-18

Query Match 3.7%; Score 9; DB 4; Length 1341;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PERDSSPA 71  
Db 900 PERDSSPA 908

Search completed: August 13, 2003, 13:41:44  
Job time : 30 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:40:28 ; Search time 56 Seconds  
(without alignments)  
568.461 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MRPOGPASPORLIGILL.....GDASTGMSVSRRIIEELPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 492763 seqs, 131003257 residues

Word size : 6

Total number of hits satisfying chosen parameters: 16488

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA.\*

1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	100.0	243	10 US-09-938-418-7	Sequence 7, Appl
2	243	100.0	243	11 US-09-946-374-352	Sequence 352, App
3	243	100.0	243	11 US-09-946-374-431	Sequence 431, App
4	243	100.0	243	12 US-10-015-387A-352	Sequence 352, App
5	243	100.0	243	12 US-10-015-387A-431	Sequence 431, App
6	243	100.0	243	12 US-10-063-735-122	Sequence 122, App
7	243	100.0	243	12 US-10-063-130A-352	Sequence 352, App
8	243	100.0	243	12 US-10-063-130A-431	Sequence 431, App
9	243	100.0	243	12 US-10-199-672-366	Sequence 366, App
10	243	100.0	243	14 US-10-052-586-366	Sequence 366, App
11	243	100.0	243	14 US-10-007-805-514	Sequence 514, App
12	243	100.0	243	14 US-10-063-547-122	Sequence 122, App
13	243	100.0	243	15 US-10-174-590-366	Sequence 366, App
14	243	100.0	243	15 US-10-176-758-366	Sequence 366, App
15	243	100.0	243	15 US-10-176-758-366	Sequence 366, App

16	243	100.0	243	15 US-10-175-737-366	Sequence 366, App
17	243	100.0	243	15 US-10-063-616-122	Sequence 122, App
18	243	100.0	243	15 US-10-173-706-366	Sequence 366, App
19	243	100.0	243	15 US-10-175-738-366	Sequence 366, App
20	243	100.0	243	15 US-10-175-752-366	Sequence 366, App
21	243	100.0	243	15 US-10-176-482-366	Sequence 366, App
22	243	100.0	243	15 US-10-176-757-366	Sequence 366, App
23	243	100.0	243	15 US-10-176-913-366	Sequence 366, App
24	243	100.0	243	15 US-10-180-552-366	Sequence 366, App
25	243	100.0	243	15 US-10-180-557-366	Sequence 366, App
26	243	100.0	243	15 US-10-076-622-514	Sequence 514, App
27	243	100.0	243	15 US-10-063-502-122	Sequence 122, App
28	243	100.0	243	15 US-10-173-700-366	Sequence 366, App
29	243	100.0	243	15 US-10-174-572-366	Sequence 366, App
30	243	100.0	243	15 US-10-174-579-366	Sequence 366, App
31	243	100.0	243	15 US-10-174-582-366	Sequence 366, App
32	243	100.0	243	15 US-10-174-588-366	Sequence 366, App
33	243	100.0	243	15 US-10-175-739-366	Sequence 366, App
34	243	100.0	243	15 US-10-175-740-366	Sequence 366, App
35	243	100.0	243	15 US-10-175-743-366	Sequence 366, App
36	243	100.0	243	15 US-10-176-488-366	Sequence 366, App
37	243	100.0	243	15 US-10-176-492-366	Sequence 366, App
38	243	100.0	243	15 US-10-176-747-366	Sequence 366, App
39	243	100.0	243	15 US-10-176-750-366	Sequence 366, App
40	243	100.0	243	15 US-10-176-985-366	Sequence 366, App
41	243	100.0	243	15 US-10-176-987-366	Sequence 366, App
42	243	100.0	243	15 US-10-176-992-366	Sequence 366, App
43	243	100.0	243	15 US-10-176-993-366	Sequence 366, App
44	243	100.0	243	15 US-10-184-658-366	Sequence 366, App
45	243	100.0	243	15 US-10-176-991-366	Sequence 366, App

## ALIGNMENTS

RESULT 1  
US-09-938-418-7  
Sequence 7, Application US/09938418  
Patent No. US20020161199A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Guney, Austin L.  
APPLICANT: Polakis, Paul  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Wu, Thomas D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TITILE OF INVENTION: TREATMENT OF TUMOR  
FILE REFERENCE: P50991  
CURRENT APPLICATION NUMBER: US/09/938,418  
PRIOR FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: 60/081,071  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: 60/085,697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/097,022  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/101,922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/103,679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: 1999-06-02  
PRIOR APPLICATION NUMBER: PCT/US99/20111  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US00/04342

```

; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-06-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-938-418-7

Query Match      100.0%; Score 243; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 6,7e-214;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPGPASPQRLKGLLLILLQLPAPSSASEIPKQKQKQRLQREVVLDLYNGMCLQGPA 60
DB      1 MRPGPASPQRLKGLLLILLQLPAPSSASEIPKQKQKQRLQREVVLDLYNGMCLQGPA 60
QY      61 GVPGDGSGPQANVLPGTGIPGRDQFKGKGECLSESESTPYKQCSMSLNYGIDL 120
DB      61 GVPGDGSGPQANVLPGTGIPGRDQFKGKGECLSESESTPYKQCSMSLNYGIDL 120
QY      121 GKIAECTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFGAGCSGPLPLEATITTDQ 180
DB      121 GKIAECTFTKMSNSALNVLFSGLRLKCRNACCORWYFTFGAGCSGPLPLEATITTDQ 180
QY      181 GSPEKNSTINIHRTSSVGEIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRIITEE 240
DB      181 GSPEKNSTINIHRTSSVGEIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRIITEE 240
QY      241 LPK 243
DB      241 LPK 243

RESULT 2
US-09-946-374-352
; Sequence 352, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Guiney, Austin J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
```

```

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PICI
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
```

;; PRIOR APPLICATION NUMBER: 60/100710  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100711  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100848  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/100849  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/100919  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100930  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/101014  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101068  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101071  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101279  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: 60/101471  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101472  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101474  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101475  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101476  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101477  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101479  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101738  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101741  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101743  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101915  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101916  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/102207  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102240  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102307  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102330  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315

;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 243; DB 11; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6,7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRRLGLLILLILLQLPAPSSASEIPKGRKQALROREVVLDYNGMCLGPA 60  
|||  
Db 1 MRPGPASPQRRLGLLILLILLQLPAPSSASEIPKGRKQALROREVVLDYNGMCLGPA 60  
61 GVPGRDGPANVITPGIPGIRGDFKGEKGECLRESFEESWTPNYKQCSWSLNYGIDL 120  
|||  
QY 121 GKTAECFTKMRSSALRVFSGSLRLKCRNACCRMYFTFNAGCSGPILEAIITLDD 180  
|||  
Db 121 GKTAECFTKMRSSALRVFSGSLRLKCRNACCRMYFTFNAGCSGPILEAIITLDD 180  
181 GSPENSTINIHRTSVGELCEGIGAGLVDAIIVGTCSDYPKDASTGNMYSRIITEE 240  
|||  
Db 181 GSPENSTINIHRTSVGELCEGIGAGLVDAIIVGTCSDYPKDASTGNMYSRIITEE 240  
241 LPK 243  
|||  
QY 241 LPK 243  
|||  
Db 241 LPK 243

RESULT 3  
US-09-946-374-431  
; Sequence 431, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661

PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01





APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C54  
CURRENT APPLICATION NUMBER: US/10/015,387A  
CURRENT FILING DATE: 2001-12-12  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 431  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-015-387A-431.

Query Match 100.0%; Score 243; DB 12; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6,7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKOKAOLRREVVLDYNGMCLQGPA 60  
DB 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKOKAOLRREVVLDYNGMCLQGPA 60  
QY 61 GVPGRDGSFGANVIGTPIGRDGFKEGECLESEFSESWTPYKOCSSSLNYGIDL 120  
DB 61 GVPGRDGSFGANVIGTPIGRDGFKEGECLESEFSESWTPYKOCSSSLNYGIDL 120  
QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLIEATITVDQ 180  
DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLIEATITVDQ 180  
QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDYPKGDASTGMSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDYPKGDASTGMSVSRITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

RESULT 6  
US-10-063-735-122  
Sequence 122, Application US/10063735  
Publication No. US20030138882A1  
GENERAL INFORMATION:  
APPLICANT: Baton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/10/063,735  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 122  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-735-122

Query Match 100.0%; Score 243; DB 12; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6,7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKOKAOLRREVVLDYNGMCLQGPA 60

DB 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKOKAOLRREVVLDYNGMCLQGPA 60  
QY 61 GVPGRDGSFGANVIGTPIGRDGFKEGECLESEFSESWTPYKOCSSSLNYGIDL 120  
DB 61 GVPGRDGSFGANVIGTPIGRDGFKEGECLESEFSESWTPYKOCSSSLNYGIDL 120  
QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLIEATITVDQ 180  
DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLIEATITVDQ 180  
QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDYPKGDASTGMSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDYPKGDASTGMSVSRITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

RESULT 7  
US-10-006-130A-352  
Sequence 352, Application US/10006130A  
Publication No. US20030148375A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C7  
CURRENT APPLICATION NUMBER: US/10/006,130A  
CURRENT FILING DATE: 2002-03-19  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 352  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-006-130A-352

Query Match 100.0%; Score 243; DB 12; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6,7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKOKAOLRREVVLDYNGMCLQGPA 60  
DB 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKOKAOLRREVVLDYNGMCLQGPA 60  
QY 61 GVPGRDGSFGANVIGTPIGRDGFKEGECLESEFSESWTPYKOCSSSLNYGIDL 120  
DB 61 GVPGRDGSFGANVIGTPIGRDGFKEGECLESEFSESWTPYKOCSSSLNYGIDL 120  
QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLIEATITVDQ 180  
DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWYFTFNGACSGPLIEATITVDQ 180  
QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDYPKGDASTGMSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIWWGTCSDYPKGDASTGMSVSRITIEE 240  
QY 241 LPK 243

Db 241 LPK 243

## RESULT 8

US-10-006-130A-431  
; Sequence 431, Application US/10006130A  
; Publication No. US20030148375A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C7  
; CURRENT APPLICATION NUMBER: US/10/006,130A  
; CURRENT FILING DATE: 2002-03-19  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 431  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-006-130A-431

Query Match 100.0%; Score 243; DB 12; Length 243;

Best Local Similarity 100.0%; Pred. No. 6,7e-214; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGLLLLLLOLPAPSSASEIPKRGKOKAOLRQREVVDLYNGMCLGPA 60  
DB 1 MRPGPASPORLRLGLLLLLLOLPAPSSASEIPKRGKOKAOLRQREVVDLYNGMCLGPA 60  
QY 61 GVPGRDSSPGANVTPGPGIPGRDGFGEKGECECLRESFESWTPNYKQCSMSLNTGIDL 120  
DB 61 GVPGRDSSPGANVTPGPGIPGRDGFGEKGECECLRESFESWTPNYKQCSMSLNTGIDL 120  
QY 121 GKIAECTFTKMRSSALRVLFSSGLRLKCRNACCORRYFTFNGAECGSPLEIAIITLDQ 180  
DB 121 GKIAECTFTKMRSSALRVLFSSGLRLKCRNACCORRYFTFNGAECGSPLEIAIITLDQ 180  
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDYPKGDASTGNNVSRIITIEE 240  
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDYPKGDASTGNNVSRIITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

## RESULT 9

US-10-199-672-366  
; Sequence 366, Application US/10199672  
; Publication No. US20030148442A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James

APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C1

CURRENT APPLICATION NUMBER: US/10/199,672

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: US/10/052,586

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 366

LENGTH: 243

TYPE: PRT

ORGANISM: Homo Sapien

US-10-199-672-366

Query Match 100.0%; Score 243; DB 12; Length 243;

Best Local Similarity 100.0%; Pred. No. 6,7e-214; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGLLLLLLOLPAPSSASEIPKRGKOKAOLRQREVVDLYNGMCLGPA 60  
DB 1 MRPGPASPORLRLGLLLLLLOLPAPSSASEIPKRGKOKAOLRQREVVDLYNGMCLGPA 60  
QY 61 GVPGRDSSPGANVTPGPGIPGRDGFGEKGECECLRESFESWTPNYKQCSMSLNTGIDL 120  
DB 61 GVPGRDSSPGANVTPGPGIPGRDGFGEKGECECLRESFESWTPNYKQCSMSLNTGIDL 120  
QY 121 GKIAECTFTKMRSSALRVLFSSGLRLKCRNACCORRYFTFNGAECGSPLEIAIITLDQ 180  
DB 121 GKIAECTFTKMRSSALRVLFSSGLRLKCRNACCORRYFTFNGAECGSPLEIAIITLDQ 180  
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDYPKGDASTGNNVSRIITIEE 240  
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDYPKGDASTGNNVSRIITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

## RESULT 10

US-10-006-867-122  
; Sequence 122, Application US/10006867  
; Publication No. US20020119130A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.  
APPLICANT: Matanade, Colin K.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/006,867  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/063435  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/064215  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090688  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091628  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/096012  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096757  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096949  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/096959  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/097954  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097971  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097979  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098749

PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105881  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106030  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106856  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108807  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/112419  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112853  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113011  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/112854  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113300  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113408  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113430  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23

;; PRIOR APPLICATION NUMBER: 60/114223  
;; PRIOR FILING DATE: 1998-12-30  
;; PRIOR APPLICATION NUMBER: 60/115614  
;; PRIOR FILING DATE: 1999-01-12  
;; PRIOR APPLICATION NUMBER: 60/116527  
;; PRIOR FILING DATE: 1999-01-20  
;; PRIOR APPLICATION NUMBER: 60/116843  
;; PRIOR FILING DATE: 1999-01-22  
;; PRIOR APPLICATION NUMBER: 60/119285  
;; PRIOR FILING DATE: 1999-02-09  
;; PRIOR APPLICATION NUMBER: 60/119287  
;; PRIOR FILING DATE: 1999-02-09  
;; PRIOR APPLICATION NUMBER: 60/119525  
;; PRIOR FILING DATE: 1999-02-10  
;; PRIOR APPLICATION NUMBER: 60/119549  
;; PRIOR FILING DATE: 1999-02-10  
;; PRIOR APPLICATION NUMBER: 60/120014  
;; PRIOR FILING DATE: 1999-02-11  
;; PRIOR APPLICATION NUMBER: 60/129122  
;; PRIOR FILING DATE: 1999-04-13  
;; PRIOR APPLICATION NUMBER: 60/129674  
;; PRIOR FILING DATE: 1999-04-16  
;; PRIOR APPLICATION NUMBER: 60/131291  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/138387  
;; PRIOR FILING DATE: 1999-06-09  
;; PRIOR APPLICATION NUMBER: 60/144791  
;; PRIOR FILING DATE: 1999-07-20  
;; PRIOR APPLICATION NUMBER: 60/169495  
;; PRIOR FILING DATE: 1999-12-07  
;; PRIOR APPLICATION NUMBER: 60/175481  
;; PRIOR FILING DATE: 2000-01-11  
;; PRIOR APPLICATION NUMBER: 60/191007  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/199397  
;; PRIOR FILING DATE: 2000-04-25  
;; PRIOR APPLICATION NUMBER: 09/380139  
;; PRIOR FILING DATE: 1998-08-25  
;; PRIOR APPLICATION NUMBER: 09/311832  
;; PRIOR FILING DATE: 1999-05-14  
;; PRIOR APPLICATION NUMBER: 09/380137  
;; PRIOR FILING DATE: 1999-08-25  
;; PRIOR APPLICATION NUMBER: 09/380138  
;; PRIOR FILING DATE: 1999-08-25  
;; PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 243; DB 14; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6,7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGRAASPORLRLGLLLLLLLLPAPSSASEIPKGRKOKAOLRORREVDLYNMGCLQGPA 60  
DB 1 MRPGRAASPORLRLGLLLLLLLLPAPSSASEIPKGRKOKAOLRORREVDLYNMGCLQGPA 60  
QY 61 GVPGRDGSFGANYIPETPGIPGRDGFKEGKECLRSFEESSWTPNTKQCSWSIANTGIDL 120  
DB 61 GVPGRDGSFGANYIPETPGIPGRDGFKEGKECLRSFEESSWTPNTKQCSWSIANTGIDL 120  
QY 121 GKIAETFTKMRNSALRVLFSGSLRLKCRNACCOWYTFPNAECSGPIPAIIYLDQ 180  
DB 121 GKIAETFTKMRNSALRVLFSGSLRLKCRNACCOWYTFPNAECSGPIPAIIYLDQ 180  
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGNSVRIITIEE 240  
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGNSVRIITIEE 240  
QY 241 LPR 243  
DB 241 LPR 243

RESULT 11  
US-10-052-586-366

;; Sequence 366, Application US/10052586  
;; Publication No. US20020127584A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3430R1c1  
;; CURRENT APPLICATION NUMBER: US/10/052,586  
;; CURRENT FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 60/059263  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/059266  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063120  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063121  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063564  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063734  
;; PRIOR FILING DATE: 1997-10-29  
;; PRIOR APPLICATION NUMBER: 60/063870  
;; PRIOR FILING DATE: 1997-10-31  
;; PRIOR APPLICATION NUMBER: 60/064103  
;; PRIOR FILING DATE: 1997-10-31  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066120  
;; PRIOR FILING DATE: 1997-11-21  
;; PRIOR APPLICATION NUMBER: 60/066466  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/066772  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/069335  
;; PRIOR FILING DATE: 1997-12-11  
;; PRIOR APPLICATION NUMBER: 60/069425  
;; PRIOR FILING DATE: 1997-12-12  
;; PRIOR APPLICATION NUMBER: 60/069870  
;; PRIOR FILING DATE: 1997-12-17  
;; PRIOR APPLICATION NUMBER: 60/068017  
;; PRIOR FILING DATE: 1997-12-18  
;; PRIOR APPLICATION NUMBER: 60/077450  
;; PRIOR FILING DATE: 1998-03-10  
;; PRIOR APPLICATION NUMBER: 60/077652  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077649  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/078886  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078939  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079664  
;; PRIOR FILING DATE: 1998-03-27



Db 181 GSPENSTINIRHTSVEGLCEIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240  
Qy 241 LPK 243  
Db 241 LPK 243

## RESULT 12

US-10-007-805-514  
; Sequence 514, Application US/10007805  
; Publication No. US20020150581A1

## GENERAL INFORMATION:

APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Durham, Margarita  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C10  
CURRENT FILING DATE: US/10/007, 805  
CURRENT FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 593  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 514  
LENGTH: 243  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-10-007-805-514

Query Match 100.0%; Score 243; DB 14; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6.7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPGPAASPORLRLGLLLLLQLPAPSSASEIPKGRKORAEVVDLYNGMCLOGPA 60  
Db 1 MRPGPAASPORLRLGLLLLLQLPAPSSASEIPKGRKORAEVVDLYNGMCLOGPA 60  
Qy 61 GVPGRGSPGANVTPGTGIPGRDGRKGEKGECLRSFESWTPNTKQCSWSSLNIGIDL 120  
Db 61 GVPGRGSPGANVTPGTGIPGRDGRKGEKGECLRSFESWTPNTKQCSWSSLNIGIDL 120  
Qy 121 GRIAECTFTKMSNSALRYLFGSLRLKCRNACCOWYTFENGACSGPLPIAIYYLDQ 180  
Db 121 GRIAECTFTKMSNSALRYLFGSLRLKCRNACCOWYTFENGACSGPLPIAIYYLDQ 180  
Qy 181 GSPENSTINIRHTSVEGLCEIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240  
Db 181 GSPENSTINIRHTSVEGLCEIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240  
Qy 241 LPK 243  
Db 241 LPK 243

## RESULT 13

US-10-063-547-122  
; Sequence 122, Application US/10063547  
; Publication No. US20020182638A1

## GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.

APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 122  
LENGTH: 243  
TYPE: PRP  
ORGANISM: Homo Sapien  
US-10-063-547-122

Query Match 100.0%; Score 243; DB 14; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6.7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPGPAASPORLRLGLLLLLQLPAPSSASEIPKGRKORAEVVDLYNGMCLOGPA 60  
Db 1 MRPGPAASPORLRLGLLLLLQLPAPSSASEIPKGRKORAEVVDLYNGMCLOGPA 60  
Qy 61 GVPGRGSPGANVTPGTGIPGRDGRKGEKGECLRSFESWTPNTKQCSWSSLNIGIDL 120  
Db 61 GVPGRGSPGANVTPGTGIPGRDGRKGEKGECLRSFESWTPNTKQCSWSSLNIGIDL 120  
Qy 121 GRIAECTFTKMSNSALRYLFGSLRLKCRNACCOWYTFENGACSGPLPIAIYYLDQ 180  
Db 121 GRIAECTFTKMSNSALRYLFGSLRLKCRNACCOWYTFENGACSGPLPIAIYYLDQ 180  
Qy 181 GSPENSTINIRHTSVEGLCEIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240  
Db 181 GSPENSTINIRHTSVEGLCEIGAGLVDAIWTGCSDPYKGDASTGMSVSRITIEE 240  
Qy 241 LPK 243  
Db 241 LPK 243

## RESULT 14

US-10-174-590-366  
; Sequence 366, Application US/10174590  
; Publication No. US20030008352A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C42  
CURRENT APPLICATION NUMBER: US/10/174,590  
CURRENT FILING DATE: 2002-06-18  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 366  
LENGTH: 243  
TYPE: PRP  
ORGANISM: Homo Sapien  
US-10-174-590-366

Query Match 100.0%; Score 243; DB 15; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6.7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: August 13, 2003, 13:49:38  
Job time : 57 secs

```
OY 1 MRPGPASPORTLRLGLLLLLQLPAPSSASEIPKQKQALROREVVLDYNGMCLQSPA 60
DB 1 MRPGPASPORTLRLGLLLLLQLPAPSSASEIPKQKQALROREVVLDYNGMCLQSPA 60
OY 61 GVPGRDGSFGANVTPGTGIPGRDGFKEGKECECLRESFEESWTPYKQCSMSLNYGIDL 120
DB 61 GVPGRDGSFGANVTPGTGIPGRDGFKEGKECECLRESFEESWTPYKQCSMSLNYGIDL 120
OY 121 GKIAECTFTKMRNSALRVLEFSGSLRLKCRNACCORWYFTFNGAECGSLPLEATITVLDQ 180
DB 121 GKIAECTFTKMRNSALRVLEFSGSLRLKCRNACCORWYFTFNGAECGSLPLEATITVLDQ 180
OY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWTCSDYPKGDASTGMNSVSRIITEE 240
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWTCSDYPKGDASTGMNSVSRIITEE 240
OY 241 LPK 243
DB 241 LPK 243
```

```
RESULT 15
US-10-176-758-366
: Sequence 366, Application US/10176758
: Publication No. US20030008353A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C104
: CURRENT APPLICATION NUMBER: US/10/176,758
: CURRENT FILING DATE: 2002-06-21
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 366
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-176-758-366
```

Query Match 100.0%; Score 243; DB 15; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6,7e-214;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MRPGPASPORTLRLGLLLLLQLPAPSSASEIPKQKQALROREVVLDYNGMCLQSPA 60
DB 1 MRPGPASPORTLRLGLLLLLQLPAPSSASEIPKQKQALROREVVLDYNGMCLQSPA 60
OY 61 GVPGRDGSFGANVTPGTGIPGRDGFKEGKECECLRESFEESWTPYKQCSMSLNYGIDL 120
DB 61 GVPGRDGSFGANVTPGTGIPGRDGFKEGKECECLRESFEESWTPYKQCSMSLNYGIDL 120
OY 121 GKIAECTFTKMRNSALRVLEFSGSLRLKCRNACCORWYFTFNGAECGSLPLEATITVLDQ 180
DB 121 GKIAECTFTKMRNSALRVLEFSGSLRLKCRNACCORWYFTFNGAECGSLPLEATITVLDQ 180
OY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWTCSDYPKGDASTGMNSVSRIITEE 240
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWTCSDYPKGDASTGMNSVSRIITEE 240
OY 241 LPK 243
DB 241 LPK 243
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:38:13 ; Search time 374 Seconds  
(without alignments)  
565.500 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MRPGSPASPORTRLGILL.....GDASTGMSVSHIIIEELPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 5580241 segs, 870357830 residues

Word size : 6

Total number of hits satisfying chosen parameters: 47375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/PCUTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*  
31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	100.0	243	1	PCT-US02-02781-4559
2	243	100.0	243	1	PCT-US02-12378-514

3	243	100.0	243	23	US-09-834-759-514	Sequence 514, App
4	243 <th>100.0</th> <td>243</td> <td>24</td> <td>US-09-938-418-7</td> <td>Sequence 7, App1</td>	100.0	243	24	US-09-938-418-7	Sequence 7, App1
5	243 <th>100.0</th> <td>243</td> <td>24</td> <td>US-09-946-374-352</td> <td>Sequence 352, App</td>	100.0	243	24	US-09-946-374-352	Sequence 352, App
6	243 <th>100.0</th> <td>243</td> <td>24</td> <td>US-09-946-374-431</td> <td>Sequence 431, App</td>	100.0	243	24	US-09-946-374-431	Sequence 431, App
7	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-041A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-041A-352	Sequence 352, App
8	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-041A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-041A-431	Sequence 431, App
9	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-063A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-063A-352	Sequence 352, App
10	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-063A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-063A-431	Sequence 431, App
11	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-116A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-116A-352	Sequence 352, App
12	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-116A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-116A-431	Sequence 431, App
13	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-117A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-117A-352	Sequence 352, App
14	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-117A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-117A-431	Sequence 431, App
15	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-130A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-130A-352	Sequence 352, App
16	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-130A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-130A-431	Sequence 431, App
17	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-172A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-172A-352	Sequence 352, App
18	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-172A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-172A-431	Sequence 431, App
19	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-485A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-485A-352	Sequence 352, App
20	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-485A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-485A-431	Sequence 431, App
21	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-746A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-746A-352	Sequence 352, App
22	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-746A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-746A-431	Sequence 431, App
23	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-768A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-768A-352	Sequence 352, App
24	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-768A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-768A-431	Sequence 431, App
25	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-818A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-818A-352	Sequence 352, App
26	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-818A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-818A-431	Sequence 431, App
27	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-856A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-006-856A-352	Sequence 352, App
28	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-856A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-006-856A-431	Sequence 431, App
29	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-006-867-122</td> <td>Sequence 122, App</td>	100.0	243	26	US-10-006-867-122	Sequence 122, App
30	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-007-194A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-007-194A-352	Sequence 352, App
31	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-007-194A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-007-194A-431	Sequence 431, App
32	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-007-236A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-007-236A-352	Sequence 352, App
33	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-007-236A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-007-236A-431	Sequence 431, App
34	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-007-805-514</td> <td>Sequence 514, App</td>	100.0	243	26	US-10-007-805-514	Sequence 514, App
35	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-671A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-011-671A-352	Sequence 352, App
36	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-671A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-011-671A-431	Sequence 431, App
37	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-692A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-011-692A-352	Sequence 352, App
38	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-692A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-011-692A-431	Sequence 431, App
39	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-795A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-011-795A-352	Sequence 352, App
40	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-795A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-011-795A-431	Sequence 431, App
41	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-795B-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-011-795B-352	Sequence 352, App
42	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-795B-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-011-795B-431	Sequence 431, App
43	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-833A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-011-833A-352	Sequence 352, App
44	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-011-833A-431</td> <td>Sequence 431, App</td>	100.0	243	26	US-10-011-833A-431	Sequence 431, App
45	243 <th>100.0</th> <td>243</td> <td>26</td> <td>US-10-012-064A-352</td> <td>Sequence 352, App</td>	100.0	243	26	US-10-012-064A-352	Sequence 352, App

#### ALIGNMENTS

RESULT 1  
PCT-US02-02781-4559  
Sequence 4559, Application PC/TUS0202781  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Benson, Darin R.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Persing, David H.  
APPLICANT: Hepler, William T.  
APPLICANT: Jiang, Yugu  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.566PC  
CURRENT APPLICATION NUMBER: PCT/US02/02781  
CURRENT FILING DATE: 2002-01-30  
NUMBER OF SEQ ID NOS: 4560  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4559  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-02781-4559  
Query Match 100.0%; Score 243; DB 1; Length 243;

Best Local Similarity 100.0%; Pred. No. 2.5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKOKAOLRQREVVDLYNGMCIQSPA 60  
DB 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKOKAOLRQREVVDLYNGMCIQSPA 60

QY 61 GVPGRDGGPGANVITPGTIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
DB 61 GVPGRDGGPGANVITPGTIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120

QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWFTFTNGACSGPLPIEAIITYDQ 180  
DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWFTFTNGACSGPLPIEAIITYDQ 180

QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240

QY 241 LPK 243  
DB 241 LPK 243

## RESULT 2

PCT-US02-12378-514  
Sequence 514, Application PC/TUS0212378  
GENERAL INFORMATION:  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Persing, David H.  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jlangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Ranger, Gary R.  
APPLICANT: Vedick, Thomas S.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Durham, Margarita  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.47003PC  
CURRENT APPLICATION NUMBER: PCT/US02/12378  
CURRENT FILING DATE: 2002-04-15  
NUMBER OF SEQ ID NOS: 627  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 514  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-12378-514

Query Match 100.0%; Score 243; DB 1; Length 243;

Best Local Similarity 100.0%; Pred. No. 2.5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKOKAOLRQREVVDLYNGMCIQSPA 60  
DB 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKOKAOLRQREVVDLYNGMCIQSPA 60

QY 61 GVPGRDGGPGANVITPGTIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
DB 61 GVPGRDGGPGANVITPGTIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120

QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWFTFTNGACSGPLPIEAIITYDQ 180  
DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWFTFTNGACSGPLPIEAIITYDQ 180

QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240

DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

## RESULT 3

US-09-834-759-514  
Sequence 514, Application US/09834759  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jlangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C9  
CURRENT APPLICATION NUMBER: US/09/834,759  
CURRENT FILING DATE: 2001-04-13  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 514  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-834-759-514

Query Match 100.0%; Score 243; DB 23; Length 243;

Best Local Similarity 100.0%; Pred. No. 2.5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKOKAOLRQREVVDLYNGMCIQSPA 60  
DB 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKOKAOLRQREVVDLYNGMCIQSPA 60

QY 61 GVPGRDGGPGANVITPGTIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120  
DB 61 GVPGRDGGPGANVITPGTIGIRGDFKGEKGECLRESEESWTPNYKCCSSSLNYGIDL 120

QY 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWFTFTNGACSGPLPIEAIITYDQ 180  
DB 121 GKIAECTFTKMRNSALRVLFSGSLRLKCRNACCORWFTFTNGACSGPLPIEAIITYDQ 180

QY 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240  
DB 181 GSPEMNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRITIEE 240

QY 241 LPK 243  
DB 241 LPK 243

## RESULT 4

US-09-938-418-7  
Sequence 7, Application US/09938418  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Gurney, Austin L.  
APPLICANT: Polakis, Paul  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Wu, Thomas D.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TITLE OF INVENTION: TREATMENT OF TUMOR  
FILE REFERENCE: P5009R1  
CURRENT APPLICATION NUMBER: US/09/938,418



```

? PRIOR APPLICATION NUMBER: 60/102484
? PRIOR FILING DATE: 1998-09-30
? PRIOR APPLICATION NUMBER: 60/102487
? PRIOR FILING DATE: 1998-09-30
? PRIOR APPLICATION NUMBER: 60/102570
? PRIOR FILING DATE: 1998-09-30
? PRIOR APPLICATION NUMBER: 60/102571
? PRIOR FILING DATE: 1998-09-30
? PRIOR APPLICATION NUMBER: 60/102684
? PRIOR FILING DATE: 1998-10-01
? PRIOR APPLICATION NUMBER: 60/102687
? PRIOR FILING DATE: 1998-10-01
? PRIOR APPLICATION NUMBER: 60/102965
? PRIOR FILING DATE: 1998-10-02
? PRIOR APPLICATION NUMBER: 60/103258
? PRIOR FILING DATE: 1998-10-06
? PRIOR APPLICATION NUMBER: 60/103314
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103315
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103328
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103395
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103396
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103401
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103449
? PRIOR FILING DATE: 1998-10-06
? PRIOR APPLICATION NUMBER: 60/103633
? PRIOR FILING DATE: 1998-10-08
? PRIOR APPLICATION NUMBER: 60/103678
? PRIOR FILING DATE: 1998-10-08
? PRIOR APPLICATION NUMBER: 60/103679
? PRIOR FILING DATE: 1998-10-08
? PRIOR APPLICATION NUMBER: 60/103711
? PRIOR FILING DATE: 1998-10-08
? PRIOR APPLICATION NUMBER: 60/104257
? PRIOR FILING DATE: 1998-10-14
? PRIOR APPLICATION NUMBER: 60/104987
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105000
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105002
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105104
? PRIOR FILING DATE: 1998-10-21
? PRIOR APPLICATION NUMBER: 60/105169
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: 60/105266
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: 60/105693
? PRIOR FILING DATE: 1998-10-26
? PRIOR APPLICATION NUMBER: 60/105694
? PRIOR FILING DATE: 1998-10-26
? PRIOR APPLICATION NUMBER: 60/105807
? PRIOR FILING DATE: 1998-10-27

Query Match 100.0%; Score 243; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,5e-210;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 MRDGPAAAPORLNGLLILLILQLPAPSSASEIPKOKAOLRQREVVDLYNGMCLQGA 60
Db 1 MRDPGAPASPRLRGLLLILLILQLPAPSSASEIPKOKAOLRQREVVDLYNGMCLQGA 60
OY 61 GVPBRDSDPGANVPIGFGTIGRGQFGKEKGECKLRSESEESMTPTMYKOCSSWLSYKIDL 120
Db 61 GVPBRDSDPGANVPIGFGTIGRGQFGKEKGECKLRSESEESMTPTMYKOCSSWLSYKIDL 120
OY 121 GKIECEFTTKRSNSALRVLEFSGSIRLKCRRNACCORWTFETNGAECSGPLPLEATITLYDQ 180

```

Db 121 GKIAECTFKMSALRVLFSGLRLKCRNACCORNYFTFNAGCSGPLEITIAITLQ 180.  
QY 181 GSPEMNSTINIHRTSVSGLEGIGAGLVDAIIVWGTCSDYPKGDASTGNNVSRIITEE 240  
Db 181 GSPEMNSTINIHRTSVSGLEGIGAGLVDAIIVWGTCSDYPKGDASTGNNVSRIITEE 240  
QY 241 LPK 243  
Db 241 LPK 243

RESULT 6  
US-09-946-374-431  
Sequence 431, Application US/09946374  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207

;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102240  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102307  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102330  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807  
;; PRIOR FILING DATE: 1998-10-27  
;;  
Query Match 100.0%; Score 243; DB 24; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPGPASPORTRLGILLILLIQLPAPSSASEIPKQKQAOURLRQREVVDLYNGMCLQGPA 60

Db |||||  
1 MRPGPASPORTRLGILLILLIQLPAPSSASEIPKQKQAOURLRQREVVDLYNGMCLQGPA 60  
Qy 61 GVPGRDGSFGANVIGTPIPGRODFKGGKGCLEESFEESWTPLYKOCSSSLWYIDL 120  
Db 61 GVPGRDGSFGANVIGTPIPGRODFKGGKGCLEESFEESWTPLYKOCSSSLWYIDL 120  
Qy 121 GKIACTFTKMSNSALRYLFGSILRLKCRNACCORWFTFTFGACSGPLPIEATITTYDQ 180  
Db 121 GKIACTFTKMSNSALRYLFGSILRLKCRNACCORWFTFTFGACSGPLPIEATITTYDQ 180  
Qy 181 GSPENNSTINIHRTSSVEGLCEGIGALVDVAIWGTCSDPYKGPASTGMSVSRITIEE 240  
Db 181 GSPENNSTINIHRTSSVEGLCEGIGALVDVAIWGTCSDPYKGPASTGMSVSRITIEE 240  
Qy 241 LPK 243  
Db 241 LPK 243

RESULT 7  
US-10-006-041A-352  
; Sequence 352, Application US/10006041A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC8  
; CURRENT APPLICATION NUMBER: US/10/006, 041A  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 352  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-041A-352

Query Match 100.0%; Score 243; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRPGPASPORTRLGILLILLIQLPAPSSASEIPKQKQAOURLRQREVVDLYNGMCLQGPA 60  
Db 1 MRPGPASPORTRLGILLILLIQLPAPSSASEIPKQKQAOURLRQREVVDLYNGMCLQGPA 60  
Qy 61 GVPGRDGSFGANVIGTPIPGRODFKGGKGCLEESFEESWTPLYKOCSSSLWYIDL 120  
Db 61 GVPGRDGSFGANVIGTPIPGRODFKGGKGCLEESFEESWTPLYKOCSSSLWYIDL 120  
Qy 121 GKIACTFTKMSNSALRYLFGSILRLKCRNACCORWFTFTFGACSGPLPIEATITTYDQ 180  
Db 121 GKIACTFTKMSNSALRYLFGSILRLKCRNACCORWFTFTFGACSGPLPIEATITTYDQ 180  
Qy 181 GSPENNSTINIHRTSSVEGLCEGIGALVDVAIWGTCSDPYKGPASTGMSVSRITIEE 240  
Db 181 GSPENNSTINIHRTSSVEGLCEGIGALVDVAIWGTCSDPYKGPASTGMSVSRITIEE 240  
Qy 241 LPK 243  
Db 241 LPK 243

```
Db      241 LPK 243

RESULT 8
US-10-006-041A-431
: Sequence 431, Application US/10006041A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan I.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Goddard, Audrey
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2830P1C3
: CURRENT APPLICATION NUMBER: US/10/006, 041A
: PRIOR FILING DATE: 2001-12-06
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 477
: SEQ ID NO 431
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-006-041A-431

Query Match      100.0%; Score 243; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.5e-210;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPGPASPQRRLGILLLLLLQLPAPSSASEIRKQKQALRQREVVDLYNGMCLGSPA 60
Db      1 MRPGPASPQRRLGILLLLLLQLPAPSSASEIRKQKQALRQREVVDLYNGMCLGSPA 60
QY      61 GVPGRDSSPGANVTPGTGIRGRDGFKEGECLEESFEESWTNYKQCSWSLNYGIDL 120
Db      61 GVPGRDSSPGANVTPGTGIRGRDGFKEGECLEESFEESWTNYKQCSWSLNYGIDL 120
QY      121 GKIAECTFTKRRNSALRVLFSGSLRLKCRNACCOMFTFNAGCSGPLTEAIYYLDQ 180
Db      121 GKIAECTFTKRRNSALRVLFSGSLRLKCRNACCOMFTFNAGCSGPLTEAIYYLDQ 180
QY      181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMSVSRIIIEE 240
Db      181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMSVSRIIIEE 240
QY      241 LPK 243
Db      241 LPK 243

RESULT 9
US-10-006-063A-352
: Sequence 352, Application US/10006063A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan I.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
US-10-006-063A-352

Db      241 LPK 243

RESULT 10
US-10-006-063A-431
: Sequence 431, Application US/10006063A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan I.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2830P1C3
: CURRENT APPLICATION NUMBER: US/10/006, 063A
: PRIOR FILING DATE: 2002-03-15
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 477
: SEQ ID NO 431
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-006-063A-431

Query Match      100.0%; Score 243; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.5e-210;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPGPASPQRRLGILLLLLLQLPAPSSASEIRKQKQALRQREVVDLYNGMCLGSPA 60
Db      1 MRPGPASPQRRLGILLLLLLQLPAPSSASEIRKQKQALRQREVVDLYNGMCLGSPA 60
QY      61 GVPGRDSSPGANVTPGTGIRGRDGFKEGECLEESFEESWTNYKQCSWSLNYGIDL 120
Db      61 GVPGRDSSPGANVTPGTGIRGRDGFKEGECLEESFEESWTNYKQCSWSLNYGIDL 120
QY      121 GKIAECTFTKRRNSALRVLFSGSLRLKCRNACCOMFTFNAGCSGPLTEAIYYLDQ 180
Db      121 GKIAECTFTKRRNSALRVLFSGSLRLKCRNACCOMFTFNAGCSGPLTEAIYYLDQ 180
QY      181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMSVSRIIIEE 240
Db      181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMSVSRIIIEE 240
QY      241 LPK 243
Db      241 LPK 243
```

Query Match 100.0%; Score 243; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2,5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLILLILLQLPAPSSASEIPKQKAOIKOREVDLYGMCLQGPA 60  
DB 1 MRPGPASPORLRLILLILLQLPAPSSASEIPKQKAOIKOREVDLYGMCLQGPA 60  
QY 61 GVPGRDGSFGANVIGTGTGIPGRDGFKEGEGECLRESEESWTPTYKQCSWSLNYGIDL 120  
DB 61 GVPGRDGSFGANVIGTGTGIPGRDGFKEGEGECLRESEESWTPTYKQCSWSLNYGIDL 120  
QY 121 GKIACTCTTKMSNALSALVYFSGSLRLKCRNACCQRMWTFTEGACSGPLPIEALITYLDQ 180  
DB 121 GKIACTCTTKMSNALSALVYFSGSLRLKCRNACCQRMWTFTEGACSGPLPIEALITYLDQ 180  
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDDYKKGASTGWNVSRIITE 240  
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDDYKKGASTGWNVSRIITE 240  
QY 241 LPK 243  
DB 241 LPK 243

RESULT 11  
US-10-006-116A-352  
; Sequence 352, Application US/10006116A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Goddard, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC15  
; CURRENT APPLICATION NUMBER: US/10/006,116A  
; PRIOR FILING DATE: 2001-12-16  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099602  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099642  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099741

; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099763  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100662  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100664  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100683  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100684  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100710  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24



;; PRIOR APPLICATION NUMBER: 60/101743  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101915  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101916  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/102207  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102240  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102307  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102330  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105653  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28  
;; PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 243; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2,5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLGLLILLLILLOLPAPSSASEIRGKOKQRLORREVVLDLNGCIGGPA 60  
Db 1 MRPGPASPORLGLLILLLILLOLPAPSSASEIRGKOKQRLORREVVLDLNGCIGGPA 60  
QY 61 GVPGRDSPGANVITPGITPGITGRDGFGEKECECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
Db 61 GVPGRDSPGANVITPGITPGITGRDGFGEKECECLRESFEESWTPNYKQCSWSSLYNGIDL 120  
QY 121 GKIAECTFTKRSALRVLFSSGLRLKCRNACCORRYTFPNGACSGPLIEAIIYLDQ 180  
Db 121 GKIAECTFTKRSALRVLFSSGLRLKCRNACCORRYTFPNGACSGPLIEAIIYLDQ 180  
QY 181 GSPENNSTINHRSSVEGLCEGIGAGLVDAIIVGTCSDYPRKGDASTGNMVSRIITIEE 240  
Db 181 GSPENNSTINHRSSVEGLCEGIGAGLVDAIIVGTCSDYPRKGDASTGNMVSRIITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

RESULT 12  
US-10-006-116A-431  
; Sequence 431, Application US/10006116A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paout, Nicholas F.  
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC15  
; CURRENT APPLICATION NUMBER: US/10/006,116A  
; CURRENT FILING DATE: 2001-12-16  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09

PRIOR APPLICATION NUMBER:	60/099596
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099598
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099602
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099642
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099741
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099754
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099763
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099792
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099808
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099812
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099815
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099816
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/100385
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100388
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100390
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100584
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100627
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100661
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100662
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100664
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100683
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100684
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100710
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100711
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100848
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100849
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100930
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/101014
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101068
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101071
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101279
PRIOR FILING DATE:	1998-09-22
PRIOR APPLICATION NUMBER:	60/101471
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101472
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101474
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101475
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101476

1	PRIOR FILING DATE: 1998-09-23
2	PRIOR APPLICATION NUMBER: 60/101477
3	PRIOR FILING DATE: 1998-09-23
4	PRIOR APPLICATION NUMBER: 60/101475
5	PRIOR FILING DATE: 1998-09-23
6	PRIOR APPLICATION NUMBER: 60/101736
7	PRIOR FILING DATE: 1998-09-24
8	PRIOR APPLICATION NUMBER: 60/101744
9	PRIOR FILING DATE: 1998-09-24
10	PRIOR APPLICATION NUMBER: 60/101744
11	PRIOR FILING DATE: 1998-09-24
12	PRIOR APPLICATION NUMBER: 60/101915
13	PRIOR FILING DATE: 1998-09-24
14	PRIOR APPLICATION NUMBER: 60/101915
15	PRIOR FILING DATE: 1998-09-24
16	PRIOR APPLICATION NUMBER: 60/102207
17	PRIOR FILING DATE: 1998-09-25
18	PRIOR APPLICATION NUMBER: 60/102207
19	PRIOR FILING DATE: 1998-09-25
20	PRIOR APPLICATION NUMBER: 60/102488
21	PRIOR FILING DATE: 1998-09-30
22	PRIOR APPLICATION NUMBER: 60/102488
23	PRIOR FILING DATE: 1998-09-30
24	PRIOR APPLICATION NUMBER: 60/102570
25	PRIOR FILING DATE: 1998-09-30
26	PRIOR APPLICATION NUMBER: 60/102571
27	PRIOR FILING DATE: 1998-09-30
28	PRIOR APPLICATION NUMBER: 60/102688
29	PRIOR FILING DATE: 1998-10-01
30	PRIOR APPLICATION NUMBER: 60/102687
31	PRIOR FILING DATE: 1998-10-01
32	PRIOR APPLICATION NUMBER: 60/102965
33	PRIOR FILING DATE: 1998-10-02
34	PRIOR APPLICATION NUMBER: 60/103255
35	PRIOR FILING DATE: 1998-10-06
36	PRIOR APPLICATION NUMBER: 60/103314
37	PRIOR FILING DATE: 1998-10-07
38	PRIOR APPLICATION NUMBER: 60/103315
39	PRIOR FILING DATE: 1998-10-07
40	PRIOR APPLICATION NUMBER: 60/103322
41	PRIOR FILING DATE: 1998-10-07
42	PRIOR APPLICATION NUMBER: 60/103395
43	PRIOR FILING DATE: 1998-10-07
44	PRIOR APPLICATION NUMBER: 60/103396
45	PRIOR FILING DATE: 1998-10-07
46	PRIOR APPLICATION NUMBER: 60/103401
47	PRIOR FILING DATE: 1998-10-07
48	PRIOR APPLICATION NUMBER: 60/103448
49	PRIOR FILING DATE: 1998-10-06
50	PRIOR APPLICATION NUMBER: 60/103633
51	PRIOR FILING DATE: 1998-10-08
52	PRIOR APPLICATION NUMBER: 60/103678
53	PRIOR FILING DATE: 1998-10-08
54	PRIOR APPLICATION NUMBER: 60/103679
55	PRIOR FILING DATE: 1998-10-08
56	PRIOR APPLICATION NUMBER: 60/103711
57	PRIOR FILING DATE: 1998-10-08
58	PRIOR APPLICATION NUMBER: 60/104257
59	PRIOR FILING DATE: 1998-10-14
60	PRIOR APPLICATION NUMBER: 60/104987
61	PRIOR FILING DATE: 1998-10-20
62	PRIOR APPLICATION NUMBER: 60/105000
63	PRIOR FILING DATE: 1998-10-20
64	PRIOR APPLICATION NUMBER: 60/105002
65	PRIOR FILING DATE: 1998-10-20
66	PRIOR APPLICATION NUMBER: 60/105104
67	PRIOR FILING DATE: 1998-10-21



Db 121 GKIACTFTKRSNSALVLSGSLRLKCRNACCORWTFTEFGAECGPILEATITVLDQ 180  
QY 181 GSPENNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGWSVSRITIEE 240  
Db 181 GSPENNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGWSVSRITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

## RESULT 15

US-10-006-130A-352  
; Sequence 352, Application US/10006130A

; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gutney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C7  
; CURRENT APPLICATION NUMBER: US/10/006,130A  
; CURRENT FILING DATE: 2002-03-19  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 352  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-130A-352

Query Match 100.0%; Score 243; DB 26; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.5e-210;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPOLRLGILLILLQLPAPSSASEIPKQKQAOI,ROREVVLDYNGMCIQGPA 60  
Db 1 MRPOGPASPOLRLGILLILLQLPAPSSASEIPKQKQAOI,ROREVVLDYNGMCIQGPA 60  
QY 61 GVPGRDGSFGANVIGTGTGIGRQDFKGEKGECLRESFEESWTPTNYKQCSWSLNYGIDL 120  
Db 61 GVPGRDGSFGANVIGTGTGIGRQDFKGEKGECLRESFEESWTPTNYKQCSWSLNYGIDL 120  
QY 121 GKIACTFTKRSNSALVLSGSLRLKCRNACCORWTFTEFGAECGPILEATITVLDQ 180  
Db 121 GKIACTFTKRSNSALVLSGSLRLKCRNACCORWTFTEFGAECGPILEATITVLDQ 180  
QY 181 GSPENNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGWSVSRITIEE 240  
Db 181 GSPENNSTINIHRTSSVGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGWSVSRITIEE 240  
QY 241 LPK 243  
Db 241 LPK 243

Search completed: August 13, 2003, 13:48:06  
Job time : 375 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 13, 2003, 13:38:43 ; Search time 21 Seconds  
(without alignments)  
252.569 Million cell updates/sec

Title: US-09-938-418-7

Perfect score: 243  
Sequence: 1 MRQGPASPRRLGILLLL.....GDASTGMSVSRITIEELPK 243

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105250 seqs, 21826969 residues

Word size : 6

Total number of hits satisfying chosen parameters: 763

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

## Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW.COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	70.0	243	1 PCT-US02-29560A-203	Sequence 203, App
2	9	3.7	80	US-10-603-113-23275	Sequence 23275, A
3	9	3.7	996	US-10-464-368-85	Sequence 85, App1
4	9	3.7	1164	US-60-487-610-2411	Sequence 2411, Ap
5	9	3.7	1164	US-60-485-450-1525	Sequence 1525, Ap
6	9	3.7	1284	US-60-487-610-2407	Sequence 2407, Ap
7	9	3.7	1284	US-60-485-450-1521	Sequence 1521, Ap
8	9	3.7	1464	PCT-US02-18638A-36	Sequence 36, App1
9	9	3.7	1464	US-10-291-265-243	Sequence 243, App
10	9	3.7	1464	US-60-487-610-2409	Sequence 2409, App
11	9	3.7	1464	US-60-485-450-1523	Sequence 1523, Ap
12	8	3.3	82	US-10-603-113-21867	Sequence 21867, A
13	8	3.3	178	US-60-487-610-2653	Sequence 2653, Ap
14	8	3.3	178	US-60-485-450-1694	Sequence 1694, Ap
15	8	3.3	181	US-08-867-587B-34	Sequence 34, App1
16	8	3.3	234	US-08-867-587B-4	Sequence 4, App1
17	8	3.3	234	US-08-867-587B-7	Sequence 7, App1
18	8	3.3	234	US-08-867-587B-19	Sequence 19, App1
19	8	3.3	234	US-08-867-587B-22	Sequence 22, App1
20	8	3.3	237	US-08-867-587B-13	Sequence 13, App1
21	8	3.3	237	US-08-867-587B-16	Sequence 16, App1
22	8	3.3	254	US-10-408-765A-509	Sequence 509, App
23	8	3.3	265	US-08-867-587B-1	Sequence 1, App1
24	8	3.3	265	US-08-867-587B-37	Sequence 37, App1
25	8	3.3	366	US-10-408-765A-492	Sequence 492, App1
26	8	3.3	486	US-60-487-636-10	Sequence 10, App1

27	8	3.3	652	6	US-10-408-765A-1422	Sequence 1422, Ap
28	8	3.3	671	7	US-60-485-450-1335	Sequence 1335, Ap
29	8	3.3	828	7	US-60-487-610-2652	Sequence 2652, Ap
30	8	3.3	828	7	US-60-485-450-1693	Sequence 1693, Ap
31	8	3.3	893	6	US-10-369-072-38	Sequence 38, App1
32	8	3.3	918	7	US-60-487-610-2650	Sequence 2650, Ap
33	8	3.3	918	7	US-60-485-450-1691	Sequence 1691, Ap
34	8	3.3	984	7	US-60-487-610-2168	Sequence 2168, Ap
35	8	3.3	984	7	US-60-485-450-1382	Sequence 1382, Ap
36	8	3.3	984	7	US-60-490-890-209	Sequence 209, App
37	8	3.3	987	7	US-60-487-610-2242	Sequence 2242, Ap
38	8	3.3	987	7	US-60-485-450-1437	Sequence 1437, Ap
39	8	3.3	1019	7	US-60-487-610-2651	Sequence 2651, Ap
40	8	3.3	1019	7	US-60-485-450-1692	Sequence 1692, Ap
41	8	3.3	1388	6	US-10-408-765A-1718	Sequence 1718, Ap
42	8	3.3	1416	7	US-60-490-890-773	Sequence 773, App
43	8	3.3	1472	7	US-60-490-890-769	Sequence 769, App
44	8	3.3	1475	7	US-60-490-890-771	Sequence 771, App
45	8	3.3	1531	7	US-60-490-890-767	Sequence 767, App

## ALIGNMENTS

RESULT 1  
PCT-US02-29560A-203  
Sequence 203, Application PC/TUS0229560A  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Gish, Kurt C.  
APPLICANT: Hevezl, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Walsen, Keith E.  
APPLICANT: Zlotnik, Albert  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OR INVENTION: Methods of Diagnosis of Cancer, Compositions and  
FILE REFERENCE: 018501-002710PC  
CURRENT APPLICATION NUMBER: PCT/US02/29560A  
CURRENT FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: US 60/323,469  
PRIOR FILING DATE: 2001-09-17  
NUMBER OF SEQ ID NOS: 412  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 203  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-29560A-203  
Query Match 70.0%: Score 170; DB 1; Length 243;  
Best Local Similarity 100.0%: Pred. No. 6.4e-143;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 IPGPGIGNDGKGEKGEKRESFEESWTPNNKQCSWSSLNTGIDGKIAECTFTMRS 133  
DB 74 IPGPGIGNDGKGEKGEKRESFEESWTPNNKQCSWSSLNTGIDGKIAECTFTMRS 133  
QY 134 NSALRYLFSSGLKRCNACCQRMFTFNGAECSSGPLIPAIITYLDOGSPEMNSTINHR 193  
DB 134 NSALRYLFSSGLKRCNACCQRMFTFNGAECSSGPLIPAIITYLDOGSPEMNSTINHR 193  
QY 194 TTSVEGICBEGIGAGLVDAIVATWGTCSYPRGDASTGMSVSRITIEELPK 243  
DB 194 TTSVEGICBEGIGAGLVDAIVATWGTCSYPRGDASTGMSVSRITIEELPK 243  
RESULT 2  
US-10-603-113-23275  
Sequence 23275, Application US/10603113  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstein et al

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US-10/603,113
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/248,796
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 23275
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-603-113-23275

Query Match
Best Local Similarity 3.7%; Score 9; DB 6; Length 80;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
DB 1 LLLLLLQL 9

RESULT 3
US-10-464-368-85
; Sequence 85, Application US/10464368
; GENERAL INFORMATION:
; APPLICANT: Krumlauf, Robb
; APPLICANT: Elies, Debra
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
; FILE REFERENCE: 40716-1P-017
; CURRENT APPLICATION NUMBER: US/10/464,368
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/388,970
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 996
; TYPE: PRT
; ORGANISM: MOUSE
US-10-464-368-85

Query Match
Best Local Similarity 3.7%; Score 9; DB 6; Length 996;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
DB 14 LLLLLLQL 22

RESULT 4
US-60-487-610-2411
; Sequence 2411, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: C1001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2411
; LENGTH: 1164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2411

Query Match 3.7%; Score 9; DB 7; Length 1164;
```

```

Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PGRDSSPCA 71
DB 724 PGRDSSPCA 732

RESULT 5
US-60-485-450-1525
; Sequence 1525, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: C1001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1525
; LENGTH: 1164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1525

Query Match
Best Local Similarity 3.7%; Score 9; DB 7; Length 1164;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PGRDSSPCA 71
DB 724 PGRDSSPCA 732

RESULT 6
US-60-487-610-2407
; Sequence 2407, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: C1001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2407
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2407

Query Match
Best Local Similarity 3.7%; Score 9; DB 7; Length 1284;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PGRDSSPCA 71
DB 844 PGRDSSPCA 852

RESULT 7
US-60-485-450-1521
; Sequence 1521, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
```

```

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1521
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1521

```

```

Query Match
Best Local Similarity 100.0%; Score 9; DB 7; Length 1284;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 63 PGRDGSFGA 71
DB 844 PGRDGSFGA 852

```

```

RESULT 8
PCT-US02-18638A-36
; Sequence 36, Application PC/TUS0218638A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035PC
; CURRENT APPLICATION NUMBER: PCT/US02/18638A
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18638A-36

```

```

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 1464;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 63 PGRDGSFGA 71
DB 1024 PGRDGSFGA 1032

```

```

RESULT 9
US-10-291-265-243
; Sequence 243, Application US/10291265
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451

```

```

; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-243

```

```

Query Match
Best Local Similarity 100.0%; Score 9; DB 6; Length 1464;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 63 PGRDGSFGA 71
DB 1024 PGRDGSFGA 1032

```

```

RESULT 10
US-60-487-610-2409
; Sequence 2409, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2409
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2409

```

```

Query Match
Best Local Similarity 100.0%; Score 9; DB 7; Length 1464;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 63 PGRDGSFGA 71
DB 1024 PGRDGSFGA 1032

```

```

RESULT 11
US-60-485-450-1523
; Sequence 1523, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1523
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1523

```

```

Query Match
Best Local Similarity 100.0%; Score 9; DB 7; Length 1464;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 63 PGDGPSCA 71  
 Db 1024 PGDGPSCA 1032

## RESULT 12

US-10-603-113-21887  
 ; Sequence 21887, Application US/10603113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstein et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
 ; FILE REFERENCE: 107196.132  
 ; CURRENT APPLICATION NUMBER: US/10/603,113  
 ; PRIOR FILING DATE: 2003-06-24  
 ; PRIOR APPLICATION NUMBER: US/09/248,796  
 ; NUMBER OF SEQ ID NOS: 28206  
 ; SEQ ID NO 21887  
 ; LENGTH: 82  
 ; TYPE: PRT  
 ; ORGANISM: Candida albicans  
 US-10-603-113-21887

Query Match 3.3%; Score 8; DB 6; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GLLLLLLL 22  
 Db 31 GLLLLLLL 38

## RESULT 13

US-60-487-610-2653  
 ; Sequence 2653, Application US/60487610  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; TITLE OF INVENTION: HUNG, Hongjin  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
 ; FILE REFERENCE: CL001469  
 ; CURRENT APPLICATION NUMBER: US/60/487,610  
 ; CURRENT FILING DATE: 2003-07-17  
 ; NUMBER OF SEQ ID NOS: 97101  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 2653  
 ; LENGTH: 178  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-487-610-2653

Query Match 3.3%; Score 8; DB 7; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GFGKEGGE 92  
 Db 32 GFGKEGGE 39

## RESULT 14

US-60-485-450-1694  
 ; Sequence 1694, Application US/60485450  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: CHANG, Sheng-Yung  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
 ; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
 ; TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001470  
 ; CURRENT APPLICATION NUMBER: US/60/485,450  
 ; CURRENT FILING DATE: 2003-07-09  
 ; NUMBER OF SEQ ID NOS: 47859  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 1694  
 ; LENGTH: 178  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-485-450-1694

Query Match 3.3%; Score 8; DB 7; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GFGKEGGE 92  
 Db 32 GFGKEGGE 39

## RESULT 15

US-08-867-587B-34  
 ; Sequence 34, Application US/08867587B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOYLE, William R.  
 ; TITLE OF INVENTION: Methods for Altering Fertility  
 ; FILE REFERENCE: MOY1-001  
 ; CURRENT APPLICATION NUMBER: US/08/867,587B  
 ; CURRENT FILING DATE: 1997-06-02  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 34  
 ; LENGTH: 181  
 ; TYPE: PRT  
 ; ORGANISM: Rat leukemia virus  
 US-08-867-587B-34

Query Match 3.3%; Score 8; DB 4; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GLLLLLLL 22  
 Db 6 GLLLLLLL 13

Search completed: August 13, 2003, 13:48:34  
 Job time : 21 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 11:07:09 ; Search time 4783 Seconds

(Without alignments)  
10751.286 Million cell updates/sec

Title: US-09-938-418-2

Perfect score: 1257  
Sequence: 1 ggaagagagcgcgcggtga.....aataaaattattcccaaca 1257

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

GenEmbl:
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_lm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_com:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	100.0	1257	6	AX092390 Sequence
2	1257	100.0	1257	6	AX376298 Sequence
3	1257	100.0	1257	6	AX454660 Sequence
4	1257	100.0	1257	6	AX459648 Sequence
5	1257	100.0	1257	6	AX491138 Sequence
6	1257	100.0	1257	6	AX697362 Sequence
7	1231.6	98.0	1342	6	AR243851 Sequence
8	1222.8	97.3	1286	6	AR243886 Sequence
9	1217.2	96.8	1245	9	BC014245 Sequence
10	1198.8	95.4	1221	9	AY136825 Sequence
11	964.6	76.7	1215	9	AF395488 Homo sapi
12	793	63.1	860	6	AX285214 Sequence
13	728.8	58.0	732	6	BD006704 Sequence
14	682.2	54.3	683	6	AX375790 Sequence
15	681.8	54.2	683	6	AR280558 Sequence
16	681.8	54.2	683	6	AR283054 Sequence
17	664.2	52.8	683	6	AX302743 Sequence
18	664.2	52.8	1217	10	AY136824 Sequence
19	640.8	51.0	687	6	AX067343 Sequence
20	539.8	42.9	160197	9	AP004221 Homo sapi
21	539.8	42.9	176922	9	AC012213 Homo sapi
22	532.2	42.3	560	6	AX339938 Sequence
23	433.2	34.5	460	6	AX351434 Sequence
24	431.2	34.3	471	6	AX340025 Sequence
25	287	22.8	111496	9	AC069351 Homo sapi
26	258	20.5	271	6	AX284686 Sequence
27	232	18.5	346	6	AX198874 Sequence
28	232	18.5	346	6	AX198975 Sequence
29	231	18.4	231	6	AX209500 Sequence
30	231	18.4	231	6	AX209501 Sequence
31	228	18.1	525	6	AX198465 Sequence
32	228	18.1	525	6	AX209011 Sequence
33	219.6	17.5	74798	2	AC069352 Homo sapi
34	196.6	15.6	270	6	AX332192 Sequence
35	190.2	15.1	323534	2	AC121173 Rattus no
36	186	14.8	235421	2	AC131363 Rattus no
37	185.6	14.8	208553	2	AC145088 Mus muscu
38	184.8	14.7	166810	9	AL590222 Human DNA
39	132.8	10.6	475	6	AX284559 Sequence
40	120.6	9.6	213269	5	AL844521 Zebrafish
41	76.8	6.1	250029	3	AE014830 Plasmodiu
42	75.2	6.0	335050	3	AL929356 Plasmodiu
43	71.8	5.7	246611	2	AC111404 Rattus no
44	71.4	5.7	9483	6	AX251786 Sequence
45	71.4	5.7	9483	6	AX345278 Sequence

#### ALIGNMENTS

```

RESULT 1
AX092390 1257 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 121 from Patent WO0116318.
DEFINITION AX092390
ACCESSION AX092390.1 GI:13444509
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Eaton,D.L., Pilvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

```

TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same						
JOURNAL	Patent: WO 0116318-A 121 08-MAR-2001;						
FEATURES	Genentech, Inc. (US)						
source	Location/Qualifiers 1..1257 /organism="Homo sapiens" /mol.type="genomic DNA" /db_xref="taxon:9606"						
BASE COUNT	324 a	264 c	299 g	370 t			
ORIGIN							
Query Match	100.0%;	Score 1257;	DB 6;	Length 1257;			
Best Local Similarity	100.0%;	Pred. No. 1,2e-213;					
Matches 1257;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
OY	1	GGAGAGAGGCGCGGGGTGAAGAAGCGCATTTGATGCAGCCTCGCGGCGCCTCGAGACGCGG	60				
Db	1	GGAGAGAGGCGCGGGGTGAAGAAGCGCATTTGATGCAGCCTCGCGGCGCCTCGAGACGCGG	60				
OY	61	CGGAGCCAGAGCCTTACCACGTTCTTCCTTCGGTCTCTCGGCCCTCCAGCTCGCGCTG	120				
Db	61	CGGAGCCAGAGCCTTACCACGTTCTTCCTTCGGTCTCTCGGCCCTCCAGCTCGCGCTG	120				
OY	121	CCCCGACCCCGGAGACCAATGCGACCCCAAGGGCCCGCGCCGCCCGGAGCGAGCTCCGG	180				
Db	121	CCCCGACCCCGGAGACCAATGCGACCCCAAGGGCCCGCGCCGCCCGGAGCGAGCTCCGG	180				
OY	181	GCTCTCTCTGCTGCTGCTGTGACAGTCCCGCGCGCTCGAAGCGCTCTGAGATCCC	240				
Db	181	GCTCTCTCTGCTGCTGCTGTGACAGTCCCGCGCGCTCGAAGCGCTCTGAGATCCC	240				
OY	241	AGGGAAACAAAAGGCGGACGCTCCGGCAGAGGAGTGTTGGACTGTATAATGGAAGT	300				
Db	241	AGGGAAACAAAAGGCGGACGCTCCGGCAGAGGAGTGTTGGACTGTATAATGGAAGT	300				
OY	301	GCTTACAAGGGCGCACAGAGTGCCTGCTCAGAGCGGAGCCCTGGGSCCAATTGTATTTC	360				
Db	301	GCTTACAAGGGCGCACAGAGTGCCTGCTCAGAGCGGAGCCCTGGGSCCAATTGTATTTC	360				
OY	361	CGGCTACACCTTGGGATCCCAAGTCGGGATGGAATTAAGAGAAAAAGGGGAATGTCTGA	420				
Db	361	CGGCTACACCTTGGGATCCCAAGTCGGGATGGAATTAAGAGAAAAAGGGGAATGTCTGA	420				
OY	421	GGGAAGGTTTGGAGAGTCTGGGACCCCACTCAACACAGTTCATGAGACTCATTTGA	480				
Db	421	GGGAAGGTTTGGAGAGTCTGGGACCCCACTCAACACAGTTCATGAGACTCATTTGA	480				
OY	481	ATTATGCGATAGATCTTGGGAAAAATTCGGAGTGTACATTTCACAAAGATGCGTTCAATA	540				
Db	481	ATTATGCGATAGATCTTGGGAAAAATTCGGAGTGTACATTTCACAAAGATGCGTTCAATA	540				
OY	541	GTGCTTAAGAAGTTTTGTTCAGTGGCTCAGTTCGGCTAAAAATGCAAAATGCATGCTGTC	600				
Db	541	GTGCTTAAGAAGTTTTGTTCAGTGGCTCAGTTCGGCTAAAAATGCAAAATGCATGCTGTC	600				
OY	601	AGCCTGGTATTTCACATTCATGAGAGCTGATGTTCAGGACCTTCCTCCATTGAAAGCTA	660				
Db	601	AGCCTGGTATTTCACATTCATGAGAGCTGATGTTCAGGACCTTCCTCCATTGAAAGCTA	660				
OY	661	TAAATTAATTTGGACCAAGGAAGCCCTGAAGAAATTAACAATTAATTAATTCAGCACTT	720				
Db	661	TAAATTAATTTGGACCAAGGAAGCCCTGAAGAAATTAACAATTAATTAATTCAGCACTT	720				
OY	721	CTTCTGTGGAAGCACTTGTGNAAGAAATGGTGTGATTTAGTAGAGTGTCTATCTGAGG	780				
Db	721	CTTCTGTGGAAGCACTTGTGNAAGAAATGGTGTGATTTAGTAGAGTGTCTATCTGAGG	780				
OY	781	TTGGCACTTGTTCAGATTTACCAAAGAGAGTCTTACTAGANAGAAATCAATTTCTC	840				
Db	781	TTGGCACTTGTTCAGATTTACCAAAGAGAGTCTTACTAGANAGAAATCAATTTCTC	840				
OY	841	GCATCATTAATGAAGAACTACCAAAATTAATGCTTTAATTTCAATTTGCTACCTCTTTTT	900				

Dd			841	GATGATTATTGGAAAGACTACCAATAAAGCTTAATTTTCATTGTCTACCTCTT	900
Oy			901	TTATTATGCCCTGGATGGTTCCATTAAATGCATTTTAAATAGTTTATGATCATCT	960
Dd			901	TTATTATGCCCTGGATGGTTCCATTAAATGCATTTTAAATAGTTTATGATCATCT	960
Oy			961	GAAATAAAAGCAAAGCCTAAATATGTGTTACACGACCAAAGTGATGTCACACTG	10200
Dd			961	GAAATAAAAGCAAAGCCTAAATATGTGTTACACGACCAAAGTGATGTCACACTG	10200
Oy			1021	AATCGACATPATTCATTTTGGCTGCAACAAAGCGCTTCAATATTTTTTTAGTGG	10800
Dd			1021	AATCGACATPATTCATTTTGGCTGCAACAAAGCGCTTCAATATTTTTTTAGTGG	10800
Oy			1081	AGAATACATTTCTTCATATGATGCATATCTCTCAACCATATATTTGGANAAT	11400
Dd			1081	AGAATACATTTCTTCATATGATGCATATCTCTCAACCATATATTTGGANAAT	11400
Oy			1141	TTTGTGTTTTCTCTTAGTATAGCATTTTAAAAAATATPAAAAGCTACCAATCT	12000
Dd			1141	TTTGTGTTTTCTCTTAGTATAGCATTTTAAAAAATATPAAAAGCTACCAATCT	12000
Oy			1201	AATTTGTAATGTTTGAAGATTTTAAAAATTTTATCTGTTAAATPAAAATTT	1257
Dd			1201	AATTTGTAATGTTTGAAGATTTTAAAAATTTTATCTGTTAAATPAAAATTT	1257
RESULT 2					
LOCUS	AX376298	1257 bp	DNA	linear	PAT 01-MAR-2002
DEFINITION	Sequence 365 from Patent WO0168848.				
ACCESSION	AX376298				
VERSION	AX376298.1	GI:19170540			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gunney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0168848-A 365 20-SEP-2001; Genentech, Inc. (US) Location/Qualifiers 1..1257 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
JOURNAL	source				
FEATURES					
BASE COUNT	324 a 264 c 299 g 370 t				
ORIGIN					
Query Match	100.0%; Score 1257;	DB 6;	Length 1257;		
Best Local Similarity	100.0%; Pred. No. 1,2e-213;				
Matches 1257;	Conservative 0;	Mismatches 0;	Gaps 0;		
Oy			1	GGAGAGAGGCGCGGGGGAAGGCGGATGATGACGACGCGGCGGCGCTCGAGCGCGG	60
Dd			1	GGAGAGAGGCGCGGGGGAAGGCGGATGATGACGACGCGGCGGCGCTCGAGCGCGG	60
Oy			61	CGAGACGAGAGCGTGACACGTTCTCTCCGCGTGCTCCGCGCTCCAGCTCGGCGTG	120
Dd			61	CGAGACGAGAGCGTGACACGTTCTCTCCGCGTGCTCCGCGCTCCAGCTCGGCGTG	120
Oy			121	CCGCGCACCGCGGAGCCATGCGACGCCAGGCCCCCGCGGCTCCCGCAGCGCTCCGCG	180
Dd			121	CCGCGCACCGCGGAGCCATGCGACGCCAGGCCCCCGCGGCTCCCGCAGCGCTCCGCG	180
Oy			181	GCTCTCTGCTGCTCTCTGCTGACGTGCCCGCGCGCTGAGAGCGCTTGAAGATCCCA	240

[illegible]

LOCUS	AX5454660	1257 bp	DNA	linear	PAT 06-JUL-2002
DEFINITION	Sequence 245 from Patent WO0208284.				
ACCESSION	AX5454660				
VERSION	AX5454660.1	GI:21713954			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 Baker,K.P., Ferrara,N., Gerber,H., Hillan,K.J., Marsters,S.A., Pan,J., Panol,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.				
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis				
JOURNAL	Patent: WO 0208284-A 245 31-JUN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gertlisen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Panol, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)				
FEATURES	Location/Qualifiers				
source	1..1257 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
BASE COUNT	324 a 264 c 299 g 370 t				
ORIGIN					
Query Match	100.0%; Score 1257; DB 6; Length 1257;				
Best Local Similarity	100.0%; Pred. No. 1.2e-213;				
Matches 1257;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 GGAGAGAGCGCGCGGGTGAAGGCGCATGTATGCAAGCTCGCGCGGCGCTCGAGCGCGG 60				
Db	1 GGAGAGAGCGCGCGGGTGAAGGCGCATGTATGCAAGCTCGCGCGGCGCTCGAGCGCGG 60				
OY	61 CGAGCGCAGAGCGCGACCGAGCTTCCTCCCGGTCCTCCGCGTCCAGCTCCAGCTCCGCGTG 120				
Db	61 CGAGCGCAGAGCGCGACCGAGCTTCCTCCCGGTCCTCCGCGTCCAGCTCCGCGTG 120				
OY	121 CCCGCGACCGCGGAGACCATGTGACGCCACCGGCGCGCGCTCCCGCAGCGGCTCGCGG 180				
Db	121 CCCGCGACCGCGGAGACCATGTGACGCCACCGGCGCGCGCTCCCGCAGCGGCTCGCGG 180				
OY	181 GCGTCCTGCTGCTCTGCTGCTGAGCTGCCCGCGCGCTCGAGCGCGCTTGAGATCCCA 240				
Db	181 GCGTCCTGCTCTCTGCTGCTGAGCTGCCCGCGCGCTCGAGCGCGCTTGAGATCCCA 240				
OY	241 AGGGGAAGCAAAAGGCGCAGCTCCGGCGAGAGGAGTGTGGACCTGTATTAATGAGATGT 300				
Db	241 AGGGGAAGCAAAAGGCGCAGCTCCGGCGAGAGGAGTGTGGACCTGTATTAATGAGATGT 300				
OY	301 GCTTACAAGGCGCAGAGAGTGGCTGGTCAGACGGGAGGCGCTGGGGCGCAATGTTATTC 360				
Db	301 GCTTACAAGGCGCAGAGAGTGGCTGGTCAGACGGGAGGCGCTGGGGCGCAATGTTATTC 360				
OY	361 CGGGTACACCTGGGATGCCAGTGGGATGATTCAAAGAGAAAAGGGGGAATGTGCA 420				
Db	361 CGGGTACACCTGGGATGCCAGTGGGATGATTCAAAGAGAAAAGGGGGAATGTGCA 420				
OY	421 GGGAAAGCTTGGAGAGTCCCTGGACACCCCACTACAGCACTGTTCAATGGAGTTCATTTGA 480				
Db	421 GGGAAAGCTTGGAGAGTCCCTGGACACCCCACTACAGCACTGTTCAATGGAGTTCATTTGA 480				
OY	481 ATTATGGCATGATCTTGGAAAAATTGGGAGTGTACTTTTACAAGAATGGCTTCAATA 540				
Db	481 ATTATGGCATGATCTTGGAAAAATTGGGAGTGTACTTTTACAAGAATGGCTTCAATA 540				
OY	541 GTGCTCTAGAAGTTTGTCTAGTGGCTCACTTGCGCTAAAATGCAAGAAATGCATGCTGTC 600				

Db	541	GTGCTCTAGAGGTTTGTTCAGTGGCTACTTCGGCTTAAATTCAGAAATTCATGCTGTCTC	600
OY	601	AGCGTTGGTATTTTCACATTTCAATGAGCTGAATGTTTCAGAGCTCTTCCATTTGAAGCTA	660
Db	601	AGCGTTGGTATTTTCACATTTCAATGAGCTGAATGTTTCAGAGCTCTTCCATTTGAAGCTA	660
OY	661	TAAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAAATTAATTAATTCATGGCACTT	720
Db	661	TAAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAAATTAATTAATTCATGGCACTT	720
OY	721	CTTCTGTGGAAGGACTTTGTGAGGAATTTGGTGTGATTTAGTGGATTTGTCTATCTGCGG	780
Db	721	CTTCTGTGGAAGGACTTTGTGAGGAATTTGGTGTGATTTAGTGGATTTGTCTATCTGCGG	780
OY	781	TTGGCACTTGTTCAGATTTACCCAAAGAGATGCTTCTACTGATGCAATTCAGTTCTGC	840
Db	781	TTGGCACTTGTTCAGATTTACCCAAAGAGATGCTTCTACTGATGCAATTCAGTTCTGC	840
OY	841	GCATCATTTATGGAAGAACTACCAAAATTAAGCTTTAATTTTCATTTGCGTACCTCTTTT	900
Db	841	GCATCATTTATGGAAGAACTACCAAAATTAAGCTTTAATTTTCATTTGCGTACCTCTTTT	900
OY	901	TTATTTATGCGCTTGGAAATGGTTCACCTTAATGACATTTTAAATTAAGTTATGATACACT	960
Db	901	TTATTTATGCGCTTGGAAATGGTTCACCTTAATGACATTTTAAATTAAGTTATGATACACT	960
OY	961	GAAATGAAGAAGCAAGCTTAATATGTTTACAGACCACCAAGTGTGATTTTCACACTGTTTTTAA	1020
Db	961	GAAATGAAGAAGCAAGCTTAATATGTTTACAGACCACCAAGTGTGATTTTCACACTGTTTTTAA	1020
OY	1021	ATTTAGCACTTTTCATTTTGGTTCATCAACCAAAAGGGTTCAAATTTTTTTTAACTGGTT	1080
Db	1021	ATTTAGCACTTTTCATTTTGGTTCATCAACCAAAAGGGTTCAAATTTTTTTTAACTGGTT	1080
OY	1081	AGAAATACCTTCCTCATAGTCAATTTCTCAACCTATTAATTTGGAATTTTGTGGGCT	1140
Db	1081	AGAAATACCTTCCTCATAGTCAATTTCTCAACCTATTAATTTGGAATTTTGTGGGCT	1140
OY	1141	TTTGTGTTTTTCTCTAGATATGCAATTTTTTAAAAAATTTAAAGCTCAATCTTTGTATC	1200
Db	1141	TTTGTGTTTTTCTCTAGATATGCAATTTTTTAAAAAATTTAAAGCTCAATCTTTGTATC	1200
OY	1201	AATTTGTAATAGTATAGAAATTTTTTTTAACTGTAAATTAATTAATTTTCCAAACA	1257
Db	1201	AATTTGTAATAGTATAGAAATTTTTTTTAACTGTAAATTAATTAATTTTCCAAACA	1257

	RESULT	4			
	AX459648				
LOCUS	AX459648	1257 bp	DNA	linear	PAT 08-JUL-2002
DEFINITION	Sequence 2 from Patent WO0216602.				
ACCESSION	AX459648				
VERSION	AX459648.1	GI:21725519			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. . . . 1				
REFERENCE	Askenazi,A.J., Goddard,A., Godowski,P.J., Gunney,A.L., Polakis,P.., Williams,P.M., Wood,W.T., Wu,T.D. and Zhang,Z. Compositions and methods for the diagnosis and treatment of tumor Patent: WO 0216602-A 2 28-FEB-2002;				
TITLE	JOURNAL	GEMENETECH, INC. (US)  Location/Qualifiers 1. 1257			
FEATURES	source	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"			
BASE COUNT	324 a	264 c	299 g	370 t	
ORIGIN					

Query Match	100.0%	Score 1257	DB 6	Length 1257	
Best Local Similarity	100.0%	Pred. No. 1,2e-213			
Matches 1257	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
OY	1	GGAGAGAGCGCGGGGCGTGAAGAGCGCATTTATGACAGCTCGCGGGCGCTCGAGCGCGG	60		
Db	1	GGAGAGAGCGCGCGGGGTGAAGAGCGCATTTATGACAGCTCGCGGGCGCTCGAGCGCGG	60		
OY	61	CGAGCGAGAGCGTGAACCGACGTTCCCTCCGCTTCGCGCTCCGCGCTCGAGCTCGCGCTG	120		
Db	61	CGAGCGCGAGAGCGTGAACCGACGTTCCCTCCGCTTCGCGCTTCGCGCTCGAGCTCGCGCTG	120		
OY	121	CCCGGACCGCGGGAGCCATGGGACCCCGAGGGCCCGCGCTCCCGGACGCGCTCGCGG	180		
Db	121	CCCGGACCGCGGGAGCCATGGGACCCCGAGGGCCCGCGCTCCCGGACGCGCTCGCGG	180		
OY	181	GCGTCTCTGCTCCTCTGCTGCTGACAGCGCCCGCGCGCTCGAGCGCTGAGATCCCA	240		
Db	181	GCGTCTCTGCTCCTCTGCTGCTGACAGCTGCGCGCGCGCTCGAGCGCTGAGATCCCA	240		
OY	241	AGGGAGCAAAAGGCGCAGCTCCGGCAGAGGGAGTGTGGACCTGTATTAATGGAATGT	300		
Db	241	AGGGAGCAAAAGGCGCAGCTCCGGCAGAGGGAGTGTGGACCTGTATTAATGGAATGT	300		
OY	301	GCTTACAGAGGGCCAGCAGAGATGCTGGTCCAGAGCGGAGCCCTGGGGCCATGTTATTC	360		
Db	301	GCTTACAGAGGGCCAGCAGAGATGCTGGTCCAGAGCGGAGCCCTGGGGCCATGTTATTC	360		
OY	361	CGGGTACACCTGCGGATGCCAGGTGGGATGGAATTCAAAGAGAAAGGGGGAATGTCTGA	420		
Db	361	CGGGTACACCTGCGGATGCCAGGTGGGATGGAATTCAAAGAGAAAGGGGGAATGTCTGA	420		
OY	421	GGGAAAGCTTTGAGAGATCTGTGACACCCCACTACAAGCAGTGTTCATGAGTTCATTTGA	480		
Db	421	GGGAAAGCTTTGAGAGATCTGTGACACCCCACTACAAGCAGTGTTCATGAGTTCATTTGA	480		
OY	481	ATTATGGCATAGATCTTGGGAAAATTTGGGAGTGTACTTTACAAAGATGCGTTCAAATA	540		
Db	481	ATTATGGCATAGATCTTGGGAAAATTTGGGAGTGTACTTTACAAAGATGCGTTCAAATA	540		
OY	541	GTGCTCTAGAGATTTTGTTCAGTGGCTCACCTCGGCTTAATTTGAGAAATGCATGCGTTC	600		
Db	541	GTGCTCTAGAGATTTTGTTCAGTGGCTCACCTCGGCTTAATTTGAGAAATGCATGCGTTC	600		
OY	601	AGCGTTGGTATTTACATTTCAATTTGAGAGTGAATGTTCAGAGCCTTCCTCCATTTGAAGTA	660		
Db	601	AGCGTTGGTATTTACATTTCAATTTGAGAGTGAATGTTCAGAGCCTTCCTCCATTTGAAGTA	660		
OY	661	TAAATTTATTTGGACCAAGAAAGCCCTGAAATGAATTCACAAATTAATTTATTCATGCACTT	720		
Db	661	TAAATTTATTTGGACCAAGAAAGCCCTGAAATGAATTCACAAATTAATTTATTCATGCACTT	720		
OY	721	CTTCGTGTGAAGACTTGTGAAGAAATTTGGTGGTATTTGATGAGATGTTCTATTCGGG	780		
Db	721	CTTCGTGTGAAGACTTGTGAAGAAATTTGGTGGTATTTGATGAGATGTTCTATTCGGG	780		
OY	781	TTGGCACTTTGTCAGATTTACCAAAAGAGATGCTTACTAGATGGAATTCAGTTCCTC	840		
Db	781	TTGGCACTTTGTCAGATTTACCAAAAGAGATGCTTACTAGATGGAATTCAGTTCCTC	840		
OY	841	GCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACGCTCTTTT	900		
Db	841	GCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACGCTCTTTT	900		
OY	901	TTATTTAGCCCTTGAAGTGGTCACTTAAATGACATTTTAAATTAAGTTATGTATACATCT	960		
Db	901	TTATTTAGCCCTTGAAGTGGTCACTTAAATGACATTTTAAATTAAGTTATGTATACATCT	960		
OY	961	GAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGGATTTACAGCTGTTTTTAA	1020		
Db	961	GAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGGATTTACAGCTGTTTTTAA	1020		
OY	1021	ATCTAGCATTTATTCATTTTGGTTCATTCAAAGTGGTTCATATATTTTTTTTATGTGGTT	1080		

|||||

Db 1021 ATCTACATATTCATTTGCTTCAATCAAAAGTGGTTTCATATTTTATAGTGGT 1080

Qy 1081 AGAATACCTTCTTCATAGTCACATCTCTCAACCACTTAATTTGGAATATGTGTGCT 1140

Db 1081 AGAATACCTTCTTCATAGTCACATCTCTCAACCACTTAATTTGGAATATGTGTGCT 1140

Qy 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAAAAATAAAGCTACCAATCTTTGTAC 1200

Db 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAAAAATAAAGCTACCAATCTTTGTAC 1200

Qy 1201 AATTTGTAATGTAAAGATTTTATATCTGTTAAATTTTATTTTCCACA 1257

Db 1201 AATTTGTAATGTAAAGATTTTATATCTGTTAAATTTTATTTTCCACA 1257

RESULT 5  
AX491138 1257 bp DNA linear PAT 16-AUG-2002

LOCUS Sequence 245 from Patent WO0200690.

DEFINITION AX491138

ACCESSION AX491138

VERSION AX491138.1 GI:22323906

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I., and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 245 03-JAN-2002;

FEATURES

source Location/Qualifiers

1..1257

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 324 a 264 c 299 g 370 t

ORIGIN

Query Match 100.0%; Score 1257; DB 6; Length 1257;

Best Local Similarity 100.0%; Pred. No. 1.2e-213;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 6GAGAGAGCGCGCGGGGTAAAGGCGCATGTATGACGCTCGGCGGCTCGAGCGCG 60

Db 1 6GAGAGAGCGCGCGGGGTAAAGGCGCATGTATGACGCTCGGCGGCTCGAGCGCG 60

Qy 61 CGAGAGCGCGCGGGGTAAAGGCGCATGTATGACGCTCGGCGGCTCGAGCGCG 120

Db 61 CGAGAGCGCGCGGGGTAAAGGCGCATGTATGACGCTCGGCGGCTCGAGCGCG 120

Qy 121 CCCGAGCGCGGAGGCGCATGCGACCCAGGCGCGCGCTCCCGAGCGGCTCGCG 180

Db 121 CCCGAGCGCGGAGGCGCATGCGACCCAGGCGCGCGCTCCCGAGCGGCTCGCG 180

Qy 181 GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Db 181 GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Qy 241 AGGGAAGCAAAAGGCGCGCATGCGCGAGAGGAGGAGTGGTGAAGCTGTAAATGGAATG 300

Db 241 AGGGAAGCAAAAGGCGCGCATGCGCGAGAGGAGGAGTGGTGAAGCTGTAAATGGAATG 300

Qy 301 GCTTACAAAGGCGCGAGAGGAGTGGTGTGAGAGCGGAGCCCTGGGCGCAATGTATTTC 360

Db 301 GCTTACAAAGGCGCGAGAGGAGTGGTGTGAGAGCGGAGCCCTGGGCGCAATGTATTTC 360

Qy 361 CGGCTACCTGCGGATCCAGGTGCGGATGATTCAAAGAGAAAGGGGGAATGTCTGA 420

|||||

Db 361 CGGCTACCTGCGGATCCAGGTGCGGATGATTCAAAGAGAAAGGGGGAATGTCTGA 420

Qy 421 GGGAAAGCTTTGAGAGTCCCTGAGACCCCAACAGCAAGAGTGTGATGAGTTCAATGA 480

Db 421 GGGAAAGCTTTGAGAGTCCCTGAGACCCCAACAGCAAGAGTGTGATGAGTTCAATGA 480

Qy 481 AATATGCAATAGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCGTCAAAAT 540

Db 481 AATATGCAATAGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCGTCAAAAT 540

Qy 541 GTGCTTAAGAGTTTGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

Db 541 GTGCTTAAGAGTTTGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

Qy 601 AGCGTGTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660

Db 601 AGCGTGTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660

Qy 661 TAAATTAATTTGAGCAAGAGAGCCCTGAATGATTTCAACATTAATTAATTCATGCACCT 720

Db 661 TAAATTAATTTGAGCAAGAGAGCCCTGAATGATTTCAACATTAATTAATTCATGCACCT 720

Qy 721 CTTCCTGAGAGACCTTTGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

Db 721 CTTCCTGAGAGACCTTTGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

Qy 781 TTGGCACTGTTGAGATTCACCAAGAGAGTCTCTCTGATGATGATGATGATGATGATGAT 840

Db 781 TTGGCACTGTTGAGATTCACCAAGAGAGTCTCTCTGATGATGATGATGATGATGATGAT 840

Qy 841 GCATCATTTATTAAGAACTACCAAAATTAATGCTTAATTTTATTTGCTACCTCTTTT 900

Db 841 GCATCATTTATTAAGAACTACCAAAATTAATGCTTAATTTTATTTGCTACCTCTTTT 900

Qy 901 TTATTTGCTTGGATGCTTCTTATTAATGATTTAATTAATTAATTAATTAATTAATTAAT 960

Db 901 TTATTTGCTTGGATGCTTCTTATTAATGATTTAATTAATTAATTAATTAATTAATTAAT 960

Qy 961 GAATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1020

Db 961 GAATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1020

Qy 1021 ATCTACATATTCATTTGCTTCAATCAAAAGTGGTTTCATATTTTATAGTGGT 1080

Db 1021 ATCTACATATTCATTTGCTTCAATCAAAAGTGGTTTCATATTTTATAGTGGT 1080

Qy 1081 AGAATACCTTCTTCATAGTCACATCTCTCAACCACTTAATTTGGAATATGTGTGCT 1140

Db 1081 AGAATACCTTCTTCATAGTCACATCTCTCAACCACTTAATTTGGAATATGTGTGCT 1140

Qy 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAAAAATAAAGCTACCAATCTTTGTAC 1200

Db 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAAAAATAAAGCTACCAATCTTTGTAC 1200

Qy 1201 AATTTGTAATGTAAAGATTTTATATCTGTTAAATTTTATTTTCCACA 1257

Db 1201 AATTTGTAATGTAAAGATTTTATATCTGTTAAATTTTATTTTCCACA 1257

RESULT 6  
AX697362 1257 bp DNA linear PAT 02-APR-2003

LOCUS Sequence 430 from Patent WO0078961.

DEFINITION AX697362

ACCESSION AX697362

VERSION AX697362.1 GI:29498494

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,





QY 248 GCAAAAGGCGAGCTCCGACAGAGGAGTGGTGCACCTGTAATGAAATGCTTACA 307  
 DB 251 GCAAAAGGCGAGCTCCGACAGAGGAGTGGTGCACCTGTAATGAAATGCTTACA 310  
 QY 308 AGGGCCAGCAGAGTCCCTGTCGAGAGGAGCCCTGGGCGCAATGTAATCCGGGTAC 367  
 DB 311 AGGGCCAGCAGAGTCCCTGTCGAGAGGAGCCCTGGGCGCAATGTAATCCGGGTAC 370  
 QY 368 ACCCTGGATCCAGGTCGGGATGATTAAGAGAGAGAGGAGGAAATGCTGAGGAGAG 427  
 DB 371 ACCCTGGATCCAGGTCGGGATGATTAAGAGAGAGAGGAGGAAATGCTGAGGAGAG 430  
 QY 428 CTTTGAAGAGTCCCTGACACCCCACTACAAGAGTGTTCATGAGTTCATTAATATG 487  
 DB 431 CTTTGAAGAGTCCCTGACACCCCACTACAAGAGTGTTCATGAGTTCATTAATATG 490  
 QY 488 CATATATCTGGGAAATTCGCGAGTGTCAATTAACAAGATCCCTCAATATGCTCT 547  
 DB 491 CATATATCTGGGAAATTCGCGAGTGTCAATTAACAAGATCCCTCAATATGCTCT 550  
 QY 548 AAGAGTTTGTTCAGTGGCTCACTTCGCTAAATGCAAGAAATGCTGTCAGGCTTG 607  
 DB 551 AAGAGTTTGTTCAGTGGCTCACTTCGCTAAATGCAAGAAATGCTGTCAGGCTTG 610  
 QY 608 GTATTTACATTCATGAGTGAATGTTCAGAGCTCTTCCCATTAAGCTATTAATTA 667  
 DB 611 GTATTTACATTCATGAGTGAATGTTCAGAGCTCTTCCCATTAAGCTATTAATTA 670  
 QY 668 TTTGACCAAGAGAGCCCTGAATGATTAACAATTAATATTCATTCGACCTCTCTCT 727  
 DB 671 TTTGACCAAGAGAGCCCTGAATGATTAACAATTAATATTCATTCGACCTCTCTCT 730  
 QY 728 GGAAGAGCTTTGTGAAGAAATGTGCTGATTAAGTATGATGATGCTGCTGCTGCTG 787  
 DB 731 GGAAGAGCTTTGTGAAGAAATGTGCTGATTAAGTATGATGATGCTGCTGCTGCTG 790  
 QY 788 TTTGTCAGATTCACCAAAAGAGATGCTTCTACTGAGAGAAATTCAGTTTCTGCAAT 847  
 DB 791 TTTGTCAGATTCACCAAAAGAGATGCTTCTACTGAGAGAAATTCAGTTTCTGCAAT 850  
 QY 848 TATTAAGAGCTTACCAAAATTAATGCTTAATTTTCATTTGCTACCTCTTTTATTAAT 907  
 DB 851 TATTAAGAGCTTACCAAAATTAATGCTTAATTTTCATTTGCTACCTCTTTTATTAAT 910  
 QY 908 GCGTTGAGATGCTCACTTAATGACATTTTAATTAATGATTAATGATGATGATGATG 967  
 DB 911 GCGTTGAGATGCTCACTTAATGACATTTTAATTAATGATTAATGATGATGATGATG 970  
 QY 968 AAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACAGTGTTTTAATCTAGC 1027  
 DB 971 AAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACAGTGTTTTAATCTAGC 1030  
 QY 1028 ATTATTCATTTGCTCAATCAAAAGTGTTCATTAATTTTATTTAGTGTGATGATG 1087  
 DB 1031 ATTATTCATTTGCTCAATCAAAAGTGTTCATTAATTTTATTTAGTGTGATGATG 1090  
 QY 1088 TTTCTTCATGATCAGATTCCTCAACCTTAATTTGATGATTTGTTGCTTTGCTT 1147  
 DB 1091 TTTCTTCATGATCAGATTCCTCAACCTTAATTTGATGATTTGTTGCTTTGCTT 1150  
 QY 1148 TTTCTTCATGATCAGATTTTAAAAAATTAATTAAGCTTCAATCTTTGATCAATTTGT 1207  
 DB 1151 TTTCTTCATGATCAGATTTTAAAAAATTAATTAAGCTTCAATCTTTGATCAATTTGT 1210  
 QY 1208 AAATGTTAAGATTTTATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 1257  
 DB 1211 AAATGTTAAGATTTTATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 1260

RESULT 8  
 AR243886  
 LOCUS AR243886 1286 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 124 from patent US 6476195.  
 ACCESSION AR243886  
 VERSION AR243886.1 GI:27291379  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1286)  
 AUTHORS Komatsoulis,G., Rosen,C.A., Ruben,S.M., Duan,R.D., Moore,P.A., Shi,Y., Lafleur,D.W., Wei,Y.-F., N.J., Florence,K.A., Young,P., Brewer,L.A., Soppet,D.R., Endress,G.A., Edner,R., Olsen,H. and Mucenski,M.  
 TITLE Secreted protein HNF20  
 JOURNAL Patent: US 6476195-A 124 05-NOV-2002;  
 FEATURES Location/Qualifiers  
 source 1..1286  
 BASE COUNT 357 a 264 c 236 g 368 t 1 others  
 ORIGIN  
 Query Match 97.3%; Score 1222.8; DB 6; Length 1286;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-207;  
 Matches 1246; Conservative 0; Mismatches 2; Indels 2; Gaps 2;  
 QY 8 GGGCGCGGGGTGAAGAGCGCATTTGATGACAGCTGCGGCGGCTCGAGGCGGAGCC 67  
 DB 2 GGGCGCGGGGTGAAGAGCGCATTTGATGACAGCTGCGGCGGCTCGAGGCGGAG-C 60  
 QY 68 AGAGCGTGACAGTTCCTCTCTGCTGCTCCGCGGCTCGAGCTCGGCGGCTCGGCGGA 127  
 DB 61 AGAGCGTGACAGTTCCTCTCTGCTGCTCCGCGGCTCGAGCTCGGCGGCTCGGCGGA 120  
 QY 128 GCGGAGGAGCATGCGACCCAGAGGCCCGCGGCTCCGCGAGCGGCTCGGCGGCTCT 187  
 DB 121 GCGGAGGAGCATGCGACCCAGAGGCCCGCGGCTCCGCGAGCGGCTCGGCGGCTCT 180  
 QY 188 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247  
 DB 181 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 248 GCAAAAGGCGAGCTCCGCGAGAGGAGTGGTGGACCTGTAATGAAATGCTTACA 307  
 DB 241 GCAAAAGGCGAGCTCCGCGAGAGGAGTGGTGGACCTGTAATGAAATGCTTACA 299  
 QY 308 AGGGCCAGCAGAGTCCCTGTCGAGAGGAGCCCTGGGCGCAATGTAATCCGGGTAC 367  
 DB 300 AGGGCCAGCAGAGTCCCTGTCGAGAGGAGCCCTGGGCGCAATGTAATCCGGGTAC 359  
 QY 368 ACCCTGGATCCAGGTCGGGATGATTAAGAGAGAGAGGAGGAAATGCTGAGGAGAG 427  
 DB 360 ACCCTGGATCCAGGTCGGGATGATTAAGAGAGAGAGGAGGAAATGCTGAGGAGAG 419  
 QY 428 CTTTGAAGAGTCCCTGACACCCCACTACAAGAGTGTTCATGAGTTCATTAATATG 487  
 DB 420 CTTTGAAGAGTCCCTGACACCCCACTACAAGAGTGTTCATGAGTTCATTAATATG 479  
 QY 488 CATAGATCTTGGGAAATTCGCGAGTGTCAATTAACAAGATGCTTCAATAGTCTCT 547  
 DB 480 CATAGATCTTGGGAAATTCGCGAGTGTCAATTAACAAGATGCTTCAATAGTCTCT 539  
 QY 548 AAGAGTTTGTTCAGTGGCTCACTTCGCTAAATTAATGCAAAATGATGCTGACAGGTTG 599  
 DB 540 AAGAGTTTGTTCAGTGGCTCACTTCGCTAAATTAATGCAAAATGATGCTGACAGGTTG 599  
 QY 608 GTATTTACATTCATGAGTGAATGTTCAGAGCTCTTCCCATTAAGCTATTAATTA 667  
 DB 600 GTATTTACATTCATGAGTGAATGTTCAGAGCTCTTCCCATTAAGCTATTAATTA 659  
 QY 668 TTTGACCAAGAGAGCCCTGAATGATTAATTAATTAATTAATTAATTAATTAATTA 727  
 DB 660 TTTGACCAAGAGAGCCCTGAATGATTAATTAATTAATTAATTAATTAATTAATTA 719  
 QY 728 GGAAGAGCTTTGTGAAGAAATGTGCTGATTAATGATGATGCTGCTGCTGCTGCTG 787

```

Db 720 GGAAGACATTTGTGAAGAAATGGTGTGATTAAGTGTGATCTACTGTGGTGGAC 779
Oy 788 TTGTTACAGATTACCCAAAAGAGATGCTTACTAGTGAATTCAGTTTCCGCAATC 847
Db 780 TTGTTACAGATTACCCAAAAGAGATGCTTACTAGTGAATTCAGTTTCCGCAATC 839
Oy 848 TATTGAGACATACCAAAATTAATGCTTAAATTTTCATGCTGCTCTTTTATATAT 907
Db 840 TATTGAGACATACCAAAATTAATGCTTAAATTTTCATGCTGCTCTTTTATATAT 899
Oy 908 GCCTTGAATGCTTACCTTAATATGATTAATTAATTAATTAATTAATTAATTAAT 967
Db 900 GCCTTGAATGCTTACCTTAATATGATTAATTAATTAATTAATTAATTAATTAAT 959
Oy 968 AAGCAAACTAAATATGTTTACAGACCAAGTGTGATTCACACGTTTAAATCTAGC 1027
Db 960 AAGCAAACTAAATATGTTTACAGACCAAGTGTGATTCACACGTTTAAATCTAGC 1019
Oy 1028 ATTATTCATTTTGGCTTCAATCAAAAAGTGTTCATTAATTTTATGTTGATGATAC 1087
Db 1020 ATTATTCATTTTGGCTTCAATCAAAAAGTGTTCATTAATTTTATGTTGATGATAC 1079
Oy 1088 TTCTCTCAGTACATCTCTCAACCTATATATGTTGATGATGCTTCTTCTTCTT 1147
Db 1080 TTCTCTCAGTACATCTCTCAACCTATATATGTTGATGATGCTTCTTCTTCTT 1139
Oy 1148 TTCTCTCAGTACATCTCTCAACCTATATATGTTGATGATGCTTCTTCTTCTT 1207
Db 1140 TTCTCTCAGTACATCTCTCAACCTATATATGTTGATGATGCTTCTTCTTCTT 1199
Oy 1208 AAAAGTTAAGAAATTTTATATGCTGTTAAATTAATTAATTTTTCACAACA 1257
Db 1200 AAAAGTTAAGAAATTTTATATGCTGTTAAATTAATTAATTTTTCACAACA 1249

```

```

RESULT 9
BC014245
LOCUS BC014245 1245 bp mRNA linear PRI 12-SEP-2001
DEFINITION Homo sapiens, similar to RIKEN cDNA 1110014B07 gene, clone
ACCESSION BC014245
VERSION BC014245.1 GI:15559789
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Strausberg, R.
1 (bases 1 to 1245)
Direct Submission
Submitted (10-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: gcgabs-remail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: http://www.nisc.nih.gov/
nisc.mgc@nih.gov
nisc.mgc@nih.gov
Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Maslejo, C., Mastrian, S.D., McCloskey, J.C.,
McGowan, J.J., Pearson, R., Snyder, B., Stentilipod, S., Thomas, P.J.,
Tsongson, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 30 Row: 1 Column: 18  
 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction.

FEATURES  
 source Location/Qualifiers

1..1245  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:20766 IMAGE:4586039"  
 /tissue\_type="Kidney, renal cell adenocarcinoma"  
 /clone\_11b="NIH MGC\_14"  
 /lab\_host="DH10B-R"  
 /note="Vector: pOTB7"  
 109..840  
 /codon\_start=1  
 /product="Similar to RIKEN cDNA 1110014B07 gene"  
 /protein\_id="AAH14245.1"  
 /db\_xref="GI:15559790"

CDS

BASE COUNT 334 a 260 c 287 g 364 t  
 ORIGIN

Query Match 96.8%; Score 1217.2; DB 9; Length 1245;  
 Best Local Similarity 99.8%; Pred. No. 1.4e-206;  
 Matches 1219; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Oy 36 AGCTGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 95
Db 7 AGCTGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 66
Oy 96 CTCTCCGCGCTCAGCTCCGCGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 155
Db 67 CTCTCCGCGCTCAGCTCCGCGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126
Oy 156 GCCGCTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 215
Db 127 GCCGCTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
Oy 216 CCGTCGAGCGGCTGAGATCCCAAGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAG 275
Db 187 CCGTCGAGCGGCTGAGATCCCAAGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAG 246
Oy 276 GTGTTGACCTGTATATGATGATGCTTACAGAGGCGGCGGCGGCGGCGGCGGCGG 335
Db 247 GTGTTGACCTGTATATGATGATGCTTACAGAGGCGGCGGCGGCGGCGGCGGCGG 306
Oy 336 GGGAGCCCTGGGCGCAATGCGGATCCAGCTGAGATCCCAAGGCGGCGGCGGCGG 395
Db 307 GGGAGCCCTGGGCGCAATGCGGATCCAGCTGAGATCCCAAGGCGGCGGCGGCGG 366
Oy 396 AAAAGAGAAAAGGGGGAATGCTGAGGGAAGCTTTGAGAGCTCTGAGACACCAACTAC 455
Db 367 AAAAGAGAAAAGGGGGAATGCTGAGGGAAGCTTTGAGAGCTCTGAGACACCAACTAC 426
Oy 456 AAGCAGTTCATGAGATTCATTAATTAATGATGATGATGATGATGATGATGATGAT 515
Db 427 AAGCAGTTCATGAGATTCATTAATTAATGATGATGATGATGATGATGATGATGAT 486
Oy 516 ACATTTCAAAGATGCGTCAATAGAGCTTAAGAGTTTGTTCAGAGCTGCTACTTCGG 575
Db 487 ACATTTCAAAGATGCGTCAATAGAGCTTAAGAGTTTGTTCAGAGCTGCTACTTCGG 546
Oy 576 CTAATAATGCAAAATGATGCTGACAGCTGATTTACATTCATTAATGAGAGTGAATGT 635
Db 547 CTAATAATGCAAAATGATGCTGACAGCTGATTTACATTCATTAATGAGAGTGAATGT 606

```



QY 636 TCAGACCTCTCCATTCAGCTATTAATTTATTTGGACCAAGAGCCCTGAATGAAT 695  
 |||||  
 DB 607 TCAGACCTCTCCATTCAGCTATTAATTTATTTGGACCAAGAGCCCTGAATGAAT 666  
 |||||  
 QY 696 TCACAAATTAATTCATTCAGCTCTCTCTGGGAAGAGCTTTGGAAGAAATGGTGT 755  
 |||||  
 DB 667 TCACAAATTAATTCATTCAGCTCTCTCTGGGAAGAGCTTTGGAAGAAATGGTGT 726  
 |||||  
 QY 756 GGATAGTGGATGGTTCATTCAGCTCTGGGTCAGCTTTGATACCCAAAGAGATGCT 815  
 |||||  
 DB 727 GGATAGTGGATGGTTCATTCAGCTCTGGGTCAGCTTTGATACCCAAAGAGATGCT 786  
 |||||  
 QY 816 TCTACTGATGGAATTCAGCTTTCTCGCATCATTTATGGAACCTACCAAAATTAATGCTT 875  
 |||||  
 DB 787 TCTACTGATGGAATTCAGCTTTCTCGCATCATTTATGGAACCTACCAAAATTAATGCTT 846  
 |||||  
 QY 876 TAAATTTCTATTCGACCTCTTTTATATGACCTTGAATAGTTCACTTAATGACAT 935  
 |||||  
 DB 847 TAAATTTCTATTCGACCTCTTTTATATGACCTTGAATAGTTCACTTAATGACAT 906  
 |||||  
 QY 936 TTTAATAAGTTTATGATATACATTCGAATGAAGCAAGCTAATATGTTTACAGACCA 995  
 |||||  
 DB 907 TTTAATAAGTTTATGATATACATTCGAATGAAGCAAGCTAATATGTTTACAGACCA 966  
 |||||  
 QY 996 AAGTGTGATTCACACCTGTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 1055  
 |||||  
 DB 967 AAGTGTGATTCACACCTGTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 1026  
 |||||  
 QY 1056 GTTCAATATTTTATGATGTTAGTGAATTAATTTCTATGATGACATTCCTCAACCT 1115  
 |||||  
 DB 1027 GTTCAATATTTTATGATGTTAGTGAATTAATTTCTATGATGACATTCCTCAACCT 1086  
 |||||  
 QY 1116 AATAATTTGAATATGTTGTCGCTTTTATTTCTCTAGTATGACATTTTAAATTA 1175  
 |||||  
 DB 1087 AATAATTTGAATATGTTGTCGCTTTTATTTCTCTAGTATGACATTTTAAATTA 1146  
 |||||  
 QY 1176 AATAATTTGAATATGTTGTCGCTTTTATTTCTCTAGTATGACATTTTAAATTA 1235  
 |||||  
 DB 1147 AATAATTTGAATATGTTGTCGCTTTTATTTCTCTAGTATGACATTTTAAATTA 1206  
 |||||  
 QY 1236 TAAATTAATTAATTTATTTCCACA 1257  
 |||||  
 DB 1207 TAAATTAATTAATTTATTTCCACA 1228  
 |||||

RESULT 10  
 AY136825 1221 bp mRNA linear PRI 01-DEC-2002  
 LOCUS  
 DEFINITION Homo sapiens collagen triple helix repeat-containing protein 1  
 (CTHRC1) mRNA, complete cds.  
 ACCESSION  
 VERSION AY136825  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1221)  
 Lehnert, W., Moore, D.P., Harmon, K.J., Mancini, M.L. and Lindner, V.  
 Expression of the novel collagen triple helix repeat-containing  
 gene (cthrcl) suggests functions in multiple organ systems  
 Unpublished  
 2 (bases 1 to 1221)  
 Lindner, V.  
 Direct Submission  
 Submitted (29-JUL-2002) Center for Molecular Medicine, Maine  
 Medical Center Research Institute, 81 Research Drive, Scarborough,  
 ME 04074, USA  
 FEATURES  
 source 1..1221  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

gene  
 CDS  
 /db\_xref="taxon:9606"  
 /chromosome="8"  
 /tissue\_type="aorta smooth muscle"  
 1..1221  
 /gene="CTHRC1"  
 104..835  
 /gene="CTHRC1"  
 /note="matrix protein"  
 /codon\_start=1  
 /product="collagen triple helix repeat-containing protein  
 1"  
 /protein\_id="AA15749.1"  
 /db\_xref="GI:25989621"  
 /translation="MRPQSPASPOLRLILLILLOLPAPSSASEIRPKQKQALQ  
 REVVDLYNMCLOGPAGVGRDSEGANIPETPGIPGDXGFKGKEGELRESFEESW  
 PPNYKCSMSISNGLDLEKIAEECTFKRSALRYLESGLRLKRNACQOHYFT  
 PFGARCSGLPIEATIIYIDGCSPEMNSRINIHRSVSVEICGIGAGLVDAIHWGTC  
 SDPKGDASTGMSYSRIITEELPK"  
 BASE COUNT 316 a 258 c 285 g 362 t  
 ORIGIN

Query Match 95.4%; Score 1198.8; DB 9; Length 1221;  
 Best Local Similarity 99.8%; Pred. No. 2.7e-203;  
 Matches 1211; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 43 GCGGGCTTCGAGCGCGGGGAGCGAGACGCTGACACGTCCTCTCTGCTCTCTCC 102  
 |||||  
 DB 9 GCGGGCTTCGAGCGCGGGGAGCGAGACGCTGACACGTCCTCTCTGCTCTCTCC 68  
 |||||  
 QY 103 GCCTCCAGCTCCGCGCTGCGCGGACCGGGAGCCATGCGACCCAGGGCCCGCGCT 162  
 |||||  
 DB 69 GCCTCCAGCTCCGCGCTGCGCGGACCGGGAGCCATGCGACCCAGGGCCCGCGCT 128  
 |||||  
 QY 163 CCGCGAGCGGGTCCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 222  
 |||||  
 DB 129 CCGCGAGCGGCTCCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 188  
 |||||  
 QY 223 GCGCTCTGAGATCCGCCAAGGGGAAAGCAAAAGCGCGAGCTCCGCGAGGAGAGTGCTG 282  
 |||||  
 DB 189 GCGCTCTGAGATCCGCCAAGGGGAAAGCAAAAGCGCGAGCTCCGCGAGGAGAGTGCTG 248  
 |||||  
 QY 283 ACCTGTATATGATATGCTCTTCAAGAGGCGACGAGAGTCCCTGCTCGAGCGGAGCC 342  
 |||||  
 DB 249 ACCTGTATATGATATGCTCTTCAAGAGGCGACGAGAGTCCCTGCTCGAGCGGAGCC 308  
 |||||  
 QY 343 CTGGGGCCAAATGTTATCCGGGTACACCTGGGATCCGAGCTGGGATGGAATCAAGAG 402  
 |||||  
 DB 309 CTGGGGCCAAATGTTATCCGGGTACACCTGGGATCCGAGCTGGGATGGAATCAAGAG 368  
 |||||  
 QY 403 AAAAGGGGAATGCTGAGAGGAAGCTTTGAGAGTCTCGACACCACTACAGACAGT 462  
 |||||  
 DB 369 AAAAGGGGAATGCTGAGAGGAAGCTTTGAGAGTCTCGACACCACTACAGACAGT 428  
 |||||  
 QY 463 GTTCATGAGTTCATTTGAATTTATGCAATGATCTTGGGAAAATTTGGCGAGTGTACTTTA 522  
 |||||  
 DB 429 GTTCATGAGTTCATTTGAATTTATGCAATGATCTTGGGAAAATTTGGCGAGTGTACTTTA 488  
 |||||  
 QY 523 CAAAGATGCGTCAATATAGTGCCTPAAGAGTTTGTTCAGTGGCTCACTTGGCTAAAT 582  
 |||||  
 DB 489 CAAAGATGCGTCAATATAGTGCCTPAAGAGTTTGTTCAGTGGCTCACTTGGCTAAAT 548  
 |||||  
 QY 583 GCAGAAATCATGCTGTCAGCGTGGTATTTACATTCATGAGAGTGAATGTCAGAGC 642  
 |||||  
 DB 549 GCAGAAATCATGCTGTCAGCGTGGTATTTACATTCATGAGAGTGAATGTCAGAGC 608  
 |||||  
 QY 643 CTCCTCCATTTAGCTATTAATTTATTTGGACCAAGAAAGCCCTGAATTAACACA 702  
 |||||  
 DB 609 CTCCTCCATTTAGCTATTAATTTATTTGGACCAAGAAAGCCCTGAATTAACACA 668  
 |||||  
 QY 703 TTAATATTCATGCACTTCTCTGTCGAGAGGACTTTGTAAGAAATGGTGTGATTAAG 762  
 |||||  
 DB 669 TTAATATTCATGCACTTCTCTGTCGAGAGGACTTTGTAAGAAATGGTGTGATTAAG 728  
 |||||

Oy		763	TGATGTGGTCAATCGGTTGGACCTTGTCAGATTACCACAAAGGAGATCCTCTACTG	822
Dd		729	TGAATGTGCTAATCTGGGTGGCCCTTGTCAGATTACCACAAAGGAGATCCTCTACTG	788
Oy		823	GATGAATTCAGTTCTTCGCATCATATTATGAGAAGTAACCAAATAATGCTTTAAATTT	882
Dd		789	GATGAATTCAGTTCTTCGCATCATATTATGAGAAGTAACCAAATAATGCTTTAAATTT	848
Oy		883	CATTGCTACTCCTTTTTTATFVAGCCTTGGAAITGGTTCACCTTAAATGACATTTTAAAT	942
Dd		849	CATTGCTACTCCTTTTTTATFVAGCCTTGGAAITGGTTCACCTTAAATGACATTTTAAAT	908
Oy		943	AAGTTTAGTATACATCGAATGAAAAGCAAGCTAAATATNGTTTACAGACCAAGGTG	1002
Dd		909	AAGTTTAGTATACATCGAATGAAAAGCAAGCTAAATATNGTTTACAGACCAAGGTG	968
Oy		1003	ATTTCACACGTGTTTTTAAATCTAGCATTATTCATTGCTTCACATCAAAAGTGTTCAA	1062
Dd		969	ATTTCACACGTGTTTTTAAATCTAGCATTATTCATTGCTTCACATCAAAAGTGTTCOA	1028
Oy		1063	TATTTTTTTAGTTGGTTAGAAATCTTCTTCATATGTCACATTCCTTCACCTTAAATTT	1122
Dd		1029	TA-TTTTTTTAGTTGGTTAGAAATCTTCTTCATATGTCACATTCCTTCACCTTAAATTT	1087
Oy		1123	GGAAATATGTTGGGTGCTTTGTTTGTTCCTTGTTGTATAGATTTTAAAAAATATATAA	1182
Dd		1088	GGAAATATGTTGGGTGCTTTGTTTGTTCCTTGTTGTATAGATTTTAAAAAATATATAA	1147
Oy		1183	AGCTACCAATCTTGTACAAATTTGTAATGTTAAGAATTTTTTTATATCTGTAAATAA	1242
Dd		1148	AGCTACCAATCTTGTACAAATTTGTAATGTTAAGAATTTTTTTATATCTGTAAATAA	1207
Oy		1243	AAATTATTTTCCAAC	1256
Dd		1208	AAATTATTTTCCAAC	1221
RESULT 11				
AF395488		LOCUS	AF395488	1215 bp mRNA linear PRI 07-JAN-2003
AF395488		DEFINITION	Homo sapiens NTMCL mRNA, complete cds.	
AF395488		ACCESSION	AF395488	
AF395488.1		VERSION	GI:27525623	
KEYWORDS				
SOURCE		ORGANISM	Homo sapiens (human)	
REFERENCE		AUTHORS	Mumtazota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
JOURNAL		TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE		AUTHORS	Sanuki,N., Fujiki,K., Kanai,A., Tanaka,Y. and Iwata,T.	
JOURNAL		TITLE	Novel polypeptide found in human cornea cDNA library	
FEATURES		location/Qualifiers	1 (bases 1 to 1215) 2 (bases 1 to 1215) Submitted (25-JUN-2001) National Center for Sensory Organs, National Tokyo Medical Center, 2-5-1 Higashiagoka, Meguro, Tokyo 152-8902, Japan	
source		1. 1215	/organism="Homo saplens" /mol_type="mRNA" /db_xref="taxon:9606" 121. 819 /codon_start=1 /product="NTMCL" /protein_id="AA017919.1" /db_xref="gi:27525624" /translation="MPPGRSRIVYKLRREKYVRSLKENNPSAFOGLIGRYNGACLOG PAGVGSDSGANGIRGPRIPIGRDFFKGEGICLRESPEESTPYKOCMSLSIAY GIDGKTABECTFKMRNSALRVLPSSSLRKCNNACCQRRYTFPNKAECGSLPIER IIVIDDSPENNSTINIHRTSVSEGLDEIGAGLVDAIIVGTCSIDYPKGDAISGMNS VSIIVIELPLTYML"	
CDS				

BASE COUNT	361 a	207 c	266 g	381 t	
Query Match	76.7%; Score 964.6; DB 9; Length 1215;				
Best Local Similarity	99.6%; Pred. No. 1,2e-161;				
Matches 967; Conservative	0; Mismatches 4; Indels 0; Gaps 0;				
OY	287	GTATAATGGAATGTGCTTACAGAGGCCACGACGAGTGCCTGTGTGAGACGGGAGCCCTGG	346		
DB	228	GTATAATGGAATGTGCTTACAGAGGCCACGACGAGTGCCTGTGTGAGACGGGAGCCCTGG	287		
OY	347	GGCCAAATGTTTCTCGGGGTACCTGGGATCCGAGTCCGAGTGGGATGATTCAAAGAGGAAA	406		
DB	288	GGCCAAATGGAATGTGCTTACAGAGGCCACGACGAGTGCCTGTGTGAGACGGGAGCCCTGG	347		
OY	407	GGGGGAATGTGTGAGGAGAAAGCTTTGAGAGTCCCTGGACACCCAACTACAAAGCAGTGTTC	466		
DB	348	GGGGGAATGTGTGAGGAGAAAGCTTTGAGAGTCCCTGGACACCCAACTACAAAGCAGTGTTC	407		
OY	467	ATGGAATTCATTGGAATTAATGACATAGATCTTGGGAAAATTCGGAGTGTACATTACAAA	526		
DB	408	ATGGAATTCATTGGAATTAATGACATAGATCTTGGGAAAATTCGGAGTGTACATTACAAA	467		
OY	527	GATCGTTTCAAAATGTGCTCTTAAGATTTTGTACAGGCTGCATCTGGCTTAAATACAG	586		
DB	468	GATCGTTTCAAAATGTGCTCTTAAGATTTTGTACAGGCTGCATCTGGCTTAAATACAG	527		
OY	587	AAATGCATGCTGTGCAGGTTGGTATTTTACATTCATATGAGCTGAAATGTTACAGACCTCT	646		
DB	528	AAATGCATGCTGTGCAGGTTGGTATTTTACATTCATATGAGCTGAAATGTTACAGACCTCT	587		
OY	647	TCCCATTTGAAGCTTAATTAATTATTGGACCAAGAGACCCCTGAAATGAATTCACAAATTA	706		
DB	588	TCCCATTTGAAGCTTAATTAATTATTGGACCAAGAGACCCCTGAAATGAATTCACAAATTA	647		
OY	707	TATTCATGCGACTCTCTCTGTGGAAGACTTTGGAAGAAATGTGCTGGATTAGAGGA	766		
DB	648	TATTCATGCGACTCTCTCTGTGGAAGACTTTGGAAGAAATGTGCTGGATTAGAGGA	707		
OY	767	TGTTGCTATCTGGGTTGGCACTTTGTTCAGATTTACCCAAAGAGAGCTTCTTACAGATG	826		
DB	708	TGTTGCTATCTGGGTTGGCACTTTGTTCAGATTTACCCAAAGAGAGCTTCTTACAGATG	767		
OY	827	GAAATTCAGTTTCTGCAATCATTAATTAAGAAAGCTACCAAAATTAATTAATTTTCATT	886		
DB	768	GAAATTCAGTTTCTGCAATCATTAATTAAGAAAGCTACCAAAATTAATTAATTTTCATT	827		
OY	887	TGTCACCTCTTTTATTAATGCTTGGAAAGGTTCACCTTAATGAATTTTAAATTAAGT	946		
DB	828	TGTCACCTCTTTTATTAATGCTTGGAAAGGTTCACCTTAATGAATTTTAAATTAAGT	887		
OY	947	TTATGTATACATCTGGAATGAAGAAAGCAAGCTTAATTAATGTTTACAGACCAAGTGTGATT	1006		
DB	888	TTATGTATACATCTGGAATGAAGAAAGCAAGCTTAATTAATGTTTACAGACCAAGTGTGATT	947		
OY	1007	CACACTGTTTTTAAATCTAGCATTAATTCATTTTGCTTCATCAACCAAAAGTGTTCATATT	1066		
DB	948	CACACTGTTTTTAAATCTAGCATTAATTCATTTTGCTTCATCAACCAAAAGTGTTCATATT	1007		
OY	1067	TTTTTTAGTGTGTAAGAAATCTTTCATGTGACATTCCTCCACCCATAAATTTTGAAA	1126		
DB	1008	TTTTTTAGTGTGTAAGAAATCTTTCATGTGACATTCCTCCACCCATAAATTTTGAAA	1067		
OY	1127	TATGTGTGTGCTTTTGTGTTTTTCTCTAGTATAGCAATTTTAAAAAATTAATTAAGCT	1186		
DB	1068	TATGTGTGTGCTTTTGTGTTTTTCTCTAGTATAGCAATTTTAAAAAATTAATTAAGCT	1127		
OY	1187	ACCAATCTTTGTACAAATTTGTAATGTTAAGAAATTTTATTAATCTGTAAATTAATAAT	1246		
DB	1128	ACCAATCTTTGTACAAATTTGTAATGTTAAGAAATTTTATTAATCTGTAAATTAATAAT	1187		
OY	1247	TATTTCCAAACA 1257			

Db	1188	TATTCCACACA	1198
RESULT 12			
AX285214/c			
LOCUS	Sequence 1019 from Patent WO0179556.	860 bp	DNA
DEFINITION			Linear
ACCESION	AX285214		PAT 20-NOV-2001
VERSION	AX285214.1	GI:17045902	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Lille,J., Brown,J.L., Bolt,A. and van Hufel,C. Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers Patent: WO 0179556-A 1019.25-OCT-2001; Millennium Predictive Medicine, Inc. (US) Location/Qualifiers 1..860		
JOURNAL	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
FEATURES			
SOURCE			
BASE COUNT	315 a 149 c 127 g 259 t		10 others
ORIGIN			
Query Match	63.1%; Score 793;	DB 6;	Length 860;
Best Local Similarity	100.0%;	Pred. No. 3.9e+131;	
Matches 793;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	465 TCATGGAGTTCATTGAATTATGATGCATAGATCTTGGAATAATGGCGAGTGTACATTTACA	524	
Db	828 TCATGGAGTTCATTGAATTATGATGCATAGATCTTGGAATAATGGCGAGTGTACATTTACA	769	
QY	525 AAGATGGCTCAATATAGTGCCTAAGAGTTTGTTCAGTGGCTCATTCCGCTAAATGC	584	
Db	768 AAGATGGCTCAATATAGTGCCTAAGAGTTTGTTCAGTGGCTCATTCCGCTAAATGC	709	
QY	585 AGAATGCATGCTGTACAGCTTGATTAATTCATTCATGAGAGCTGATGTTTCAGAGCT	644	
Db	708 AGAATGCATGCTGTACAGCTTGATTAATTCATTCATGAGAGCTGATGTTTCAGAGCT	649	
QY	645 CTTCGCATGGAAGCTATATTTATTTGGAGCCAGGAAGCCCTGGAATGAATCAACTT	704	
Db	648 CTTCGCATGGAAGCTATATTTATTTGGAGCCAGGAAGCCCTGGAATGAATCAACTT	589	
QY	705 AATTTATGATGCATCTTCTCTGTGGAAGAGCTTTGTGAAGAATGGTGTCTGATTTAGTG	764	
Db	588 AATTTATGATGCATCTTCTCTGTGGAAGAGCTTTGTGAAGAATGGTGTCTGATTTAGTG	529	
QY	765 GATGTGCTCATCTGGGTGGGATGTCATGATTAACCAAAAAGAGATGCTTACTAGGA	824	
Db	528 GATGTGCTCATCTGGGTGGGATGTCATGATTAACCAAAAAGAGATGCTTACTAGGA	469	
QY	825 TGAATTCAGTTTTCTGCCATCATTTATGGAAGAACATACCAAATAATGCTTTAATTTCA	884	
Db	468 TGAATTCAGTTTTCTGCCATCATTTATGGAAGAACATACCAAATAATGCTTTAATTTCA	409	
QY	885 TTTCCTACCTCTTTTTTTTATTTATTTAGCCCTGGAGTGGTCACTTAATGACATTTAAATAA	944	
Db	408 TTTCCTACCTCTTTTTTTTATTTATTTAGCCCTGGAGTGGTCACTTAATGACATTTAAATAA	349	
QY	945 GTTATGATATATCATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAAATGTGAT	1004	
Db	348 GTTATGATATATCATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAAATGTGAT	289	
QY	1005 TTCACAGTGTTTTAAATCTAGCAATTTATTTATTTGGTTCATATAAAAAGTGGTTTCATA	1064	
Db	288 TTCACAGTGTTTTAAATCTAGCAATTTATTTATTTGGTTCATATAAAAAGTGGTTTCATA	229	
QY	1065 TTTTTTTTAGTGGTTAGCAATACCTTTCTTCACTAGTCAACATTCCTCAACCTATATTTGG	1124	

QY	258	CAGCTCCGGCAGAGGAGGTGGTGGACCTGTTATTTGAAATGCTTACAAAGGGCCACGA	317
Db	121	CAGCTTCGGCAGAGGAGGTGGTGGACCTGTTATTTGAAATGCTTACAAAGGGCCACGA	180
QY	318	GGAGTGGCTGGTGGCAGAGGAGGGGCCCTGGGCAATGTTATTCGGGATACACCTGGATC	377
Db	181	GGAGTGGCTGGTGGCAGAGGAGGGGCCCTGGGCAATGTTATTCGGGATACACCTGGATC	240
QY	378	CCAGTCCGGGATGATTCAAAGGAGAAAAGGGGCAATGTCGAGGAAAGCTTTGAGAG	437
Db	241	CCAGTCCGGGATGATTCAAAGGAGAAAAGGGGCAATGTCGAGGAAAGCTTTGAGAG	300
QY	438	TCCTGGACACCCAACTACAGACAGTGTTCATGAGTTCATGTAATGTAATGGCATAGATCT	497
Db	301	TCCTGGACACCCAACTACAGACAGTGTTCATGAGTTCATGTAATGTAATGGCATAGATCT	360
QY	498	GGGAAAATTCGGAGTGTATTCATTTCAAAAGATGCGTTCAAAATAGTCTCTAAGATTTTG	557
Db	361	GGGAAAATTCGGAGTGTATTCATTTCAAAAGATGCGTTCAAAATAGTCTCTAAGATTTTG	420
QY	558	TTTCATGGCTCACTTCGCGCTAAATATGCAAGAAATGATGCTGTACAGCTTTGGTATTTCACA	617
Db	421	TTTCATGGCTCACTTCGCGCTAAATATGCAAGAAATGATGCTGTACAGCTTTGGTATTTCACA	480
QY	618	TTTCATGAGAGCTGATGTTTCAGAGACCTCTCCCATTTGAAGCTATATTAATTTTGGACGA	677
Db	481	TTTCATGAGAGCTGATGTTTCAGAGACCTCTCCCATTTGAAGCTATATTAATTTTGGACGA	540
QY	678	GGAGCCCTGAATGATTCACAAATTAATTCATGACCTCTTCTGTGGAGGACTT	737
Db	541	GGAGCCCTGAATGATTCACAAATTAATTCATGACCTCTTCTGTGGAGGACTT	600
QY	738	TGTGAAGAAATTTGGTGGAGATTTAGTGGATGTTGCTATCTGGGTGGACCTGTCAAT	797
Db	601	TGTGAAGAAATTTGGTGGAGATTTAGTGGATGTTGCTATCTGGGTGGACCTGTCAAT	660
QY	798	TACCCAAAAGAGATGCTTCTACTGAGATGGAATTCAGTTCTCGCATCATTTATGAGAA	857
Db	661	TACCCAAAAGAGATGCTTCTACTGAGATGGAATTCAGTTCTCGCATCATTTATGAGAA	720
QY	858	CTACCAAAATTA 869	
Db	721	CTACCAAAATTA 732	
RESULT 14			
LOCUS	AX375790	683 bp	DNA
DEFINITION	Sequence 3 from Patent WO0173031.		linear
ACCESSION	AX375790		
VERSION	AX375790.1	GI:19170293	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS	1	Xu,J. and Stolk,J.A.	
TITLE	Compositions and methods for the therapy and diagnosis of ovarian		
JOURNAL	Cancer		
	Patent: WO 0173031-A 3 04-OCT-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	location/Qualifiers		
	1..683		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	256 a	118 c	108 g
ORIGIN		199 t	2 others
Query Match	54.3%	Score 682.2;	DB 6; Length 683;
Best Local Similarity	99.7%;	Pred. No. 1.9e-111;	

Matches	681: Conservative	2: Mismatches	0: Indels	0: Gaps	0:
QY	516 ACATTTCACAAAGATCCGTTCAAAATAGTCTCTAAGAGCTTTGGTTCAGTGCCTACCTCGG	575			
Db	516 ACATTTCACAAAGATCCGTTCAAAATAGTCTCTAAGAGCTTTGGTTCAGTGCCTACCTCGG	575			
QY	576 CTAATATGCAGAAATGCATGCGTGCAGGGTGGATTTCAATTCAAATGAGAGCGAATGT	635			
Db	576 CTAATATGCAGAAATGCATGCGTGCAGGGTGGATTTCAATTCAAATGAGAGCGAATGT	635			
QY	636 TCAGAGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCAAGAGAGCCCTGAATGAT	695			
Db	636 TCAGAGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCAAGAGAGCCCTGAATGAT	695			
QY	696 TCAACAATTAATATTCATGCGACTCTCTGTGGAGAGCACTTTGGAGGAATGTGGCT	755			
Db	696 TCAACAATTAATATTCATGCGACTCTCTGTGGAGAGCACTTTGGAGGAATGTGGCT	755			
QY	756 GGATTAGTGGATGTTGCTATCGGGTGGCACTTGTTCAGATTAACCCAAAAGAGAGCT	815			
Db	756 GGATTAGTGGATGTTGCTATCGGGTGGCACTTGTTCAGATTAACCCAAAAGAGAGCT	815			
QY	443 GGATTAGTGGATGTTGCTATCGGGTGGCACTTGTTCAGATTAACCCAAAAGAGAGCT	384			
Db	443 GGATTAGTGGATGTTGCTATCGGGTGGCACTTGTTCAGATTAACCCAAAAGAGAGCT	384			
QY	816 TCTACTGCATGCAATTCAGTTCTTCGCCATCATTTATGGAAGACTACCAAAATTAATGCTT	875			
Db	816 TCTACTGCATGCAATTCAGTTCTTCGCCATCATTTATGGAAGACTACCAAAATTAATGCTT	875			
QY	876 TAATTTGATTTGGTACCTCTTTTATTAATGAGCTTTGATGAGTGGTCACTTAATGACAT	935			
Db	876 TAATTTGATTTGGTACCTCTTTTATTAATGAGCTTTGATGAGTGGTCACTTAATGACAT	935			
QY	936 TTTAAATTAAGTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACA	995			
Db	936 TTTAAATTAAGTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACA	995			
QY	996 AAGTGTGATTCACACCTGTTTTTAAATGTACATATTCATTTGGTCTCAATCAAAAGTG	1055			
Db	996 AAGTGTGATTCACACCTGTTTTTAAATGTACATATTCATTTGGTCTCAATCAAAAGTG	1055			
QY	203 AAGTGTGATTCACACCTGTTTTTAAATGTACATATTCATTTGGTCTCAATCAAAAGTG	144			
Db	203 AAGTGTGATTCACACCTGTTTTTAAATGTACATATTCATTTGGTCTCAATCAAAAGTG	144			
QY	1056 GTTTCAAATATTTTTTTAGTGGTGTAGAAATCTTTCTCATAGTACATTCCTCAACT	1115			
Db	1056 GTTTCAAATATTTTTTTAGTGGTGTAGAAATCTTTCTCATAGTACATTCCTCAACT	1115			
QY	1116 ATAAATTTGGAATATTTGTGGTCTTTGTTTTCCTTGTGATAGATTTTAAAAAA	1175			
Db	1116 ATAAATTTGGAATATTTGTGGTCTTTGTTTTCCTTGTGATAGATTTTAAAAAA	1175			
QY	83 ATAAATTTGGAATATTTGTGGTCTTTGTTTTCCTTGTGATAGATTTTAAAAAA	24			
Db	83 ATAAATTTGGAATATTTGTGGTCTTTGTTTTCCTTGTGATAGATTTTAAAAAA	24			
QY	1176 ATATTAAGCTACCAATCTTGT	1198			
Db	23 ATATTAAGCTACCAATCTTGT	1			
RESULT 15					
LOCUS	AR280558	683 bp	DNA	linear	PAT 10-Apr-2003
DEFINITION	Sequence 63 from patent US 6518237.				
ACCESSION	AR280558				
KEYWORDS	AR280558.1 GI:29716028				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 683)				
TITLE	Yuglu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.				
JOURNAL	Compositions for treatment and diagnosis of breast cancer and				
FEATURES	methods for their use				
source	Patent: US 6518237-A 63 11-FEB-2003;				
	Location/Qualifiers				
	1..683				
	/organism="unknown"				
BASE COUNT	255 a 118 c 107 g 200 t				
ORIGIN					
Query Match	54.2%	Score 681.8;	DB 6;	Length 683;	

Best Local Similarity 99.6%; Pred. No. 2.3e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
OY 516 ACATTTACAAGATGGCTCAATAGTGGCTAGAGATTTTGTGAGTGGCTACCTGGG 575
    |||||||
Db 683 ACATTTACAAGATGGCTCAATAGTGGCTAGAGATTTTGTGAGTGGCTACCTGGG 624
OY 576 CTAATAATGCAAGAAATGCATGCTGTCAGCGTTGGTATTTCAATCAATGAGCTGAATGT 635
    |||||||
Db 623 CTAATAATGCAAGAAATGCATGCTGTCAGCGTTGGTATTTCAATCAATGAGCTGAATGT 564
OY 636 TAGGACCTCTCCCATTTAAGCTATATTTATTGGACCAAGAAAGCCCTGAATGAAT 695
    |||||||
Db 563 TCAGGACCTCTCCCATTTAAGCTATATTTATTGGACCAAGAAAGCCCTGAATGAAT 504
OY 696 TCACAAATTAATTAATTCATGCACTCTCTGGAAGGACTTTGGAAGAAATGTGGCT 755
    |||||||
Db 503 TCACAAATTAATTAATTCATGCACTCTCTGGAAGGACTTTGGAAGAAATGTGGCT 444
OY 756 GGATTAGTGAATGTCATCTGGGTTGGCACTTTTCAGATTACCAAAAGAGATGCT 815
    |||||||
Db 443 GGATTAGTGAATGTCATCTGGGTTGGCACTTTTCAGATTACCAAAAGAGATGCT 384
OY 816 TCTACTGGATGGAATTCATGTTCTGCGCATATTATTGAAGAACTACCAAAATTAATGCTT 875
    |||||||
Db 383 TCTACTGGATGGAATTCATGTTCTGCGCATATTATTGAAGAACTACCAAAATTAATGCTT 324
OY 876 TAATTTTCATTTGCTACCTCTTTTATTTATGCGCTGGAATGGTCACTTAATGACAT 935
    |||||||
Db 323 TAATTTTCATTTGCTACCTCTTTTATTTATGCGCTGGAATGGTCACTTAATGACAT 264
OY 936 TTTAATAATAGTTATGTAATACATCTGAATGAAGCAAAAGCTAAATATGTTTACAGACCA 995
    |||||||
Db 263 TTTAATAATAGTTATGTAATACATCTGAATGAAGCAAAAGCTAAATATGTTTACAGACCA 204
OY 996 AAGTGTGATTCACACTGTTTAAATCTAGCATATTATTGCTTCAATCAAAAGTG 1055
    |||||||
Db 203 AAGTGTGATTCACACTGTTTAAATCTAGCATATTATTGCTTCAATCAAAAGTG 144
OY 1056 GTTCAATATTTTATAGTTAGTGTAGAAATACCTTCTCATAGTCAATTCCTCAAGCT 1115
    |||||||
Db 143 GTTCAATATTTTATAGTTAGTGTAGAAATACCTTCTCATAGTCAATTCCTCAAGCT 84
OY 1116 ATAATTGGAATATGTTGTGCTTTTGTGTTTCTCTTAGATAGCATTTTAAAAA 1175
    |||||||
Db 83 ATAATTGGAATATGTTGTGCTTTTGTGTTTCTCTTAGATAGCATTTTAAAAA 24
OY 1176 ATATAAAGCTACCAATCTTTGT 1198
    |||||||
Db 23 ATATAAAGCTACCAATCTTTGT 1
```

Search completed: August 20, 2003, 13:48:00  
Job time : 4791 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 11:55:54 ; Search time 381 Seconds  
(without alignments)  
8906.020 Million cell updates/sec

Title: US-09-938-418-2  
Perfect score: 1257  
Sequence: 1 ggaagagagcgcgaggtga.....ataaaattattccaca 1257

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: N.Geneseq.19Jun03.\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
26: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	100.0	1257	21	AAA37144 Human PRO1550 cDNA
2	1257	100.0	1257	22	AA546107 Human DNA encoding
3	1257	100.0	1257	22	AA546107 Human DNA encoding
4	1257	100.0	1257	22	AA546107 Human DNA encoding
5	1257	100.0	1257	24	AB574438 Human cDNA encoding
6	1257	100.0	1257	24	AB574438 Human cDNA encoding
7	1257	100.0	1257	24	AB574438 Human cDNA encoding
8	1257	100.0	1257	24	AB574438 Human cDNA encoding

9	1257	100.0	1257	25	ACA57865 Human PRO1550 cDNA
10	1257	100.0	1257	25	ACA58870 Human PRO1550 cDNA
11	1257	100.0	1257	25	ACA60423 Human PRO1550 cDNA
12	1257	100.0	1257	25	ACA63433 Human PRO1550 cDNA
13	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
14	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
15	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
16	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
17	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
18	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
19	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
20	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
21	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
22	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
23	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
24	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
25	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
26	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
27	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
28	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
29	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
30	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
31	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
32	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
33	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
34	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
35	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
36	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
37	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
38	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
39	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
40	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
41	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
42	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
43	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
44	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA
45	1257	100.0	1257	25	ABX98335 Human PRO1550 cDNA

ALIGNMENTS

RESULT 1	AAA37144	standard; cDNA; 1257 BP.
ID	AAA37144	
XX	AAA37144	
AC	AAA37144	
XX	08-AUG-2000 (first entry)	
DT	08-AUG-2000 (first entry)	
DE	Human PRO1550 cDNA sequence SEQ ID NO:430.	
XX	Human: PRO polypeptide; membrane bound protein; receptor; diagnosis;	
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening;	
XX	ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200012708-A2.	
XX	09-MAR-2000.	
PD	09-MAR-2000.	
PF	01-SEP-1999;	99WO-US20111.
XX	01-SEP-1999;	98US-0098716.
PR	01-SEP-1998;	98US-0098749.
PR	01-SEP-1998;	98US-0098750.
PR	01-SEP-1998;	98US-0098750.
PR	02-SEP-1998;	98US-0098803.
PR	02-SEP-1998;	98US-0098821.
PR	02-SEP-1998;	98US-0098843.
PR	09-SEP-1998;	98US-0099536.
PR	09-SEP-1998;	98US-0099596.
PR	09-SEP-1998;	98US-0099598.

```

PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099806.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 15-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100399.
PR 16-SEP-1998; 98US-0100384.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100663.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 24-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103318.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103637.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.

PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 18-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.

XX PA (GETH ) GENENTECH INC.
XX PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX DR WPI: 2000-237871/20.
XX DR P-PSDB: AAY99462.
XX PT New mammalian DNA sequences encoding transmembrane, receptor or
XX PT secreted PRO polypeptides, useful for screening of potential peptide or
XX PT small molecule inhibitors of the relevant receptor/ligand interactions
XX PS Claim 2; Fig 245; 773pp; English.
XX CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX CC transmembrane and receptor PRO proteins can be used for screening of
XX CC potential peptide or small molecule inhibitors of the relevant
XX CC receptor/ligand interactions. The polypeptides and nucleotide sequences
XX CC encoding them have various industrial applications, including uses as
XX CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX CC PCR primers and hybridisation probes used in the isolation of the PRO
XX CC polypeptides from the present invention.
XX SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 21; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1,7e-251;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGAGAGCGCGGGTGAAGGCGATGATGACGCTGGCGGCTCGAGAGCGG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGATGATGACGCTGGCGGCTCGAGAGCGG 60

```



[illegible]

QY	1141	TTTGTCTTCTCTAGATAGCATTTTAAAAAATATTAAGCTCCATCTTGTAC	1200
Db	1141	TTGTGTTTTTCTCTAGATAGCATTTTAAAAAATATTAAGCTCCATCTTGTAC	1200
QY	1201	AATTTGTAAAGTTAAAGATTTTTTTTATCTGTTAAATATAATTTTCCACA	1257
Db	1201	AATTTGTAAAGTTAAAGATTTTTTTTATCTGTTAAATATAATTTTCCACA	1257
RESULT 2			
ID	AAS46107	standard; cDNA; 1257 BP.	
XX	AC	AAS46107;	
XX	DT	18-DEC-2001 (first entry)	
XX	DE	Human DNA encoding PRO polypeptide sequence #183.	
XX	OS	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;	
XX	PN	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;	
XX	PF	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;	
XX	PD	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;	
XX	XX	PCR primer.	
XX	XX	Homo sapiens.	
XX	XX	WO20016848-A2.	
XX	XX	20-SEP-2001.	
XX	PF	28-FEB-2001; 2001WO-US06520.	
PR	01-MAR-2000; 2000WO-US05601.		
PR	02-MAR-2000; 2000WO-US05841.		
PR	03-MAR-2000; 2000US-187202P.		
PR	06-MAR-2000; 2000US-186968P.		
PR	14-MAR-2000; 2000US-189320P.		
PR	14-MAR-2000; 2000US-189328P.		
PR	15-MAR-2000; 2000WO-US06884.		
PR	21-MAR-2000; 2000US-190828P.		
PR	21-MAR-2000; 2000US-191007P.		
PR	21-MAR-2000; 2000US-191048P.		
PR	21-MAR-2000; 2000US-191314P.		
PR	28-MAR-2000; 2000US-192655P.		
PR	29-MAR-2000; 2000US-193032P.		
PR	29-MAR-2000; 2000US-193053P.		
PR	30-MAR-2000; 2000WO-US08439.		
PR	04-APR-2000; 2000US-194449P.		
PR	04-APR-2000; 2000US-194647P.		
PR	11-APR-2000; 2000US-195975P.		
PR	11-APR-2000; 2000US-196000P.		
PR	11-APR-2000; 2000US-196187P.		
PR	11-APR-2000; 2000US-196690P.		
PR	11-APR-2000; 2000US-196820P.		
PR	18-APR-2000; 2000US-198121P.		
PR	18-APR-2000; 2000US-198585P.		
PR	25-APR-2000; 2000US-199397P.		
PR	25-APR-2000; 2000US-199550P.		
PR	25-APR-2000; 2000US-199654P.		
PR	03-MAY-2000; 2000US-201516P.		
PR	17-MAY-2000; 2000WO-US13705.		
PR	22-MAY-2000; 2000WO-US14042.		
PR	30-MAY-2000; 2000WO-US14941.		
PR	02-JUN-2000; 2000WO-US15264.		
PR	05-JUN-2000; 2000US-209832P.		
PR	28-JUL-2000; 2000WO-US20710.		
PR	22-AUG-2000; 2000US-0644848.		
PR	24-AUG-2000; 2000WO-US23328.		
PR	08-NOV-2000; 2000WO-US30952.		
PR	01-DEC-2000; 2000WO-US32678.		
PR	20-DEC-2000; 2000WO-US34956.		
XX	XX		

PA (GETH ) GENE/TECH INC.  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI: 2001-602746/68.  
 DR P-PSDB: AAU29206.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 PS Claim 2; Fig 365; 774pp: English.  
 XX  
 CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood, when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX  
 SO Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 22; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGAGCGCGCGGGTGAAGAGCGCATGATGACAGCTCGCGCGCGCTGGAGCGCG 60  
 DB 1 GGAAGAGAGCGCGCGGGTGAAGAGCGCATGATGACAGCTCGCGCGCGCTGGAGCGCG 60  
 QY 61 CGAGAGCAGAGCG 120  
 DB 61 CGAGAGCAGAGCG 120  
 QY 121 CCGGCGAGCGCGGAGCGCATGCGAGCCGAGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 DB 121 CCGGCGAGCGCGGAGCGCATGCGAGCCGAGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 QY 181 GCCGCGAGCG 240  
 DB 181 GCCGCGAGCG 240  
 QY 241 AGGGAGAGCAAAAGCG 300  
 DB 241 AGGGAGAGCAAAAGCG 300  
 QY 301 GCTTACAAGGGCGCGAGAGTGCCTGCTGAGAGCGGAGCGCGCGCGCGCGCGCGCG 360  
 DB 301 GCTTACAAGGGCGCGAGAGTGCCTGCTGAGAGCGGAGCGCGCGCGCGCGCGCGCG 360  
 QY 361 CGGGTACAGCTGGGATCCGAGGTGCGATGATCAAGGAGGAGGAGGAGGAGTGTCTGA 420  
 DB 361 CGGGTACAGCTGGGATCCGAGGTGCGATGATCAAGGAGGAGGAGGAGGAGTGTCTGA 420  
 QY 421 GGGAAAGCTTTGAGAGCTGCGAGACCAACTCAAGAGCGAGTTCATGAGGATTCATGA 480  
 DB 421 GGGAAAGCTTTGAGAGCTGCGAGACCAACTCAAGAGCGAGTTCATGAGGATTCATGA 480  
 QY 481 ATTATGCAATAGATCTTGGGAAATTCGAGAGTGTACATTACAAAGATGCGTCAATA 540  
 DB 481 ATTATGCAATAGATCTTGGGAAATTCGAGAGTGTACATTACAAAGATGCGTCAATA 540

QY 541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGGTAATAAGCAAAATGATGCTGTC 600  
 DB 541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGGTAATAAGCAAAATGATGCTGTC 600  
 QY 601 AGCGTTGATTTTACATTAATGAGTGAATTTTACAGACCTTCCATTAAGCTA 660  
 DB 601 AGCGTTGATTTTACATTAATGAGTGAATTTTACAGACCTTCCATTAAGCTA 660  
 QY 661 TAATTTATTTGAGCAAGAGAGCCCGTAATTAATTAATTAATTAATTAATTAATTAAT 720  
 DB 661 TAATTTATTTGAGCAAGAGAGCCCGTAATTAATTAATTAATTAATTAATTAATTAAT 720  
 QY 721 CTCTGTGGAAGACTTGTGAAGAAATGGTGTGATTAAGTATGATGCTATGCTGG 780  
 DB 721 CTCTGTGGAAGAGCTTGTGAAGAAATGGTGTGATTAAGTATGATGCTATGCTGG 780  
 QY 781 TTGCACTGTGTCAGTATTAACCAAGAGAGTGTGTCTGATTAAGTATGATGCTATGCT 840  
 DB 781 TTGCACTGTGTCAGTATTAACCAAGAGAGTGTGTCTGATTAAGTATGATGCTATGCT 840  
 QY 841 GCATCATTTATGAAGAACTACCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 900  
 DB 841 GCATCATTTATGAAGAACTACCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 900  
 QY 901 TTATTTATGCTTGAAGTGTGCTCACTTAATTAATTAATTAATTAATTAATTAATTAAT 960  
 DB 901 TTATTTATGCTTGAAGTGTGCTCACTTAATTAATTAATTAATTAATTAATTAATTAAT 960  
 QY 961 GAATGAAGAAAGCAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020  
 DB 961 GAATGAAGAAAGCAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020  
 QY 1021 ATCTAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080  
 DB 1021 ATCTAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080  
 QY 1081 AGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140  
 DB 1081 AGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140  
 QY 1141 TTGTTTATTTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200  
 DB 1141 TTGTTTATTTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200  
 QY 1201 AATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1257  
 DB 1201 AATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1257

RESULT 3  
 AAF92118  
 ID AAF92118 standard; cDNA; 1257 BP.  
 XX  
 AC AAF92118;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Human PRO1550 cDNA.  
 XX  
 KW Human; PRO protein; mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200116318-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000WO-US23328.  
 XX  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 07-DEC-1999; 99US-0169495.  
 PR 09-DEC-1999; 99US-0170262.

PR 11-JAN-2000: 2000US-0175481.  
 PR 18-FEB-2000: 2000MO-US04341.  
 PR 18-FEB-2000: 2000MO-US04342.  
 PR 22-FEB-2000: 2000MO-US04414.  
 PR 01-MAR-2000: 2000MO-US05601.  
 PR 03-MAR-2000: 2000US-0187202.  
 PR 25-APR-2000: 2000US-0199397.  
 PR 22-MAY-2000: 2000MO-US14042.  
 PR 05-JUN-2000: 2000US-0209832.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PI Baton DL, Flyaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
 XI  
 DR WPI: 2001-183260/18.  
 DR P-PSDB: AAB87586.  
 XX  
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
 PT molecular biology, including use as hybridization probes, and in  
 PT chromosome and gene mapping.  
 XX  
 XX  
 PS Claim 2: Fig 121; 278pp; English.  
 CC  
 CC The present sequence is the coding sequence for a human PRO polypeptide  
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
 CC antagonists or anti-PRO antibodies are useful for preparation of a  
 CC medicament useful in the treatment of a condition which is responsive to  
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
 CC protein may also be employed as molecular weight markers for protein  
 CC electrophoresis. The PRO coding sequence has applications in molecular  
 CC biology, including use as hybridisation probes, and in chromosome and  
 CC gene mapping.  
 CC  
 SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 22; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGAGCGCATTTGATGACGCTGCGGCGGCGCATCGAGGCGG 60  
 DB 1 GGAGAGAGCGCGCGGGTGAAGAGCGCATTTGATGACGCTGCGGCGGCGCATCGAGGCGG 60  
 QY 61 CGAGAGCGAGCGCTGACACAGCTTCTCTCGTCTCTCTCGGCTTCAGACTTCGCGCTG 120  
 DB 61 CGAGAGCGAGCGCTGACACAGCTTCTCTCGTCTCTCTCGGCTTCAGACTTCGCGCTG 120  
 QY 121 CCCGCGAGCGCGGAGCGCATGCGACCCCGCGCGCGCGCGCTCCCGCAGCGGCTCCGG 180  
 DB 121 CCCGCGAGCGCGGAGCGCATGCGACCCCGCGCGCGCGCGCTCCCGCAGCGGCTCCGG 180  
 QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 QY 241 AGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGTGTGAGCTGTAAATGAGATGT 300  
 DB 241 AGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGTGTGAGCTGTAAATGAGATGT 300  
 QY 301 GCTTACAGGCGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 DB 301 GCTTACAGGCGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 361 CGGGTACCTGCGAGTCCAGGTCGGAGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAG 420  
 DB 361 CGGGTACCTGCGAGTCCAGGTCGGAGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAG 420  
 QY 421 GGGAAAGCTTTGAGAGTCTTGAGACCACTACAGAGAGTGTTCAGTTCAGTTCAGTTCAG 480  
 DB 421 GGGAAAGCTTTGAGAGTCTTGAGACCACTACAGAGAGTGTTCAGTTCAGTTCAGTTCAG 480  
 QY 481 ATTATGCGATAGATCTTGGGAAAATTGCGAGTGTACATTTACAAAAGATGCGTTCAATA 540

DB 481 ATTATGCGATAGATCTTGGGAAAATTGCGAGTGTACATTTACAAAAGATGCGTTCAATA 540  
 QY 541 GTGCTTAAGAGTTTGTTCAGTGGCTTCCTGCTTAAGAGAGAGAGAGAGAGAGAGAGAG 600  
 DB 541 GTGCTTAAGAGTTTGTTCAGTGGCTTCCTGCTTAAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 601 AGCGTGTATTTACATTCAGATGAGTGAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 660  
 DB 601 AGCGTGTATTTACATTCAGATGAGTGAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 660  
 QY 661 TAATTTATTTGACCAAGAGAGCGCTGAATGATTCAGCAATTAATTAATTCATTCGACCT 720  
 DB 661 TAATTTATTTGACCAAGAGAGCGCTGAATGATTCAGCAATTAATTAATTCATTCGACCT 720  
 QY 721 CTCTGCTGAGAGACTTGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 DB 721 CTCTGCTGAGAGACTTGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 781 TTGGCACTTGTTCAGATTCACCAAGAGAGATGCTTCTACTGATGAGATTCAGTTCAC 840  
 DB 781 TTGGCACTTGTTCAGATTCACCAAGAGAGATGCTTCTACTGATGAGATTCAGTTCAC 840  
 QY 841 GCATCATTTATGAGAGACTACCAAAATTAATGCTTAATTTTCAATTTGCTACCTTTT 900  
 DB 841 GCATCATTTATGAGAGACTACCAAAATTAATGCTTAATTTTCAATTTGCTACCTTTT 900  
 QY 901 TTTATTTGCTGCTGAGATGCTTCAATTAATGATTTAAATTAATTAATTAATTAATTAAT 960  
 DB 901 TTTATTTGCTGCTGAGATGCTTCAATTAATGATTTAAATTAATTAATTAATTAATTAAT 960  
 QY 961 GAATGAAGCAAGCAAGTAAATATGTTTACAGCAAGAGTGTGATTCACAGCTTTTAA 1020  
 DB 961 GAATGAAGCAAGCAAGTAAATATGTTTACAGCAAGAGTGTGATTCACAGCTTTTAA 1020  
 QY 1021 ATCTACATTTATTCATTTTGTCTTCATTCAGCAAGAGTGTTCATTTTAAATTTTAA 1080  
 DB 1021 ATCTACATTTATTCATTTTGTCTTCATTCAGCAAGAGTGTTCATTTTAAATTTTAA 1080  
 QY 1081 AGAATACCTTCTTCATGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1140  
 DB 1081 AGAATACCTTCTTCATGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1140  
 QY 1141 TTTGTTTTTCTCTGATGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200  
 DB 1141 TTTGTTTTTCTCTGATGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200  
 QY 1201 AATTGTAATGTTAAGAAATTTTATATATCTGTTAAATTAATTAATTTTCCACACA 1257  
 DB 1201 AATTGTAATGTTAAGAAATTTTATATATCTGTTAAATTAATTAATTTTCCACACA 1257

RESULT 4  
 AAF54507  
 ID AAF54507 standard; DNA; 1257 BP.  
 XX  
 XX AAF54507;  
 AC  
 AC  
 XX  
 XX  
 XX 02-APR-2001 (first entry)  
 DE Probe #60 used in the identification of proteins.  
 DE  
 DE Secreted; transmembrane; gene therapy; ss.  
 OS Unidentified.  
 OS  
 PN WO200078961-A1.  
 PN  
 XX  
 XX 28-DEC-2000.  
 PD  
 XX  
 XX 18-FEB-2000: 2000MO-US04342.  
 PF  
 XX  
 XX 23-JUN-1999; 990S-0141037.

PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99MO-US20111.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 02-DEC-1999; 99MO-US28551.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 05-JAN-2000; 2000MO-US00219.  
 PR 06-JAN-2000; 2000MO-US00376.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PI Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D,  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI: 2001-071395/08.  
 DR  
 XX  
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy -  
 PS  
 XX  
 PS Example 124; Page 489; 787pp; English.  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of  
 CC anti-sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents.  
 CC The nucleic acids may also be used in gene therapy.  
 CC  
 XX  
 XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 1257; DB 22; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 481 ATTATGCAATAGATCTTGGGAAAATTGGGAGTGATACATTTACAAAGATGGCTTCAATA 540  
 Qy GTGCTCTAAGAGTTTGTTCAGTGCTACTTGGCTAAATGCAAGAAATGCATGCTGTC 600  
 Db 541 GTGCTCTAAGAGTTTGTTCAGTGCTACTTGGCTAAATGCAAGAAATGCATGCTGTC 600  
 Qy 601 AGCGTTGGTATTTACATTCATGAGAGCTGAATGTTGAGAGCTCTTCCCAATGAAGCTA 660  
 Db 601 AGCGTTGGTATTTACATTCATGAGAGCTGAATGTTGAGAGCTCTTCCCAATGAAGCTA 660  
 Qy 661 TAAATTTATTTGGACCAAGAGCCCTGAAATGAATTCACAAATTAATTCATGGCACT 720  
 Db 661 TAAATTTATTTGGACCAAGAGCCCTGAAATGAATTCACAAATTAATTCATGGCACT 720  
 Qy 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGGTGTGATATGATGAGATTTGCTATGCGG 780  
 Db 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGGTGTGATATGATGAGATTTGCTATGCGG 780  
 Qy 781 TTGGCAGCTTGTACAGATTTACCCAAAGAGATGCTTCTACATGATGCAATTCAGTTCTC 840  
 Db 781 TTGGCAGCTTGTACAGATTTACCCAAAGAGATGCTTCTACATGATGCAATTCAGTTCTC 840  
 Qy 841 GCATCATTTATGGAAGAACTACCAAAATTAATGCTTAAATTTTCAATTTGCTACCTTTT 900  
 Db 841 GCATCATTTATGGAAGAACTACCAAAATTAATGCTTAAATTTTCAATTTGCTACCTTTT 900  
 Qy 901 TTATTTATGCTTGAATGTTGCTACTTAATGACATTTTAAATTAATTAATGATATACATCT 960  
 Db 901 TTATTTATGCTTGAATGTTGCTACTTAATGACATTTTAAATTAATTAATGATATACATCT 960  
 Qy 961 CAATGAAAGCAAGCTTAATATGTTTACACACCAAGTGTGATTTTACACTGTTTAA 1020  
 Db 961 CAATGAAAGCAAGCTTAATATGTTTACACACCAAGTGTGATTTTACACTGTTTAA 1020  
 Qy 1021 ATCTGATTTATTTATTTGCTCATCAATCAAAAGTGTTCATATTTTATTTAGTGGTT 1080  
 Db 1021 ATCTGATTTATTTATTTGCTCATCAATCAAAAGTGTTCATATTTTATTTAGTGGTT 1080  
 Qy 1081 AGAATACCTTCTTCATACATCTCTCAACCTATATTAATTTGGAATATTTGTGTGCT 1140  
 Db 1081 AGAATACCTTCTTCATACATCTCTCAACCTATATTAATTTGGAATATTTGTGTGCT 1140  
 Qy 1141 TTGTGTTTCTCTTACATATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200  
 Db 1141 TTGTGTTTCTCTTACATATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200  
 Qy 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTAAATTAATTAATTTTCCAA 1257  
 Db 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTAAATTAATTAATTTTCCAA 1257  
 RESULT 5  
 ABS74438  
 ID ABS74438 standard; cDNA; 1257 BP.  
 XX  
 XX ABS74438;  
 AC  
 XX  
 XX 10-DEC-2002 (first entry)  
 DT  
 XX  
 XX Human cDNA encoding secreted/transmembrane protein PRO1550.  
 DE  
 XX  
 XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;  
 KW antiarthritic; osteopathic; sports-related joint problem;  
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.  
 OS  
 XX  
 XX Homo sapiens.  
 PN  
 XX US2002119130-A1.  
 PD  
 XX 29-AUG-2002.  
 XX  
 XX 06-DEC-2001; 2001US-0006867.  
 PF  
 XX









Query Match 100.0%; Score 1257; DB 24; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGAGAGAGGGGGGGGGGGAAGGCGATGATGACACCTCGGGCGGCTCGAGCGCG 60
   1 GGGAGAGAGGGGGGGGGTGAAGGCGATGATGACACCTCGGGCGGCTCGAGCGCG 60
DB 1 GGGAGAGAGGGGGGGGGTGAAGGCGATGATGACACCTCGGGCGGCTCGAGCGCG 60
QY 61 CGGAGCGAGAGCGTGCACGATTCCTCTCTCGGTCTCTCGGCTCGAGCTCGAGCTG 120
   61 CGGAGCGAGAGCGTGCACGATTCCTCTCTCGGTCTCTCGGCTCGAGCTCGAGCTG 120
DB 61 CGGAGCGAGAGCGTGCACGATTCCTCTCTCGGTCTCTCGGCTCGAGCTCGAGCTG 120
QY 121 CCCGCGAGCGCGGAGCCATGCGAGCCCGAGGCCCCCGCGCTCCCGCGAGCGCT 180
   121 CCCGCGAGCGCGGAGCCATGCGAGCCCGAGGCCCCCGCGCTCCCGCGAGCGCT 180
DB 121 CCCGCGAGCGCGGAGCCATGCGAGCCCGAGGCCCCCGCGCTCCCGCGAGCGCT 180
QY 181 GCCCTCGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
   181 GCCCTCGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCCTCGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGGTGTGGACCTGTATATGAAATGT 300
   241 AGGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGGTGTGGACCTGTATATGAAATGT 300
DB 241 AGGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGGTGTGGACCTGTATATGAAATGT 300
QY 301 GCTTACAGAGGCGCGACAGAGAGTGCCTGTGAGACGGAGCCCTGGGCGCAATGTATTC 360
   301 GCTTACAGAGGCGCGACAGAGAGTGCCTGTGAGACGGAGCCCTGGGCGCAATGTATTC 360
DB 301 GCTTACAGAGGCGCGACAGAGAGTGCCTGTGAGACGGAGCCCTGGGCGCAATGTATTC 360
QY 361 CGGGTACACCTGGGATCCGAGGTGGGATGATCAAGGAGAAAGGGGGAATGTCTGA 420
   361 CGGGTACACCTGGGATCCGAGGTGGGATGATCAAGGAGAAAGGGGGAATGTCTGA 420
DB 361 CGGGTACACCTGGGATCCGAGGTGGGATGATCAAGGAGAAAGGGGGAATGTCTGA 420
QY 421 GGGAGAGCTTTGAGAGAGTCTGTGACACCACTACAAAGCACTGTTCATGAGTTCAATGA 480
   421 GGGAGAGCTTTGAGAGAGTCTGTGACACCACTACAAAGCACTGTTCATGAGTTCAATGA 480
DB 421 GGGAGAGCTTTGAGAGAGTCTGTGACACCACTACAAAGCACTGTTCATGAGTTCAATGA 480
QY 481 AATATGACATATGATCTGGGAAATGCGAGTGTATATGACAAATATGCTTCAATA 540
   481 AATATGACATATGATCTGGGAAATGCGAGTGTATATGACAAATATGCTTCAATA 540
DB 481 AATATGACATATGATCTGGGAAATGCGAGTGTATATGACAAATATGCTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTCTAGTGTCTACCTTCGGTAAATGCGAAGATCATGCTGTC 600
   541 GTGCTCTAAGAGTTTGTCTAGTGTCTACCTTCGGTAAATGCGAAGATCATGCTGTC 600
DB 541 GTGCTCTAAGAGTTTGTCTAGTGTCTACCTTCGGTAAATGCGAAGATCATGCTGTC 600
QY 601 AGCGTGTATATTCACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
   601 AGCGTGTATATTCACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
DB 601 AGCGTGTATATTCACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
QY 661 TAATTTATTTGAGCAAGGAAAGCCCTGAATGATGAACTAATTAATTCATGAGCACTT 720
   661 TAATTTATTTGAGCAAGGAAAGCCCTGAATGATGAACTAATTAATTCATGAGCACTT 720
DB 661 TAATTTATTTGAGCAAGGAAAGCCCTGAATGATGAACTAATTAATTCATGAGCACTT 720
QY 721 CTTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTTAGTGAATGTTGCTATCTGAG 780
   721 CTTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTTAGTGAATGTTGCTATCTGAG 780
DB 721 CTTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTTAGTGAATGTTGCTATCTGAG 780
QY 781 TTGGCACTTTGTCAGATTTACCAAAAGAGATGCTTACTGATGGAATTCAGTTCTC 840
   781 TTGGCACTTTGTCAGATTTACCAAAAGAGATGCTTACTGATGGAATTCAGTTCTC 840
DB 781 TTGGCACTTTGTCAGATTTACCAAAAGAGATGCTTACTGATGGAATTCAGTTCTC 840
QY 841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTAAATTTCTGACCTCTTTT 900
   841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTAAATTTCTGACCTCTTTT 900
DB 841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTAAATTTCTGACCTCTTTT 900
QY 901 TTATTTATGCTTGAAGATGTTCACTTAATGACATTTTAAATTAATTAATTAATTAATTA 960
   901 TTATTTATGCTTGAAGATGTTCACTTAATGACATTTTAAATTAATTAATTAATTAATTA 960
DB 901 TTATTTATGCTTGAAGATGTTCACTTAATGACATTTTAAATTAATTAATTAATTAATTA 960
QY 961 GAATGAAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTACACACTGTTTTAA 1020
   961 GAATGAAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTACACACTGTTTTAA 1020
DB 961 GAATGAAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTACACACTGTTTTAA 1020

```

```

QY 1021 ATCTAGCATATATTCATTTTGTCTCAATCAATCAAAAGTGTTCATATATTTTTTAACTGGT 1080
   1021 ATCTAGCATATATTCATTTTGTCTCAATCAATCAAAAGTGTTCATATATTTTTTAACTGGT 1080
DB 1021 ATCTAGCATATATTCATTTTGTCTCAATCAATCAAAAGTGTTCATATATTTTTTAACTGGT 1080
QY 1081 AGAATACCTTCTCTATGTCATCTCTCTCACTTCTCACTTCTCACTTCTCACTTCTCT 1140
   1081 AGAATACCTTCTCTATGTCATCTCTCTCACTTCTCACTTCTCACTTCTCTCTCTCTCT 1140
DB 1081 AGAATACCTTCTCTATGTCATCTCTCTCACTTCTCACTTCTCACTTCTCTCTCTCTCT 1140
QY 1141 TTTGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
   1141 TTTGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
DB 1141 TTTGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1201 AATTTGTAATGTTTGAAGATTTTTTTTATATCTGTAAATTAATTAATTAATTCACACA 1257
   1201 AATTTGTAATGTTTGAAGATTTTTTTTATATCTGTAAATTAATTAATTAATTCACACA 1257
DB 1201 AATTTGTAATGTTTGAAGATTTTTTTTATATCTGTAAATTAATTAATTAATTCACACA 1257

RESULT 8
ABL88194
ID ABL88194 standard; cDNA; 1257 BP.
XX
AC ABL88194;
XX
DE 16-MAY-2002 (first entry)
XX
DE Human PRO1550 cDNA sequence SEQ ID NO:245.
XX
KW Human; angiogenesis; cardiac; cytosolic; antilangogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PE 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 28-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000US-220710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23522.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001US-0806666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.

```



PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Ferrara N, Gerder H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Guney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI; 2002-090516/12.  
 DR P-PSDB; ABB84939.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 PS  
 PS Claim 2; Fig 245; 565pp; English.  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cyostatic,  
 CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 XX  
 XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 1257; DB 24; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 GGGAAAGCTTTGAGAGATCTGGACACCCACTACAGCAGTGTTCATGAGACTTATGA 480  
 Qy 481 ATTATGAGATAGATCTTGGGAAATTTGGGAGTGTACATTTTCAAAAGATGCTTCAATA 540  
 Db 481 ATTATGAGATAGATCTTGGGAAATTTGGGAGTGTACATTTTCAAAAGATGCTTCAATA 540  
 Qy 541 GTGCTCTAAGAGATTTTGTTCAGTGTCTCAGTCTGCTTAATATGCAAAATGATGCTGTC 600  
 Db 541 GTGCTCTAAGAGATTTTGTTCAGTGTCTCAGTCTGCTTAATATGCAAAATGATGCTGTC 600  
 Qy 601 AGCGTTGGATTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 660  
 Db 601 AGCGTTGGATTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 660  
 Qy 661 TAATTTATTTGGACCAAGAGACCCCTGAATATTCACAAATTAATATTCATTCACACTT 720  
 Db 661 TAATTTATTTGGACCAAGAGACCCCTGAATATTCACAAATTAATATTCATTCACACTT 720  
 Qy 721 CTTCGTGAGAGACTTTGTGAGAGATTTGTGTGAGATTTAGTGTGATTTGCTATCTGGG 780  
 Db 721 CTTCGTGAGAGACTTTGTGAGAGATTTGTGTGAGATTTAGTGTGATTTGCTATCTGGG 780  
 Qy 781 TTGGCACTTTGTCACATTTACCCAAAGAGATGCTTCTCTGATGAGATTTGATTTCTC 840  
 Db 781 TTGGCACTTTGTCACATTTACCCAAAGAGATGCTTCTCTGATGAGATTTGATTTCTC 840  
 Qy 841 GCATCATTTATTAAGAGACACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
 Db 841 GCATCATTTATTAAGAGACACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
 Qy 901 TTATTTATGCTTTGGAATGTTGCTTAAATGACATTTTAAATTAATTTGATTAACACT 960  
 Db 901 TTATTTATGCTTTGGAATGTTGCTTAAATGACATTTTAAATTAATTTGATTAACACT 960  
 Qy 961 GAATGAAAGCAAGGATTAATTTGTTACAGCAAGGATGATTTTACAGCTTTTAA 1020  
 Db 961 GAATGAAAGCAAGGATTAATTTGTTACAGCAAGGATGATTTTACAGCTTTTAA 1020  
 Qy 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTTTATTTTATTTAGTGT 1080  
 Db 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTTTATTTTATTTAGTGT 1080  
 Qy 1081 AGAATACCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Db 1081 AGAATACCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Qy 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 Db 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 Qy 1201 AATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1257  
 Db 1201 AATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1257  
 RESULT 9  
 ACAS7865  
 ID ACAS7865 standard; cDNA; 1257 BP.  
 XX  
 XX ACAS7865;  
 AC 10-JUN-2003 (first entry)  
 XX  
 XX Human PRO1550 cDNA.  
 DE Human; PRO: secreted; transmembrane; cytosolic; TNF-alpha; blood; gene;  
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;  
 XX differential; tumour; gene therapy; ss.  
 OS Homo sapiens.  
 XX  
 XX US2003036143-A1.

PD 20-FEB-2003.  
XX  
XX 02-JUL-2002; 2002US-0187600.  
XX  
PR 16-SEP-1998; 98WO-US19330.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 14-MAY-1999; 99WO-US1073.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US21011.  
PR 15-SEP-1999; 99WO-US21090.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28351.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23338.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2001WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 29-AUG-2001; 2001WO-US27099.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 17-OCT-1997; 97US-062250P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 28-OCT-1997; 97US-063540P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063734P.  
PR 31-OCT-1997; 97US-063870P.  
PR 31-OCT-1997; 97US-064103P.  
PR 13-NOV-1997; 97US-065311P.  
PR 21-NOV-1997; 97US-066120P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066772P.  
PR 11-DEC-1997; 97US-069335P.  
PR 12-DEC-1997; 97US-069425P.  
PR 17-DEC-1997; 97US-069870P.  
PR 18-DEC-1997; 97US-068017P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077649P.  
PR 20-MAR-1998; 98US-078886P.  
PR 20-MAR-1998; 98US-078939P.  
PR 27-MAR-1998; 98US-079664P.  
PR 31-MAR-1998; 98US-080107P.  
PR 31-MAR-1998; 98US-080194P.  
PR 01-APR-1998; 98US-080327P.  
PR 01-APR-1998; 98US-080333P.  
PR 08-APR-1998; 98US-081049P.  
PR 08-APR-1998; 98US-081070P.  
  
PR 09-APR-1998; 98US-081195P.  
PR 15-APR-1998; 98US-081838P.  
PR 21-APR-1998; 98US-082568P.  
PR 22-APR-1998; 98US-082569P.  
PR 22-APR-1998; 98US-082704P.  
PR 28-APR-1998; 98US-082797P.  
PR 28-APR-1998; 98US-083222P.  
PR 29-APR-1998; 98US-083495P.  
PR 29-APR-1998; 98US-083496P.  
PR 29-APR-1998; 98US-083559P.  
PR 05-MAY-1998; 98US-084366P.  
PR 06-MAY-1998; 98US-084414P.  
PR 07-MAY-1998; 98US-084639P.  
PR 07-MAY-1998; 98US-084640P.  
PR 15-MAY-1998; 98US-084643P.  
PR 15-MAY-1998; 98US-084649P.  
PR 15-MAY-1998; 98US-085580P.  
PR 15-MAY-1998; 98US-085582P.  
PR 15-MAY-1998; 98US-085700P.  
PR 18-MAY-1998; 98US-086023P.  
PR 22-MAY-1998; 98US-086392P.  
PR 22-MAY-1998; 98US-086466P.  
PR 28-MAY-1998; 98US-087098P.  
PR 28-MAY-1998; 98US-087208P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087659P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088722P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088740P.  
PR 10-JUN-1998; 98US-088811P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088825P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088863P.  
PR 12-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089090P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 24-JUN-1998; 98US-090422P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090688P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 25-JUN-1998; 98US-090696P.

```

PR 26-JUN-1998: 98US-090862P.
PR 26-JUN-1998: 98US-090863P.
PR 26-JUN-1998: 98US-091010P.
PR 01-JUL-1998: 98US-091359P.
PR 01-JUL-1998: 98US-091544P.
PR 02-JUL-1998: 98US-091478P.
PR 02-JUL-1998: 98US-091486P.
PR 02-JUL-1998: 98US-091626P.
PR 02-JUL-1998: 98US-091628P.
PR 02-JUL-1998: 98US-091632P.
PR 24-JUL-1998: 98US-094006P.
PR 04-AUG-1998: 98US-095282P.
PR 10-AUG-1998: 98US-095998P.
PR 10-AUG-1998: 98US-096012P.
PR 17-AUG-1998: 98US-096757P.
PR 17-AUG-1998: 98US-096766P.
PR 17-AUG-1998: 98US-096867P.
PR 17-AUG-1998: 98US-096891P.
PR 17-AUG-1998: 98US-096897P.
PR 18-AUG-1998: 98US-096949P.
PR 18-AUG-1998: 98US-096959P.
PR 18-AUG-1998: 98US-097022P.
PR 26-AUG-1998: 98US-097952P.
PR 26-AUG-1998: 98US-097954P.
PR 26-AUG-1998: 98US-097955P.
PR 26-AUG-1998: 98US-097971P.
PR 26-AUG-1998: 98US-097974P.
PR 26-AUG-1998: 98US-098014P.
PR 01-SEP-1998: 98US-098716P.
PR 01-SEP-1998: 98US-098723P.
PR 02-SEP-1998: 98US-098803P.
PR 02-SEP-1998: 98US-098821P.
PR 02-SEP-1998: 98US-098843P.
PR 02-SEP-1998: 98US-099602P.
PR 10-SEP-1998: 98US-099741P.
PR 10-SEP-1998: 98US-099754P.
PR 10-SEP-1998: 98US-099763P.
PR 10-SEP-1998: 98US-099812P.

```

Query Match Best Local Similarity 100.0%; Score 1257; DB 25; Length 1257;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATGTGATGACGCTCGCGCGGCTCGAGCGCGG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATGTGATGACGCTCGCGCGGCTCGAGCGCGG 60
QY 61 CGAGAGCAGACGCTGACACAGCTCTCTCGGTCTCTCTCGGCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCAGACGCTGACACAGCTCTCTCGGTCTCTCTCTCGGCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGAGCGCGGAGCATATGCGACGCCAGAGCGCGCGCGCGCTCCCGCGAGCGGCTCGCG 180
DB 121 CCCGAGCGCGGAGCATATGCGACGCCAGAGCGCGCGCGCGCGCTCCCGCGAGCGGCTCGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGGAAGCAAAAGGCGCAGCTCCGCGCAGAGGAGGTGGACCTGTATTAAGGAATGT 300
DB 241 AGGGGAAGCAAAAGGCGCAGCTCCGCGCAGAGGAGGTGGACCTGTATTAAGGAATGT 300
QY 301 GCTTACAGGCGCAGAGAGTGTCTGTCTGAGAGCGGAGCCCTTG6GGCCATGTATTTC 360
DB 301 GCTTACAGGCGCAGAGAGTGTCTGTCTGAGAGCGGAGCCCTTG6GGCCATGTATTTC 360
QY 361 CGGGTACACTGGGATCCAGAGTCTGGAGTGGATTCAAGAGAGAGAGAGAGAGAGAGTCTCTGA 420
DB 361 CGGGTACACTGGGATCCAGAGTCTGGAGTGGATTCAAGAGAGAGAGAGAGAGAGTCTCTGA 420
QY 421 GGGAAAGCTTTGAGAGTCTCTGACACCCCACTACAGCAGTGTATGATGAGTTCAATGA 480
DB 421 GGGAAAGCTTTGAGAGTCTCTGACACCCCACTACAGCAGTGTATGATGAGTTCAATGA 480

```

```

DB 421 GGGAAAGCTTTGAGAGTCTCTGACACCCCACTACAGCAGTGTATGATGAGTTCAATGA 480
QY 481 ATTATGCAATAGATCTTGGGAAATTCGCGAGTGTACATTTACAAAGATCGTTCAATA 540
DB 481 ATTATGCAATAGATCTTGGGAAATTCGCGAGTGTACATTTACAAAGATCGTTCAATA 540
QY 541 GTGCTCTAGAGATTTGTTCTCAGTGCTCAGCTTGGGCTAAATGCGAATGATGCTGTC 600
DB 541 GTGCTCTAGAGATTTGTTCTCAGTGCTCAGCTTGGGCTAAATGCGAATGATGCTGTC 600
QY 601 AGCGTGTGATTTTACATTTCAATGAGCTGAATGTTGAGACCTCTTCCATTGAAGCTA 660
DB 601 AGCGTGTGATTTTACATTTCAATGAGCTGAATGTTGAGACCTCTTCCATTGAAGCTA 660
QY 661 TAAATTTATTTGAGCAAGAGAGCCCTGAATGAATTCACATTAATATTCATCGCACTT 720
DB 661 TAAATTTATTTGAGCAAGAGAGCCCTGAATGAATTCACATTAATATTCATCGCACTT 720
QY 721 CTCTGTGAGAGACTTTGTGAAGAAATGCTGTGATTTGATGATGATGATGATGATGATG 780
DB 721 CTCTGTGAGAGACTTTGTGAAGAAATGCTGTGATTTGATGATGATGATGATGATGATG 780
QY 781 TTGGCACTTTGTAGATTTACCAAGAGATGCTTCTACTGATGATGATGATGATGATGATG 840
DB 781 TTGGCACTTTGTAGATTTACCAAGAGATGCTTCTACTGATGATGATGATGATGATGATG 840
QY 841 GCATCATTTATTTGAGCAAGAGAGCCCTGAATGAATTCACATTAATATTCATCGCACTT 900
DB 841 GCATCATTTATTTGAGCAAGAGAGCCCTGAATGAATTCACATTAATATTCATCGCACTT 900
QY 901 TTAATTAAGCTTGAATGTTCACTTAATGATTTTAAATGATTTATGATGATGATGATG 960
DB 901 TTAATTAAGCTTGAATGTTCACTTAATGATTTTAAATGATTTATGATGATGATGATG 960
QY 961 GAATGAAAGCAAGCAATATGATTTAGACCAAGTGTGATTTACACCTGTTTTTAA 1020
DB 961 GAATGAAAGCAAGCAATATGATTTAGACCAAGTGTGATTTACACCTGTTTTTAA 1020
QY 1021 ATCTAGCATTTATTTGATTTGCTTCAATCAAAAGTGTTCATATTTTATTTTATTTT 1080
DB 1021 ATCTAGCATTTATTTGATTTGCTTCAATCAAAAGTGTTCATATTTTATTTTATTTT 1080
QY 1081 AGAATACCTTTCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 AGAATACCTTTCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 TTTGTTTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 TTTGTTTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AATTTGAAATGTTAAGAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1257
DB 1201 AATTTGAAATGTTAAGAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1257

RESULT 10
ACAS8870
ID ACAS8870 standard; cDNA; 1257 BP.
ACAS8870:
10-JUN-2003 (first entry)
cDNA encoding human secreted polypeptide PRO1550.
Human; ss; gene; gene therapy; tumour; cancer.
Homo sapiens.
US2003013855-A1.
16-JAN-2003.

```

PF 03-MAY-2002; 2002US-0063616.  
 XX 30-DEC-1998; 98KR-0062142.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 14-MAY-1999; 99US-0311832.  
 PR 25-AUG-1999; 99US-0380137.  
 PR 25-AUG-1999; 99US-0380137.  
 PR 25-AUG-1999; 99US-0380139.  
 PR 25-AUG-1999; 99US-0380142.  
 PR 15-SEP-1999; 99US-0397342.  
 PR 18-OCT-1999; 99US-0403297.  
 PR 12-NOV-1999; 99US-0423844.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 18-SEP-2000; 2000US-0646110.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 10-MAY-2001; 2001US-0834208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 29-JUN-2001; 2001US-0869599.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-DEC-2001; 2001US-0006867.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Eaton DL, Filvaroff E, Gerlitsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WJ;  
 XX WPI: 2003-330485/31.  
 DR P-PSDB; AB071566.  
 DR  
 XX  
 PT New isolated antibody specifically binding a PRO polypeptide, useful  
 PT for the preparation of a medicament for treating disorders with the  
 PT aberrant expression or activity of the PRO polypeptide, such as tumor  
 PT conditions and cancer -  
 PS  
 PS Example 4; Page 193-194; 406pp; English.  
 XX  
 CC The invention relates to an antibody that binds to a polypeptide with a  
 CC fully defined sequence given in the specification. The methods and  
 CC compositions (containing antibodies that specifically bind a PRO  
 CC polypeptide) of the present invention are useful for the preparation of a  
 CC medicament for the treatment of disorders associated with the aberrant  
 CC expression or activity of the PRO polypeptide, such as tumor conditions  
 CC and cancer. They can also be used to generate transgenic or knockout  
 CC animals useful in the development and screening of therapeutically useful  
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
 CC molecular weight markers for protein electrophoresis, chromosome  
 CC identification and tissue typing. The PRO polypeptides are useful to  
 CC induce angiogenesis e.g. wound healing. In the treatment of sports-related  
 CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
 CC antibodies may be used in various diagnostic, competitive binding and/or  
 CC immunoprecipitation assays. The present sequence represents a cDNA  
 CC encoding a PRO polypeptide of the invention.  
 XX

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;  
 Query Match 100.0%; Score 1257; DB 25; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-251;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTCGGGGCGCTCGAGCGCGG 60  
 DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTCGGGGCGCTCGAGCGCGG 60  
 QY CGGAGCCAGACGCTGACACGCTTCCTCCCTCGCTCGCTCGCTCGCTCGCTCGCTCG 120  
 DB CGGAGCCAGACGCTGACACGCTTCCTCCCTCGCTCGCTCGCTCGCTCGCTCGCTCG 120  
 QY 61 CGGAGCCAGACGCTGACACGCTTCCTCCCTCGCTCGCTCGCTCGCTCGCTCGCTCG 180  
 DB CGGAGCCAGACGCTGACACGCTTCCTCCCTCGCTCGCTCGCTCGCTCGCTCGCTCG 180  
 QY 121 CCGGAGCCAGACGCTGACACGCTTCCTCCCTCGCTCGCTCGCTCGCTCGCTCGCTCG 240  
 DB CCGGAGCCAGACGCTGACACGCTTCCTCCCTCGCTCGCTCGCTCGCTCGCTCGCTCG 240  
 QY 181 GCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 DB GCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 241 AGGGAGAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGGAGCTGTAATGGAAGT 300  
 DB AGGGAGAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGGAGCTGTAATGGAAGT 300  
 QY 301 GCTTACAGAGGCGCAGAGAGTGCCTGCTGCGAGAGGAGGCGGCGGCAATGTTATTC 360  
 DB GCTTACAGAGGCGCAGAGAGTGCCTGCTGCGAGAGGAGGCGGCGGCAATGTTATTC 360  
 QY 361 CGGGTACACCTGGAGATCCAGAGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGTCTGA 420  
 DB CGGGTACACCTGGAGATCCAGAGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGTCTGA 420  
 QY 421 GGGAGAGCTTGGAGAGTCTGAGACACCACTACAGAGGCTCATGAGATCATGTA 480  
 DB GGGAGAGCTTGGAGAGTCTGAGACACCACTACAGAGGCTCATGAGATCATGTA 480  
 QY 481 ATTATGCAATAGATCTGGAGAAATTTGGAGGTGATTCAGAAATGATGCTCAATA 540  
 DB ATTATGCAATAGATCTGGAGAAATTTGGAGGTGATTCAGAAATGATGCTCAATA 540  
 QY 541 GTGCTCTAAGAGTTTGTTCAGTGTGCTCACTTGGCTTAAATGCAAGATGATGCTCTC 600  
 DB GTGCTCTAAGAGTTTGTTCAGTGTGCTCACTTGGCTTAAATGCAAGATGATGCTCTC 600  
 QY 601 AGCGTGTATTTGATTCATTCATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 660  
 DB AGCGTGTATTTGATTCATTCATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 660  
 QY 661 TAATTTATTTGGAGCAAGAGCCCTGAATGATTCAGCAATTAATTTATTCAGCACTT 720  
 DB TAATTTATTTGGAGCAAGAGCCCTGAATGATTCAGCAATTAATTTATTCAGCACTT 720  
 QY 721 CTTCGTGGAGAGCTTTGTGAGAGATTTGTGAGATTTGTGAGATTTGTGAGATTTGT 780  
 DB CTTCGTGGAGAGCTTTGTGAGAGATTTGTGAGATTTGTGAGATTTGTGAGATTTGT 780  
 QY 781 TTGGAGCTTTGATTCATTCATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 840  
 DB TTGGAGCTTTGATTCATTCATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 840  
 QY 841 GCATCATTTATGAGAGAACTACCAAAATTAATGCTTAATTTTCAATTCCTACCTTTT 900  
 DB GCATCATTTATGAGAGAACTACCAAAATTAATGCTTAATTTTCAATTCCTACCTTTT 900  
 QY 901 TTATTTATGCTTGGAGATGCTTCAATTAATGATTTTAATTAATTTATTTATTTATTC 960  
 DB TTATTTATGCTTGGAGATGCTTCAATTAATGATTTTAATTAATTTATTTATTTATTC 960  
 QY 961 GAATGAAGAGAGAGCTTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1020  
 DB GAATGAAGAGAGAGCTTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1020

QY 1021 ATCTACGATTTATTCATTTGCTTCATCAATCAAAAGTGTTCATATTTTGTAGTTGGTT 1080  
DB 1021 ATCTACGATTTATTCATTTGCTTCATCAAAAGTGTTCATATTTTGTAGTTGGTT 1080  
QY 1081 AGAATACCTTCTTCATGATGACATTCCTCAACCTATATTTGGATATTTGTGTCT 1140  
DB 1081 AGAATACCTTCTTCATGATGACATTCCTCAACCTATATTTGGATATTTGTGTCT 1140  
QY 1141 TTTGTTTTTCTCTAGTATGATGATTTTAAAAAATATATAAGCTACATCTTTGTAC 1200  
DB 1141 TTTGTTTTTCTCTAGTATGATGATTTTAAAAAATATATAAGCTACATCTTTGTAC 1200  
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATATAAATTTATTTCCAA 1257  
DB 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATATAAATTTATTTCCAA 1257

RESULT 11  
ID ACA60423 standard; cDNA; 1257 BP.  
AC ACA60423:  
AC ACA60423:  
XX 11-JUN-2003 (first entry)  
DE Novel human secreted and transmembrane protein PRO1550 cDNA.  
XX  
XX Human: secreted and transmembrane polypeptide; gene: ss.  
KM chromosome mapping; gene mapping; transgenic animal; knockout animal;  
KM therapeutic agent screening; chromosome identification; tissue typing;  
KW gene therapy.  
XX Homo sapiens.  
XX US2003018183-A1.  
PN 23-JAN-2003.  
XX 01-MAY-2002; 2002US-0063512.  
PF 06-DEC-2001; 2001US-0006867.  
PR (GENT) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;  
XX WPI; 2003-330984/31.  
DR P-SDB; AB072012.  
XX  
XX New secreted and transmembrane PRO polypeptides and nucleic acid  
PT molecules encoding the polypeptides, useful in gene therapy or  
PT preparing a medicament for treating a condition that is responsive to  
PT the PRO polypeptide or antibody -  
XX  
XX Disclosure: Fig 121; 409pp; English.  
XX The invention describes novel isolated PRO polypeptides. The PRO  
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
CC for treating a condition that is responsive to the PRO polypeptide or  
CC antibody. The PRO nucleotide sequences may be used as hybridisation  
CC probes in chromosome and gene mapping, or in generating antisense RNA  
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,  
CC in assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knockout animals, which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides and nucleic acid molecules are also useful in gene  
CC therapy, and as molecular weight markers for protein electrophoresis  
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
CC PRO or for the affinity purification of PRO from recombinant cell  
CC culture or natural sources. This sequence encodes a novel human

CC secreted and transmembrane PRO polypeptide.  
XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;  
SQ  
Query Match 100.0%; Score 1257; DB 25; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAGAGAGGCGCGGGGTGAAGAGCGATGATGACAGCCGCGGCGCTCGAGGCGG 60  
DB 1 GGAGAGAGGCGCGGGGTGAAGAGCGATGATGACAGCCGCGGCGCTCGAGGCGG 60  
QY CGAGAGCGAGCGCTGACACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB CGAGAGCGAGCGCTGACACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CCGGCGAGCGGGAGAGCGATGCGACCCAGGCGCGCGCGCGCTCGGCGAGCGGCTCGCG 180  
DB 121 CCGGCGAGCGGGAGAGCGATGCGACCCAGGCGCGCGCGCGCTCGGCGAGCGGCTCGCG 180  
QY 181 GCGTCTGCTGCT 240  
DB 181 GCGTCTGCTGCT 240  
QY 241 AGGGGAAGCAAAAGCGCGACCTCCGGCAGAGGAGGTGTGGAAGCTGTATATGAAATGT 300  
DB 241 AGGGGAAGCAAAAGCGCGACCTCCGGCAGAGGAGGTGTGGAAGCTGTATATGAAATGT 300  
QY 301 GCTTTACAGAGGCGCAGCAGAGGTGCTGTGTGAACGAGGAGCCCTGGGGCCATGTATTC 360  
DB 301 GCTTTACAGAGGCGCAGCAGAGGTGCTGTGTGAACGAGGAGCCCTGGGGCCATGTATTC 360  
QY 361 CGGGTACACCTGGGATCCAGGTGCGGATGGATTCAAGGAAAGGAGGAAATGTCTGA 420  
DB 361 CGGGTACACCTGGGATCCAGGTGCGGATGGATTCAAGGAAAGGAGGAAATGTCTGA 420  
QY 421 GGGAAAGCTTTGAGAGAGTCTGTGACACCACTACAGAGGTTCATGAGATTGA 480  
DB 421 GGGAAAGCTTTGAGAGAGTCTGTGACACCACTACAGAGGTTCATGAGATTGA 480  
QY 481 ATTATGGCATAGATCTGGGAAATGCGGAGGTTCATTTACAAAGATCCGTCAATTA 540  
DB 481 ATTATGGCATAGATCTGGGAAATGCGGAGGTTCATTTACAAAGATCCGTCAATTA 540  
QY 541 GTGCTCTAGAGATTTGTTTCTAGTGGCTCACTTGGCTAAATATCAGAAATGATGCTGTC 600  
DB 541 GTGCTCTAGAGATTTGTTTCTAGTGGCTCACTTGGCTAAATATCAGAAATGATGCTGTC 600  
QY 601 AGCGTTGGTATTTTACATTCATGACAGCTGAATGTTCAGGACCTCTCCATTTGAAGCTA 660  
DB 601 AGCGTTGGTATTTTACATTCATGACAGCTGAATGTTCAGGACCTCTCCATTTGAAGCTA 660  
QY 661 TAATTTATTTGGACCAAGAGAGCCCTGAATATGAAATTAATTAATTAATTAATTAATTA 720  
DB 661 TAATTTATTTGGACCAAGAGAGCCCTGAATATGAAATTAATTAATTAATTAATTAATTA 720  
QY 721 CTCTGTGAGAGACTTTGTGAAGAAATTTGCTGTGATGATGATGATGATGATGATGATG 780  
DB 721 CTCTGTGAGAGACTTTGTGAAGAAATTTGCTGTGATGATGATGATGATGATGATGATG 780  
QY 781 TTGGCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
DB 781 TTGGCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
QY 841 GCATCATTTATGGAAGAACTACCAAAATTAATGCTTTAATTTTATTTGCTACTCTTTT 900  
DB 841 GCATCATTTATGGAAGAACTACCAAAATTAATGCTTTAATTTTATTTGCTACTCTTTT 900  
QY 901 TTTATTTGCTTTGGAATGTTTCACTTAATTAATGATTTTAAATAGTTTATGATATCT 960  
DB 901 TTTATTTGCTTTGGAATGTTTCACTTAATTAATGATTTTAAATAGTTTATGATATCT 960  
QY 961 GAATGAAAGCAAAAGCTAAATATATGTTTACAGACCAAAAGTGTGATTTACACTGTTTAA 1020

|||||  
Db 961 GAATGAAAGCAAGCTAAATATGTTACAGACCAAGGTGATTTCACTGTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTTGGCTGCATCAAAAGTGTTCATATTTTATTTAGTGGT 1080  
Db 1021 ATCTAGCATTTATTCATTTTGGCTGCATCAAAAGTGTTCATATTTTATTTAGTGGT 1080  
QY 1081 AGAATACCTTTCTCATAGTACATCTCTCAACCTATATATTTGGAAATATGTTGGTCT 1140  
Db 1081 AGAATACCTTTCTCATAGTACATCTCTCAACCTATATATTTGGAAATATGTTGGTCT 1140  
QY 1141 TTGCTTTTCTCTAGTATAGCATTTTAAATAATTAAGTACCATTCTGTGAC 1200  
Db 1141 TTGCTTTTCTCTAGTATAGCATTTTAAATAATTAAGTACCATTCTGTGAC 1200  
QY 1201 AATTTGTAATGTATAGAAATTTTATCTGTTAAATTAATTAATTTTCCAAACA 1257  
Db 1201 AATTTGTAATGTATAGAAATTTTATCTGTTAAATTAATTAATTTTCCAAACA 1257

RESULT 12  
ACA63433  
ID ACA63433 standard; cDNA; 1257 BP.  
XX ACA63433;  
AC  
XX 13-JUN-2003 (first entry)  
DT  
XX  
DE cDNA encoding human PRO polypeptide #61.  
XX  
KW Human: PRO polypeptide; secreted and transmembrane protein;  
KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003023042-A1.  
PD 30-JAN-2003.  
XX  
PF 01-MAY-2002; 2002US-0063502.  
PR 06-DEC-2001; 2001US-0006867.  
XX  
PA (GENE ) GENENTECH INC.  
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX MPI: 2003-331484/31.  
DR P-PSDB; AB072169.  
XX  
XX Novel monoclonal antibody that binds to secreted and transmembrane  
PT polypeptide, useful for detecting and purifying the polypeptide and  
PT also for treating conditions responsive to the antibody  
XX  
PS Disclosure: Fig 121; 408pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a  
CC medicament useful in the treatment of a condition responsive to  
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells,  
CC tissues or serum, and for affinity purification of PRO from  
CC recombinant cell culture or natural sources. ACA63373-ACA63456  
CC represent cDNA sequences encoding the human PRO polypeptides of  
CC the invention.  
XX  
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 25; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 1.7e-251;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACGCTCGCGCGCGCTGGAGCGCG 60  
Db 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACGCTCGCGCGCGCTGGAGCGCG 60  
QY 61 CGAGAGCGAGCGCTGACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 61 CGAGAGCGAGCGCTGACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CCGGAGAGCGGGGACCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 121 CCGGAGAGCGGGGACCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
QY 181 GCGCT 240  
Db 181 GCGCT 240  
QY 241 AGGGAGAGCAAAAGCGCGAGCTCCGGCAGAGGAGGTGAGACCTGTATATGAAATGT 300  
Db 241 AGGGAGAGCAAAAGCGCGAGCTCCGGCAGAGGAGGTGAGACCTGTATATGAAATGT 300  
QY 301 GCTTACAGAGGCGAGAGAGTGGCTGGTGGAGACGGGAGCGCGCGCGCGCATGTATTC 360  
Db 301 GCTTACAGAGGCGAGAGAGTGGCTGGTGGAGACGGGAGCGCGCGCGCATGTATTC 360  
QY 361 CGGGTACACCTGGGATCCAGGTGGGATGATTCAAAGAGAAAGGGGGAATGTCTGA 420  
Db 361 CGGGTACACCTGGGATCCAGGTGGGATGATTCAAAGAGAAAGGGGGAATGTCTGA 420  
QY 421 GGGAAAGTTTGGAGAGTCTGAGACCCCACTACAGCATGTTCATGAGTTCAATTGA 480  
Db 421 GGGAAAGTTTGGAGAGTCTGAGACCCCACTACAGCATGTTCATGAGTTCAATTGA 480  
QY 481 ATTAATGCGATAGCTTTGGGAAATTTGGGAGTGTATACAAAGATGCGTCAATA 540  
Db 481 ATTAATGCGATAGCTTTGGGAAATTTGGGAGTGTATACAAAGATGCGTCAATA 540  
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTTAAATTTGAGAAATGCATGCTGC 600  
Db 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTTAAATTTGAGAAATGCATGCTGC 600  
QY 601 AGCGTTGATTTTCAATTCATATGAGTGAATGTTCAGAGCTCTTCCATTGAAGCTA 660  
Db 601 AGCGTTGATTTTCAATTCATATGAGTGAATGTTCAGAGCTCTTCCATTGAAGCTA 660  
QY 661 TAAATTTATTTGGACCAAGAGAGCCCTGAAATGAATTCACAAATTAATTTATGACACT 720  
Db 661 TAAATTTATTTGGACCAAGAGAGCCCTGAAATGAATTCACAAATTAATTTATGACACT 720  
QY 721 CTCTGTGGAAGAGCTTTGTAAGGAATTTGGTGTGATTTAGTGAATGTTCTATCTGGG 780  
Db 721 CTCTGTGGAAGAGCTTTGTAAGGAATTTGGTGTGATTTAGTGAATGTTCTATCTGGG 780  
QY 781 TTGGACCTGTTGAGATTAACCAAAAGAGAGTGTCTTACGTGAGATTCAGCTTCTC 840  
Db 781 TTGGACCTGTTGAGATTAACCAAAAGAGAGTGTCTTACGTGAGATTCAGCTTCTC 840  
QY 841 GCATCATTTTGAAGAGTACCAAAATTAATTTTCAATTTTCAATTTTCAATTTTCAATTT 900  
Db 841 GCATCATTTTGAAGAGTACCAAAATTAATTTTCAATTTTCAATTTTCAATTTTCAATTT 900  
QY 901 TTAATTTATTTGGAAGAGTACCAATTAATTTTCAATTTTCAATTTTCAATTTTCAATTT 960  
Db 901 TTAATTTATTTGGAAGAGTACCAATTAATTTTCAATTTTCAATTTTCAATTTTCAATTT 960  
QY 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTCACTGTTTAA 1020  
Db 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTCACTGTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTTGGCTGCATCAAAAGTGTTCATATTTTATTTAGTGGT 1080  
Db 1021 ATCTAGCATTTATTCATTTTGGCTGCATCAAAAGTGTTCATATTTTATTTAGTGGT 1080

QY 1081 AGAATCTTCTTCATGACATCTCTCACCCATTAATTTGGAATATGTTGCTCTP 1140  
DB 1081 AGAATCTTCTTCATGACATCTCTCACCCATTAATTTGGAATATGTTGCTCTP 1140  
QY 1141 TTTGTTTTCTCTGTATGATGATTTTAAAAAATTAAGCTACCAATCTTTGTAC 1200  
DB 1141 TTTGTTTTCTCTGTATGATGATTTTAAAAAATTAAGCTACCAATCTTTGTAC 1200  
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257  
DB 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257  
RESULT 13  
ABX98335  
ID ABX98335 standard; cDNA; 1257 BP.  
XX ABX98335;  
AC  
XX  
XX 19-MAY-2003 (first entry)  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.  
XX  
XX  
XX Human; ss; gene; PRO; secreted protein; transmembrane protein;  
XX cytosolic; antiarthritic; osteopathic; adrenal tumour; lung tumour;  
XX colon tumour; breast tumour; prostate tumour; rectal tumour;  
XX cervical tumour; liver tumour; TNF-alpha release; arthritis;  
XX tumour necrosis factor alpha; chondrocyte cell; bone disorder;  
XX cartilage disorder; sports injury.  
XX  
XX Homo sapiens.  
XX US2003036156-A1.  
XX  
XX 20-FEB-2003.  
XX  
XX 02-JUL-2002; 2002US-0186767.  
XX  
XX  
XX 16-SEP-1998; 98WO-US19330.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 08-MAR-1999; 99WO-US05028.  
XX 14-MAY-1999; 99WO-US10733.  
XX 02-JUN-1999; 99WO-US12252.  
XX 01-SEP-1999; 99WO-US20111.  
XX 15-SEP-1999; 99WO-US21090.  
XX 01-DEC-1999; 99WO-US28301.  
XX 02-DEC-1999; 99WO-US28551.  
XX 30-DEC-1999; 99WO-US31274.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 18-FEB-2000; 2000WO-US04342.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 01-MAR-2000; 2000WO-US05601.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 20-DEC-2000; 2000WO-US34956.  
XX 28-FEB-2001; 2001WO-US106520.  
XX 01-JUN-2001; 2001WO-US117800.  
XX 20-JUN-2001; 2001WO-US119692.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 09-JUL-2001; 2001WO-US21735.

PR 29-AUG-2001; 2001WO-US27099.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 17-OCT-1997; 97US-062250P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 28-OCT-1997; 97US-063540P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063734P.  
PR 31-OCT-1997; 97US-063870P.  
PR 13-NOV-1997; 97US-064103P.  
PR 21-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066120P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066772P.  
PR 11-DEC-1997; 97US-069335P.  
PR 12-DEC-1997; 97US-069425P.  
PR 17-DEC-1997; 97US-069870P.  
PR 18-DEC-1997; 97US-068017P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077649P.  
PR 20-MAR-1998; 98US-078886P.  
PR 20-MAR-1998; 98US-078939P.  
PR 27-MAR-1998; 98US-079664P.  
PR 31-MAR-1998; 98US-079786P.  
PR 31-MAR-1998; 98US-080107P.  
PR 31-MAR-1998; 98US-080194P.  
PR 01-APR-1998; 98US-080327P.  
PR 08-APR-1998; 98US-081043P.  
PR 08-APR-1998; 98US-081070P.  
PR 09-APR-1998; 98US-081195P.  
PR 15-APR-1998; 98US-081838P.  
PR 21-APR-1998; 98US-082568P.  
PR 21-APR-1998; 98US-082569P.  
PR 22-APR-1998; 98US-082704P.  
PR 22-APR-1998; 98US-082797P.  
PR 28-APR-1998; 98US-083322P.  
PR 29-APR-1998; 98US-083495P.  
PR 29-APR-1998; 98US-083496P.  
PR 29-APR-1998; 98US-083499P.  
PR 29-APR-1998; 98US-083559P.  
PR 05-MAY-1998; 98US-084366P.  
PR 06-MAY-1998; 98US-084414P.  
PR 07-MAY-1998; 98US-084639P.  
PR 07-MAY-1998; 98US-084640P.  
PR 15-MAY-1998; 98US-084643P.  
PR 15-MAY-1998; 98US-085579P.  
PR 15-MAY-1998; 98US-085860P.  
PR 15-MAY-1998; 98US-085882P.  
PR 18-MAY-1998; 98US-085700P.  
PR 22-MAY-1998; 98US-086023P.  
PR 22-MAY-1998; 98US-086392P.  
PR 22-MAY-1998; 98US-086486P.  
PR 28-MAY-1998; 98US-087098P.  
PR 28-MAY-1998; 98US-087208P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087837P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088036P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.



PR	10-JUN-1998;	98US-088722P.
PR	10-JUN-1998;	98US-088738P.
PR	10-JUN-1998;	98US-088740P.
PR	10-JUN-1998;	98US-088811P.
PR	10-JUN-1998;	98US-088824P.
PR	10-JUN-1998;	98US-088825P.
PR	10-JUN-1998;	98US-088826P.
PR	11-JUN-1998;	98US-088861P.
PR	11-JUN-1998;	98US-088863P.
PR	11-JUN-1998;	98US-088876P.
PR	12-JUN-1998;	98US-089090P.
PR	12-JUN-1998;	98US-089105P.
PR	16-JUN-1998;	98US-089512P.
PR	16-JUN-1998;	98US-089514P.
PR	17-JUN-1998;	98US-089538P.
PR	17-JUN-1998;	98US-089598P.
PR	17-JUN-1998;	98US-089653P.
PR	18-JUN-1998;	98US-089908P.
PR	19-JUN-1998;	98US-089952P.
PR	22-JUN-1998;	98US-090246P.
PR	22-JUN-1998;	98US-090252P.
PR	22-JUN-1998;	98US-090254P.
PR	24-JUN-1998;	98US-090429P.
PR	24-JUN-1998;	98US-090435P.
PR	24-JUN-1998;	98US-090444P.
PR	24-JUN-1998;	98US-090461P.
PR	24-JUN-1998;	98US-090535P.
PR	24-JUN-1998;	98US-090540P.
PR	25-JUN-1998;	98US-090676P.
PR	25-JUN-1998;	98US-090678P.
PR	25-JUN-1998;	98US-090688P.
PR	25-JUN-1998;	98US-090690P.
PR	25-JUN-1998;	98US-090694P.
PR	25-JUN-1998;	98US-090695P.
PR	25-JUN-1998;	98US-090696P.
PR	26-JUN-1998;	98US-090862P.
PR	26-JUN-1998;	98US-090863P.
PR	26-JUN-1998;	98US-091010P.
PR	01-JUL-1998;	98US-091359P.
PR	01-JUL-1998;	98US-091544P.
PR	02-JUL-1998;	98US-091478P.
PR	02-JUL-1998;	98US-091486P.
PR	02-JUL-1998;	98US-091626P.
PR	02-JUL-1998;	98US-091628P.
PR	02-JUL-1998;	98US-091632P.
PR	04-JUL-1998;	98US-094006P.
PR	04-AUG-1998;	98US-095282P.
PR	10-AUG-1998;	98US-095988P.
PR	10-AUG-1998;	98US-096012P.
PR	17-AUG-1998;	98US-096757P.
PR	17-AUG-1998;	98US-096766P.
PR	17-AUG-1998;	98US-096867P.
PR	17-AUG-1998;	98US-096891P.
PR	17-AUG-1998;	98US-096897P.
PR	18-AUG-1998;	98US-096949P.
PR	18-AUG-1998;	98US-096959P.
PR	18-AUG-1998;	98US-097022P.
PR	26-AUG-1998;	98US-097952P.
PR	26-AUG-1998;	98US-097954P.
PR	26-AUG-1998;	98US-097955P.
PR	26-AUG-1998;	98US-097971P.
PR	26-AUG-1998;	98US-097974P.
PR	26-AUG-1998;	98US-098014P.
PR	01-SEP-1998;	98US-098716P.
PR	01-SEP-1998;	98US-098723P.
PR	02-SEP-1998;	98US-098803P.
PR	02-SEP-1998;	98US-098821P.
PR	02-SEP-1998;	98US-098843P.
PR	09-SEP-1998;	98US-099602P.
PR	10-SEP-1998;	98US-099741P.

Query Match 100.0%; Score 1257; DB 25; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 1,7e-251;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1	GGAGAGAGCGCGGGGTGAAGCGCATTCATGACGCTCGGCGGCTCGAGCGGG	60	
Db	1	GGAGAGAGCGCGGGGTGAAGCGCATTCATGACGCTCGGCGGCTCGAGCGGG	60	
OY	61	CGAGCCAGAGCGTGACACGCTTCCTCCTCGGCTTCCTCCGCTCCAGCTCCGCGTG	120	
Db	61	CGAGCCAGAGCGTGACACGCTTCCTCCTCGGCTTCCTCCGCTCCAGCTCCGCGTG	120	
OY	121	CCCGGACCGCGGGGACATGCGACCCGAGGGCCCGCGCTCCCGGAGGGCTCCGGC	180	
Db	121	CCCGGACCGCGGGGACATGCGACCCGAGGGCCCGCGCTCCCGGAGGGCTCCGGC	180	
OY	181	GCTCTCTGCTCTCTCTGCTGAGCTGCCCGCGCGCTCGAGCGCTGAGATCCCA	240	
Db	181	GCTCTCTGCTCTCTCTGCTGAGCTGCCCGCGCGCTCGAGCGCTGAGATCCCA	240	
OY	241	AGGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGTGCTGACCTGTATATGGAATGT	300	
Db	241	AGGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGTGCTGACCTGTATATGGAATGT	300	
OY	301	GCTTACAAAGGCGCAGCAGAGTGGCTGTGAGACGGAGCCCGGGCCAAATGTATTC	360	
Db	301	GCTTACAAAGGCGCAGCAGAGTGGCTGTGAGACGGAGCCCGGGCCAAATGTATTC	360	
OY	361	CGGCTACACCTGGGATCCAGCTCGGATGATTCAAAGGAGGAGGAGATGTCTGA	420	
Db	361	CGGCTACACCTGGGATCCAGCTCGGATGATTCAAAGGAGGAGGAGATGTCTGA	420	
OY	421	GGGAAGCTTTGAGAGTCTGACACCCAACTACAAAGCACTGTCATGAGTTCAATGA	480	
Db	421	GGGAAGCTTTGAGAGTCTGACACCCAACTACAAAGCACTGTCATGAGTTCAATGA	480	
OY	481	ATTATGGCATGATCTTGGGAAATTTGGGAGTGTACATTACAAAGATGGCTCAATA	540	
Db	481	ATTATGGCATGATCTTGGGAAATTTGGGAGTGTACATTACAAAGATGGCTCAATA	540	
OY	541	GTGCTTAAAGATTTTGTTCAGTGCTCACTTGGCTAAATTCAGAAATGCATGCTGTC	600	
Db	541	GTGCTTAAAGATTTTGTTCAGTGCTCACTTGGCTAAATTCAGAAATGCATGCTGTC	600	
OY	601	AGCGTTGGTATTTACATTCATGAGCTGATGTCAGGCCCTCCCTCCATTAAGCTA	660	
Db	601	AGCGTTGGTATTTACATTCATGAGCTGATGTCAGGCCCTCCCTCCATTAAGCTA	660	
OY	661	TAAATTTATTTGGACCAAGAAAGCCCTGAATGAATTCACATTAATTTATGCACTT	720	
Db	661	TAAATTTATTTGGACCAAGAAAGCCCTGAATGAATTCACATTAATTTATGCACTT	720	
OY	721	CTTCTGTGAAGACTTTGTGAAGAAATGGTGTGATTAAGATGTTGCTACTGGG	780	
Db	721	CTTCTGTGAAGACTTTGTGAAGAAATGGTGTGATTAAGATGTTGCTACTGGG	780	
OY	781	TTGGCAGCTGTTCAGATTAACCAAGAGATGCTTCTACAGATGGAATTCAGTTCTC	840	
Db	781	TTGGCAGCTGTTCAGATTAACCAAGAGATGCTTCTACAGATGGAATTCAGTTCTC	840	
OY	841	GCATCATTTATGAAGAACTACCAAAATTAATGCTTATTTCAATTTGCTACCTTTT	900	
Db	841	GCATCATTTATGAAGAACTACCAAAATTAATGCTTATTTCAATTTGCTACCTTTT	900	
OY	901	TTATTTATGCTTGAATGTTCACTTAATGACATTTTAATTAATGTTATATACATCT	960	
Db	901	TTATTTATGCTTGAATGTTCACTTAATGACATTTTAATTAATGTTATATACATCT	960	
OY	961	GAATGAAGCAAAAGCTTAATATGTTTACAGACCAAAAGTGATTCACACTGTTTTAA	1020	
Db	961	GAATGAAGCAAAAGCTTAATATGTTTACAGACCAAAAGTGATTCACACTGTTTTAA	1020	
OY	1021	ATCTAGCATTAATTAATTTGCTTCAATCAAAAGGTTTCAATATTTTATTTATGTT	1080	
Db	1021	ATCTAGCATTAATTAATTTGCTTCAATCAAAAGGTTTCAATATTTTATTTATGTT	1080	



QY	1081	AGAAATCTTCTCACTAGTACATTCCTCTCAACCTAAATTTGGAAATATTGTGGCTCT	1140	PR	18-SEP-1997	9705-059263P
Db	1081	AGAAATCTTCTCACTAGTACATTCCTCTCAACCTAAATTTGGAAATATTGTGGCTCT	1140	PR	17-OCT-1997	9705-059263P
QY	1141	TTGTGTTTCTCTAGATAGCATTTTAAATAAATNAAAGTACCAACTTGTGTC	1200	PR	21-OCT-1997	9705-063486P
Db	1141	TTGTGTTTCTCTAGATAGCATTTTAAATAAATNAAAGTACCAACTTGTGTC	1200	PR	24-OCT-1997	9705-063120P
QY	1201	AAATTTGTAATGTTAAGATTTTATTTTATCTGTTAAATAAATTTATTTCCACA	1257	PR	28-OCT-1997	9705-063112P
Db	1201	AAATTTGTAATGTTAAGATTTTATTTTATCTGTTAAATAAATTTATTTCCACA	1257	PR	28-OCT-1997	9705-063540P
RESULT 14						
ABX98837		ABX98837 standard; cDNA; 1257 BP.				
AC	ABX98837					
XX	20-MAY-2003	(first entry)				
DE	Novel human secreted and transmembrane protein PRO1550 cDNA.					
XX	Human; secreted protein; transmembrane protein; cytosolic;					
KW	gene therapy; TNF-Agonist-alpha; chondrocyte stimulator; tumour;					
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;					
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour;					
XX	gene; ss.					
XX	Homo sapiens.					
OS	US2003036157-A1.					
PN	20-FEB-2003.					
PD	02-JUL-2002; 2002US-0188769.					
XX	16-SEP-1998; 98WO-US19330.					
XX	07-OCT-1998; 98WO-US21141.					
PR	01-DEC-1998; 98WO-US25108.					
PR	08-MAR-1999; 99WO-US05028.					
PR	14-MAY-1999; 99WO-US10733.					
PR	02-JUN-1999; 99WO-US12252.					
PR	01-SEP-1999; 99WO-US20111.					
PR	15-SEP-1999; 99WO-US21090.					
PR	01-DEC-1999; 99WO-US28301.					
PR	02-DEC-1999; 99WO-US28551.					
PR	30-DEC-1999; 99WO-US31274.					
PR	05-JAN-2000; 2000WO-US00219.					
PR	18-FEB-2000; 2000WO-US04341.					
PR	18-FEB-2000; 2000WO-US04342.					
PR	22-FEB-2000; 2000WO-US04411.					
PR	24-FEB-2000; 2000WO-US05004.					
PR	01-MAR-2000; 2000WO-US05601.					
PR	02-MAR-2000; 2000WO-US05841.					
PR	15-MAR-2000; 2000WO-US06884.					
PR	30-MAR-2000; 2000WO-US08439.					
PR	17-MAY-2000; 2000WO-US13705.					
PR	22-MAY-2000; 2000WO-US14042.					
PR	30-MAY-2000; 2000WO-US14941.					
PR	02-JUN-2000; 2000WO-US15264.					
PR	28-JUL-2000; 2000WO-US20710.					
PR	24-AUG-2000; 2000WO-US23328.					
PR	08-NOV-2000; 2000WO-US30952.					
PR	01-DEC-2000; 2000WO-US32678.					
PR	20-DEC-2000; 2000WO-US34956.					
PR	28-FEB-2001; 2001WO-US06520.					
PR	01-JUN-2001; 2001WO-US17800.					
PR	20-JUN-2001; 2001WO-US19692.					
PR	29-JUN-2001; 2001WO-US21066.					
PR	09-JUL-2001; 2001WO-US21735.					
PR	29-AUG-2001; 2001WO-US27099.					
PR	10-JUN-1998; 98US-088157P					
PR	05-JUN-1998; 98US-088202P					
PR	05-JUN-1998; 98US-088212P					
PR	05-JUN-1998; 98US-088217P					
PR	05-JUN-1998; 98US-088555P					
PR	05-JUN-1998; 98US-088722P					
PR	05-JUN-1998; 98US-088727P					
PR	05-JUN-1998; 98US-088802P					
PR	05-JUN-1998; 98US-088802P					
PR	05-JUN-1998; 98US-088803P					
PR	05-JUN-1998; 98US-088832P					
PR	05-JUN-1998; 98US-088816P					
PR	05-JUN-1998; 98US-088820					

PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088740P.  
PR 10-JUN-1998; 98US-088811P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088825P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088851P.  
PR 11-JUN-1998; 98US-088863P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089090P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089608P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 24-JUN-1998; 98US-090299P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090461P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090688P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 25-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 26-JUN-1998; 98US-091010P.  
PR 01-JUL-1998; 98US-091359P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091486P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091632P.  
PR 04-JUL-1998; 98US-094006P.  
PR 04-AUG-1998; 98US-095282P.  
PR 10-AUG-1998; 98US-095998P.  
PR 10-AUG-1998; 98US-096012P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-097022P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-098014P.  
PR 01-SEP-1998; 98US-098716P.  
PR 01-SEP-1998; 98US-098723P.  
PR 02-SEP-1998; 98US-098803P.  
PR 02-SEP-1998; 98US-098821P.  
PR 02-SEP-1998; 98US-098843P.  
PR 09-SEP-1998; 98US-099602P.  
PR 10-SEP-1998; 98US-099741P.  
PR 10-SEP-1998; 98US-099754P.  
Query Match 100.0%; Score 1257; DB 25; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 1.7e-251;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAGAGAGCGCGGGGTGAAGCGCATTTGATGACCTGCGCGGCTGAGCGCG 60  
1 GGAGAGAGCGCGGGGTGAAGCGCATTTGATGACCTGCGCGGCTGAGCGCG 60  
DB 1 GGAGAGAGCGCGGGGTGAAGCGCATTTGATGACCTGCGCGGCTGAGCGCG 60  
QY 61 CGAGCCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
CGAGCCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 61 CGAGCCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CCGGCAAGCGCGGCGCATGCGACCCAGCGCGCGCGCGCGCGCGCGCGCG 180  
CCGGCAAGCGCGGCGCATGCGACCCAGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 121 CCGGCAAGCGCGGCGCATGCGACCCAGCGCGCGCGCGCGCGCGCGCG 180  
QY 181 GCT 240  
GCT 240  
DB 181 GCT 240  
QY 241 AGGGGAAGCAAAAGCGCGAGCTCCGCGAGAGAGGTGTGACCTGTATTA 300  
AGGGGAAGCAAAAGCGCGAGCTCCGCGAGAGAGGTGTGACCTGTATTA 300  
DB 241 AGGGGAAGCAAAAGCGCGAGCTCCGCGAGAGAGGTGTGACCTGTATTA 300  
QY 301 GCTTACAAAGGCGCGAGAGTGGCTGAGAGGAGGAGCGCGCGCAATGTAT 360  
GCTTACAAAGGCGCGAGAGTGGCTGAGAGGAGGAGCGCGCGCAATGTAT 360  
DB 301 GCTTACAAAGGCGCGAGAGTGGCTGAGAGGAGGAGCGCGCGCAATGTAT 360  
QY 361 CGGCTACACCTGGGATCCAGTCCAGTGGGATGATTAAGAGAGAGGAGAT 420  
CGGCTACACCTGGGATCCAGTCCAGTGGGATGATTAAGAGAGAGGAGAT 420  
DB 361 CGGCTACACCTGGGATCCAGTCCAGTGGGATGATTAAGAGAGAGGAGAT 420  
QY 421 GGGGAAGCTTGAAGAGTCCCTGGACACCCAACTCAAGCACTGTTCATG 480  
GGGGAAGCTTGAAGAGTCCCTGGACACCCAACTCAAGCACTGTTCATG 480  
DB 421 GGGGAAGCTTGAAGAGTCCCTGGACACCCAACTCAAGCACTGTTCATG 480  
QY 481 ATTATGCAATGATCTTGGGAAATGCGAGTGTATTAACAAGTGGCTCAATA 540  
ATTATGCAATGATCTTGGGAAATGCGAGTGTATTAACAAGTGGCTCAATA 540  
DB 481 ATTATGCAATGATCTTGGGAAATGCGAGTGTATTAACAAGTGGCTCAATA 540  
QY 541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAGATGCT 600  
GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAGATGCT 600  
DB 541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAGATGCT 600  
QY 601 AGCGTTGGTATTTACATTAATGAGTGTATTTAGAGGCTCTTCCATTA 660  
AGCGTTGGTATTTACATTAATGAGTGTATTTAGAGGCTCTTCCATTA 660  
DB 601 AGCGTTGGTATTTACATTAATGAGTGTATTTAGAGGCTCTTCCATTA 660  
QY 661 TAAATTTTGGACCAAGAGAGCCCTGAATGAATTAATTAATTCATGCACT 720  
TAAATTTTGGACCAAGAGAGCCCTGAATGAATTAATTAATTCATGCACT 720  
DB 661 TAAATTTTGGACCAAGAGAGCCCTGAATGAATTAATTAATTCATGCACT 720  
QY 721 CTCTGTGGAAGACTTGTGAAGAAATGGTGTGATTAAGTGAATGCTAT 780  
CTCTGTGGAAGACTTGTGAAGAAATGGTGTGATTAAGTGAATGCTAT 780  
DB 721 CTCTGTGGAAGACTTGTGAAGAAATGGTGTGATTAAGTGAATGCTAT 780  
QY 781 TTGGCAGCTGTTCAGATTTACCAAAAGAGATGCTTACAGATGGAATTC 840  
TTGGCAGCTGTTCAGATTTACCAAAAGAGATGCTTACAGATGGAATTC 840  
DB 781 TTGGCAGCTGTTCAGATTTACCAAAAGAGATGCTTACAGATGGAATTC 840  
QY 841 GCATCATTTATGAAGACTTACCAAAATGAATGCTTATTTTCAATTCACCT 900  
GCATCATTTATGAAGACTTACCAAAATGAATGCTTATTTTCAATTCACCT 900  
DB 841 GCATCATTTATGAAGACTTACCAAAATGAATGCTTATTTTCAATTCACCT 900  
QY 901 TTATTTATGCGTTGAATGCTTCAATTAATGATTAATTAATTAATTAAT 960  
TTATTTATGCGTTGAATGCTTCAATTAATGATTAATTAATTAATTAAT 960  
DB 901 TTATTTATGCGTTGAATGCTTCAATTAATGATTAATTAATTAATTAAT 960  
QY 961 GAATGAAGCAAGAGTAAATATGTTTACAGACCAAGTGTGATTTCACT 1020  
GAATGAAGCAAGAGTAAATATGTTTACAGACCAAGTGTGATTTCACT 1020  
DB 961 GAATGAAGCAAGAGTAAATATGTTTACAGACCAAGTGTGATTTCACT 1020  
QY 1021 ATCTAGCATTTATTTATTTTGTCTCAATCAAAAGGTTTCAATTTTAT 1080  
ATCTAGCATTTATTTATTTTGTCTCAATCAAAAGGTTTCAATTTTAT 1080  
DB 1021 ATCTAGCATTTATTTATTTTGTCTCAATCAAAAGGTTTCAATTTTAT 1080

```

OY      1081 AGAATACCTTCTTCATAGTCACATTCCTCAACCTAATATTTGATATTTGGTGTCT 1140
        |||
DB      1081 AGAATACCTTCTTCATAGTCACATTCCTCAACCTAATATTTGATATTTGGTGTCT 1140
OY      1141 TTTGTTTTTCTCTAGTATACATTTTAAAAAATATAAAAAGTACCAATCTTTGTAC 1200
        |||
DB      1141 TTTGTTTTTCTCTAGTATACATTTTAAAAAATATAAAAAGTACCAATCTTTGTAC 1200
OY      1201 AATTTGTAATGTAAAGATTTTATATCTGTTAAATATTAATTTATTTCCACA 1257
        |||
DB      1201 AATTTGTAATGTAAAGATTTTATATCTGTTAAATATTAATTTATTTCCACA 1257

RESULT 15
ACAO5882
ID      ACA05882 standard; cDNA; 1257 BP.
XX
AC      ACA05882;
XX
DT      29-MAY-2003 (first entry)
XX
DE      Human secreted/transmembrane protein (PRO) CDNA #183.
XX
KM      Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KM      tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM      tissue typing.
XX
OS      Homo sapiens.
XX
PN      US2003036162-A1.
XX
PD      20-FEB-2003.
XX
PF      12-JUL-2002; 2002US-0194423.
XX
PR      16-SEP-1998; 98WO-US19330.
PR      07-OCT-1998; 98WO-US21141.
PR      01-DEC-1998; 98WO-US21108.
PR      08-MAR-1999; 99WO-US05028.
PR      14-MAY-1999; 99WO-US10733.
PR      02-JUN-1999; 99WO-US12252.
PR      01-SEP-1999; 99WO-US20111.
PR      15-SEP-1999; 99WO-US21090.
PR      01-DEC-1999; 99WO-US28301.
PR      02-DEC-1999; 99WO-US28551.
PR      30-DEC-1999; 99WO-US31274.
PR      05-JAN-2000; 2000WO-US00219.
PR      18-FEB-2000; 2000WO-US04341.
PR      22-FEB-2000; 2000WO-US04342.
PR      24-FEB-2000; 2000WO-US04414.
PR      01-MAR-2000; 2000WO-US05004.
PR      02-MAR-2000; 2000WO-US05601.
PR      15-MAR-2000; 2000WO-US05841.
PR      30-MAR-2000; 2000WO-US06884.
PR      17-MAY-2000; 2000WO-US13705.
PR      22-MAY-2000; 2000WO-US14042.
PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15264.
PR      28-JUL-2000; 2000WO-US20710.
PR      24-AUG-2000; 2000WO-US23328.
PR      08-NOV-2000; 2000WO-US30952.
PR      01-DEC-2000; 2000WO-US32678.
PR      20-DEC-2000; 2000WO-US34956.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
PR      29-AUG-2001; 2001WO-US27099.
PR      26-OCT-1998; 98US-0105413.
PR      07-OCT-1998; 98US-0168978.

```

```

PR      06-NOV-1998; 98US-0187368.
PR      07-DEC-1998; 98US-0202054.
PR      03-MAR-1999; 99US-0254311.
PR      14-MAY-1999; 99US-0311832.
PR      14-MAY-1999; 99US-0380137.
PR      25-AUG-1999; 99US-0380138.
PR      25-AUG-1999; 99US-0380139.
PR      25-AUG-1999; 99US-0380142.
PR      18-OCT-1999; 99US-0403297.
PR      12-NOV-1999; 99US-0423844.
PR      22-AUG-2000; 2000US-0644848.
PR      18-SEP-2000; 2000US-0664610.
PR      18-SEP-2000; 2000US-0665350.
PR      08-NOV-2000; 2000US-0709238.
PR      20-DEC-2000; 2000US-0747259.
PR      22-MAR-2001; 2001US-0816744.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866028.
PR      05-JUN-2001; 2001US-0874503.
PR      18-JUL-2001; 2001US-0908827.
PR      30-JUL-2001; 2001US-0919585.
PR      06-AUG-2001; 2001US-0924419.
PR      13-AUG-2001; 2001US-0929404.
PR      16-AUG-2001; 2001US-0931836.
PR      28-AUG-2001; 2001US-0941992.
PR      04-SEP-2001; 2001US-0946374.
PR      15-JAN-2002; 2002US-0052586.

```

(GETH ) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI, 2003-332039/31.  
P-PSDB; AB067588.

New secreted and transmembrane PRO polypeptides and nucleic acids,  
useful in gene therapy, in chromosome and gene mapping, as chromosome  
markers, in tissue typing, and in chromosome identification

Claim 2; Fig 365; 706pp; English.

The invention discloses human nucleic acids encoding secreted and  
transmembrane (PRO) polypeptides. Also disclosed is an antibody that  
specifically binds to the PRO polypeptide, a method for stimulating the  
release of tumour necrosis factor alpha (TNF-alpha) from human blood by  
contacting the blood a PRO polypeptide, a method for stimulating the  
proliferation or differentiation of chondrocyte cells by contacting the  
cells with a PRO polypeptide, a method for detecting the presence of a  
tumour in a mammal and an oligonucleotide probe derived from any of the  
PRO nucleotide sequences. The nucleotide sequences are useful as probes,  
in chromosome and gene mapping, in generating antisense RNA and DNA, in  
preparing PRO polypeptides by recombinant techniques and in gene therapy  
(e.g. for replacement of defective gene). The PRO polypeptides are useful  
as molecular weight markers for protein electrophoresis purposes, for  
chromosome identification, as chromosome markers, as therapeutic agents,  
for stimulating the release of TNF-alpha from human blood, for  
stimulating the proliferation or differentiation of chondrocytes and  
detecting the presence of a tumour. The PRO polypeptides and nucleic  
acids may also be used diagnostically for tissue typing. The sequences  
presented in ACA05700-ACA06004 are the cDNAs encoding the PRO  
polypeptides of the invention.

Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 25; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 1.7e-251;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 GGAGAGAGGCGCGGGGTGAAGGCGCATGTATGACGCTTGGCGGCGCTCGAGCGCG 60
        |||
DB      1 GGAGAGAGGCGCGGGGTGAAGGCGCATGTATGATGACGCTTGGCGGCGCTCGAGCGCG 60

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 12:23:44 ; Search time 2967 Seconds

(without alignments)  
10296.841 Million cell updates/sec

Title: US-09-938-418-2

Perfect score: 1257  
Sequence: 1 ggaagagagcgcgcggtga.....ataaaattatccaca 1257

Scoring table: IDENTITY\_NTC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estdb:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estrov:\*  
6: em\_estropl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_hiv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_ping:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252.2	99.6	1288	11	BC021025
2	999	79.5	1201	9	AL532456
3	951.8	75.7	1190	9	AL575307
4	946.6	75.3	1201	9	AL564395

5	914.2	72.7	1201	9	AL551834
6	861.6	68.5	1201	13	BX387691
7	842.6	67.0	1201	13	BX387690
8	842.2	67.0	1132	12	BM560093
9	815.2	64.9	903	12	BT763295
10	811.2	64.5	887	9	AL544722
11	739.4	58.8	851	13	BQ425266
12	716.4	57.0	922	13	BQ425098
13	705.4	56.1	1037	12	BM15926
14	700.4	55.7	747	14	CA115410
15	695.6	55.3	796	12	BQ008675
16	693.2	55.1	734	14	BX114800
17	691	55.0	723	14	CA431413
18	690	54.9	724	12	BQ009009
19	682.2	54.3	716	14	CA413294
20	682	54.3	702	12	BQ010155
21	681.4	54.2	683	10	BE607413
22	681.4	54.2	683	10	BE607414
23	679.8	54.1	837	9	AL570753
24	679.6	54.1	949	9	AL553798
25	679	54.0	730	13	BT729033
26	678.2	54.0	1099	12	BM15288
27	672.6	53.5	986	13	BQ48112
28	672.4	53.5	1046	13	BX386416
29	672.2	53.5	902	13	BQ424201
30	658.2	52.4	1161	11	AK003674
31	655.4	52.1	723	12	BQ005403
32	651.6	51.8	1168	11	AK076498
33	649.8	51.7	671	13	BQ624465
34	641.8	51.1	688	10	BE387335
35	641	51.0	688	10	BE896915
36	637.4	50.7	1045	13	BX386415
37	633.8	50.4	654	13	BQ624261
38	629.2	50.1	956	9	AL553771
39	608.8	48.4	798	14	CB959810
40	606.2	48.2	1023	10	BG421228
41	597	47.5	849	14	CB201936
42	581.4	46.3	610	12	BC013605
43	577	45.9	814	14	CB991371
44	569.6	45.3	617	13	BQ574527
45	567.4	45.1	569	9	AM071610

#### ALIGNMENTS

RESULT 1  
LOCUS BC021025 1288 bp mRNA  
DEFINITION Homo sapiens, clone IMAGE:3617432, mRNA.  
ACCESSION BC021025  
VERSION BC021025.1 GI:18045042  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: ATCC/DCPD/TPP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amadan@systemsbiology.org](mailto:amadan@systemsbiology.org)

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
 Series: IRAL Plate: 24 Row: 1 Column: 7  
 This clone was selected for full length screening because it passed the following selection criteria: Hexamer frequency ORF analysis  
 This clone has the following problem: no cloning site / microdeletion.

FEATURES  
 source location/Qualifiers

1..1288  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3617432"  
 /issue\_type="Skin, melanotic melanoma."  
 /clone\_lib="NHL\_MGC\_20"  
 /lab\_host="DH10B-R"  
 /note="Vector: pOTB7"  
 BASE COUNT 346 a 268 c 303 g 371 t  
 ORIGIN

Query Match 99.6%; Score 1252.2; DB 11; Length 1288;  
 Best Local Similarity 99.8%; Pred. No. 3.1e-198;  
 Matches 1234; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGAGAGAGCGCGGGGTGAAGGCGCATGTGATGACGCTCGCGCGCTCGAGCGCGG 60  
 6 GGAGAGAGCGCGGGGTGAAGGCGCATGTGATGACGCTCGCGCGCTCGAGCGCGG 65  
 61 CGAGAGAGCGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 66 CGAGAGCGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125  
 121 CCCGAGAGCGCGGGGTGAAGGCGCATGTGACGCTCGCGCGCTCGAGCGCGG 180  
 126 CCCGAGAGCGCGGGGTGAAGGCGCATGTGACGCTCGCGCGCTCGAGCGCGG 185  
 181 GCGTCTGCT 240  
 186 GCGTCTGCT 245  
 241 AGGAGAGCGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
 246 AGGAGAGCGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 305  
 301 GCTTACAGAGCGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
 306 GCTTACAGAGCGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 365  
 361 CGGATACAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
 366 CGGATACAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 425  
 421 GGGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
 426 GGGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 485  
 481 ATTATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
 486 ATTATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545  
 541 GTGCTAAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 546 GTGCTAAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 605  
 601 AGCGTTGATTTACATTTCAATGAGAGTGTTCAGACCTCTCTCTCTCTCTCTCT 660  
 606 AGCGTTGATTTACATTTCAATGAGAGTGTTCAGACCTCTCTCTCTCTCTCTCT 665  
 661 TAATTATTGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720

|||||  
 666 TAATTATTGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 725  
 721 CTTCTGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 726 CTTCTGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 785  
 781 TTGCACTGTTGAGATTTACCAAAAGAGAGTCTTCTCTGATGAGATTCAGTTCTC 840  
 786 TTGCACTGTTGAGATTTACCAAAAGAGAGTCTTCTCTGATGAGATTCAGTTCTC 845  
 841 GCATCATTTATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
 846 GCATCATTTATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 905  
 901 TTATTTAGCGCTTGAATGCTTCACTTAAATGACATTTTAAATGATTTATGATACAT 960  
 906 TTATTTAGCGCTTGAATGCTTCACTTAAATGACATTTTAAATGATTTATGATACAT 965  
 961 GAATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020  
 966 GAATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1025  
 1021 ATCTAGCATTTATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080  
 1026 ATCTAGCATTTATGAGAGCGGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1085  
 1081 AGAATACCTTCTCTGATGACATTTCTCTCACTTAAATGATTTATGATACATTT 1140  
 1086 AGAATACCTTCTCTGATGACATTTCTCTCACTTAAATGATTTATGATACATTT 1145  
 1141 TTGCTTTTCTCTGATGACATTTCTCTCACTTAAATGATTTATGATACATTT 1200  
 1146 TTGCTTTTCTCTGATGACATTTCTCTCACTTAAATGATTTATGATACATTT 1205  
 1201 AATTGTAAATGATTTATGATTTCTCTCACTTAAATGATTTATGATACATTT 1257  
 1206 AATTGTAAATGATTTATGATTTCTCTCACTTAAATGATTTATGATACATTT 1262

RESULT 2  
 AL532456 1201 bp mRNA linear EST 23-MAY-2003  
 LOCUS AL532456 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
 DEFINITION CS0DM014YN20 5-PRIME, mRNA sequence.  
 VERSION AL532456  
 ACCESSION AL532456.2 GI:31070288  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayres, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12795949.  
 Contact: Genoscope  
 BP 191 91006 Evry cedex - France  
 Email: [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 4941.f for  
 more information about this cluster, see  
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DM014G100P1&cluster=4941.f>  
 Feng Liang Email: [filiang@lifetech.com](mailto:filiang@lifetech.com) URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID: CS0DM014G100P1.

FEATURES  
 source location/Qualifiers  
 1..1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

```

/db_xref="taxon:9606"
/clone="CSODM01.4YN20"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

```

Query Match	79.5%	Score 999	DB 9	Length 1201
Best Local Similarity	96.2%	Pred. NO. 3.6e-156		
Matches 1059	Conservative 15	Mismatches 20	Indels 7	Gaps 5

QY	140	GCAGACCAGGAGCCCGCGCCCTCCCGGAGGCGCCCGCGCCTCTCGTGGCTCGCT	199
Db	60	GGCGCCCCAGGGCCCCCGCCGCTCCCGCGAGCGGCTCCCGGCTCTCTGCTCTCTGCT	119
QY	200	GCTGCAGCTGCCCGCGCCGCTGAGCGCCTGTAGATCCCCAAAGGGAGCAAAAGCGCA	259
Db	120	GCTGAGCTGCCCGCGCCGCTGAGCGCCTGTAGATCCCCAAAGGGAGCAAAAGGSGCA	179
QY	260	GCTCCGCGAGAGGAGGCTGTGTGTGACCTGTATATAGGAATGTGCTTACAAAGGCCACAGG	319
Db	180	G-TCCGGAGAGGGAGGTGTGTGACCTGTATATAGGAATGTGCTTACAAAGGGCCACAGG	238
QY	320	AGTGCCTGTGTGAGAGCGGAGCCCTGGGGCCCAATGTATTATCCGGGATACCTGGATGCC	379
Db	239	AGTGCCTGTGTGAGAGCGGAGCCCTGGGGCCCAATGTGATCCCGGTACACTGTGGATCCC	298
QY	380	AGTGGGAGTGGATTCAAAAGGAGAAAAGGGGGAATGCTGTAGAGGAAAGCTTTGAGAGTC	439
Db	299	AGTGGGAGTGGATTCAAAAGGAGAAAAGGGGGAATGCTGTAGAGGAAAGCTTTGAGAGTC	358
QY	440	CTGAGACACCCACTCTACAGCAGTGTCTCATGTGAGTTCATGTGATTAAGCATAGATCTTGG	499
Db	359	CTGAGACACCCACTCTACAGCAGTGTCTCATGTGAGTTCATGTGATTAAGCATAGATCTTGG	418
QY	500	GAATATTCGCGAGTGTACATTTTACAAAGATGGCTTCAATATGCTCTCTAAAGATTTTGT	559
Db	419	GAATATTCGCGAGTGTACATTTTACAAAGATGGCTTCAATATGCTCTCTAAAGATTTTGT	478
QY	560	CATGTGCTCACTTGTGGCTTAAAAATGACAGAAATGCAATGCTGTCAAGCTGTATTTACAT	619
Db	479	CATGTGCTCACTTGTGGCTTAAAAATGACAGAAATGCAATGCTGTCAAGCTGTATTTACAT	538
QY	620	CAATGAGACTCAATGTATTAGACACCTCTCCCATTTAGAGCTATAATTTATTTGGACCAAG	679
Db	539	CAATGAGACTCAATGTATTAGACACCTCTCCCATTTAGAGCTATAATTTATTTGGACCAAG	598
QY	680	AAGCCCTGAAATGAATTCACAAATTAATTCATGCGACTTCTGTGTGGAAGGACTTTG	739
Db	599	AAGCCCTGAAATGAATTCACAAATTAATTCATGCGACTTCTGTGTGGAAGGACTTTG	658
QY	740	TGAAGGAATTTGCTGTGTATAGTGTGATGTCTCATGTGGGTTGGGCACTTGTTCAGATTA	799
Db	659	TGAAGGAATTTGCTGTGTATAGTGTGATGTCTCATGTGGGTTGGGCACTTGTTCAGATTA	718
QY	800	CCCAAAAGAGATGCTTCTACGTAGTGAATTCAGTTCTCCATCATTAATTTGAAGAACT	859
Db	719	CCCAAAAGAGATGCTTCTACGTAGTGAATTCAGTTCTCCATCATTAATTTGAAGAACT	778
QY	860	ACCAAAATTAATTTGCTTAAATTTTCATTTTGTACCTCTTTTATTAATGCTTGTGAATG	919
Db	779	ACCAAAATTAATTTGCTTAAATTTTCATTTTGTACCTCTTTTATTAATGCTTGTGAATG	838
QY	920	TTCACTTAAATGACATTTTAAATTAAGTTATATATACATATCAATGAAAGAAAGCAACTAA	979
Db	839	TTCACTTAAATGACATTTTAAATTAAGTTATATATACATATCAATGAAAGAAAGCAACTAA	898

Oy	980	TTATGTTACAGACCAAGGTGATTCACACTGTTTTAAATCAGATTAATCATTTT	1039
Db	899	ATAAGTTACAGACCAAGGTGATTCACACTGTTTTAAATCAGATTAATCATTTT	958
Oy	1040	GCTTCATCAAAAGTGTTTCATATTTTTTTTAAAGTGTAGATACTTCTCATAGT	1099
Db	959	GCTTCATCAAAAGTGKTTCTAAATTTTTTTTAAAGTGTAGATACTTCTCATAGT	1018
Oy	1100	CACATTCGCGACCTAATTAATTTGGAATATGTGTGTGTTGTTTCTCTGATA	1159
Db	1019	CACAT--CTCGACACTAATTAATTTGGRANATGTGTGTGTC--TTTGKTTTGCTCTTGAKA	1075
Oy	1160	TAGCATTTTTAAAAAATATAAAGCTAACCAATCTTGTACAAATTTGTAATGTTAAGAA	1219
Db	1076	TAGCATTTTTAAAAAATATAAAGC--GCCAATCTTTTACAA--TTTGTATGTTAAGAT	1132
Oy	1220	TTTTTTTAAATCTGTAAAT	1240
Db	1133	TTTTTTTAAATCTGTAAAT	1153

RESULT 3	AL575307/c	1190 bp	mRNA	linear	EST 01-JUN-2003
LOCUS	AL575307				
DEFINITION	AL575307 Homo sapiens PLAGENRA COT 25-NORMALIZED Homo sapiens cDNA clone CSOD1061YA20 3-PRIME, mRNA sequence.				
ACCESSION	AL575307				
VERSION	AL575307.2	GI:31313615			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	On Feb 16, 2001 this sequence version replaced gi:12936346.				
COMMENT	Unpublished				

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologists, a division of  
Invitrogen. This sequence belongs to sequence cluster 4941.f For  
more information about this cluster, see  
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cg4-bln/cluster.cg4?seq=CS0D1061BA10NP1a&cluster=4941.f)  
Peng Liang Email : [liangell@etech.com](mailto:liangell@etech.com) URL :  
<http://fulllength.invitrogen.com/invitrogen/cluster/1600>  
Faraday Avenue genoscope sequence ID : CS0D1061BA10NP1.

```

FEATURES
    source
        1. .1190
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS010617A20"
                /issue_type="PLACENTA COT 25-NORMALIZED"
                /clone_1b="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with NotI and cloned into the NotI and EcoRV
                    sites of the pCMVSPORT 6 vector. Library was normalized."
            370 a
                248 c
                    212 g
                        321 t
                            39 others
BASE COUNT
ORIGIN

```

Query Match	75.7%	Score 951.8	DB 9	Length 1190
Best Local Similarity	95.6%	Pred. No. 2.5e-148		
Matches 992	Conservative 5	Mismatches 38	Indels 3	Gaps 2

  

Oy	199	TGCTGCAGC	CCCCGCGCCCTCGAGCGCCTTCGTGAGATCC	CCCAAGGGGAGCAAAAGGCGC	258
Ob	1037	TTTCGGYSTC	CAATGCGCCCGCGCGCGCTTATGATCTCCCAAGGAGCAAAAGGCGC	978	

QY 259 AGCTCCGCGAGAGGAGGAGTGGACCTGTATATATGAAATGTCTTACAAAGGCCACAG 318  
 Db 977 AGCTCCGCGAGAGGAGTGGT-GACTGTATATATGAAATGTCTTACAAAGGCCACAG 919  
 QY 319 GAGTGCCTGGTTCAGAGCGGAGCCCTGGGCGCAATGTATTCGGGTACACCTGGATCC 378  
 Db 918 GAGTGCCTGGTTCAGAGCGGAGCCCTGGGCGCAATGTATTCGGGTACACCTGGATCC 859  
 QY 379 CAGGTGGGATGATTCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438  
 Db 858 CAGGTGGGATGATTCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 799  
 QY 439 CCGGACACCCACTCAACAGCTGTCAGAGTGTATGAAATATGAGATAGATCTTG 498  
 Db 798 CCGGACACCCACTCAACAGCTGTCAGAGTGTATGAAATATGAGATAGATCTTG 739  
 QY 499 GGAATATGCGAGATGATTCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 558  
 Db 738 GGAATATGCGAGATGATTCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 679  
 QY 559 TCAGTGGCTCAGTGGCTTAAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 618  
 Db 678 TCAGTGGCTCAGTGGCTTAAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 619  
 QY 619 TCATGAGAGCTGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 678  
 Db 618 TCATGAGAGCTGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 559  
 QY 679 GAAAGCCCTGAATGAATTCACAAATTAATATATGACAGCTCTCTGAGAGAGAT 738  
 Db 558 GAAAGCCCTGAATGAATTCACAAATTAATATATGACAGCTCTCTGAGAGAGAT 499  
 QY 739 GTAGAGAGATGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 798  
 Db 498 GTAGAGAGATGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 439  
 QY 799 ACCCAAGAGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 858  
 Db 438 ACCCAAGAGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 379  
 QY 859 TACCAAAATGAATGCTTAAATTTTCAATTTTCACTCTCTCTCTCTCTCTCTCT 918  
 Db 378 TACCAAAATGAATGCTTAAATTTTCAATTTTCACTCTCTCTCTCTCTCTCTCT 319  
 QY 919 GTTCACTTAAATGATTTTAAATAGTATGATGATGATGATGATGATGATGATGAT 978  
 Db 318 GTTCACTTAAATGATTTTAAATAGTATGATGATGATGATGATGATGATGATGAT 259  
 QY 979 AATATGTTTACAGAT 1038  
 Db 258 AATATGTTTACAGAT 199  
 QY 1039 TCGTCAATCAAAAGAGTTCATATTTTCTAGTGTAGATGATGATGATGATGATGAT 1098  
 Db 198 TCGTCAATCAAAAGAGTTCATATTTTCTAGTGTAGATGATGATGATGATGATGAT 139  
 QY 1098 TCGTCAATCAAAAGAGTTCATATTTTCTAGTGTAGATGATGATGATGATGATGAT 1158  
 Db 138 TCGTCAATCAAAAGAGTTCATATTTTCTAGTGTAGATGATGATGATGATGATGAT 79  
 QY 1159 ATAGCATTTTAAAGAGTTCATATTTTCTAGTGTAGATGATGATGATGATGATGAT 1216  
 Db 78 ATAGCATTTTAAAGAGTTCATATTTTCTAGTGTAGATGATGATGATGATGATGAT 19  
 QY 1217 GAATTTTCTATATCTG 1234  
 Db 18 AATTTTCTATATCTD 1

RESULT 4  
 AL564395 1201 bp mRNA linear EST 31-MAY-2003  
 LOCUS AL564395 Homo sapiens FETAL LIVER Homo sapiens CDNA clone  
 DEFINITION

ACCESSION CS0DM014YN20 3-PRIME, mRNA sequence.  
 VERSION AL564395  
 KEYWORDS GI:31288373  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS L.W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12914757.  
 CONTACT Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4941.f For more information about this cluster, see:  
 http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CS0DM014DGI0NP1&cluster=4941.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DM014DGI0NP1.  
 Location/Qualifiers  
 1..1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DM014YN20"  
 /rname="FETAL LIVER"  
 /dev\_stage="fetal"  
 /clone\_1b="Homo sapiens FETAL LIVER"  
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."  
 BASE COUNT 346 a 249 c 238 g 336 t 32 others  
 ORIGIN  
 Query Match 75.3% Score 946.6; DB 9; Length 1201;  
 Best Local Similarity 93.9%; Pred. No. 1-be-147;  
 Matches 1028; Conservative 9; Mismatches 53; Indels 5; Gaps 5;  
 QY 127 AGCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 186  
 Db 1091 AGAGGTGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1032  
 QY 187 TGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246  
 Db 1031 CTCTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974  
 QY 247 AGCAAAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 306  
 Db 973 AGCAAAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 915  
 QY 307 AAGGGCAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 366  
 Db 914 AAGGGCAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 855  
 QY 367 CACCTGGAGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGAT 426  
 Db 854 CACCTGGAGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGAT 795  
 QY 427 GCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486  
 Db 794 GCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 735  
 QY 487 GCATAGATCTTGGGAAATTTGGGAGATGATCATTTCAAAAGATGATGATGATGATGATGAT 546  
 Db 734 GCATAGATCTTGGGAAATTTGGGAGATGATCATTTCAAAAGATGATGATGATGATGATGAT 675



OY	547	TTAAGAGTTTGTTCAGTGGCTCACTTGC - GGTAAATGACAAATATGCATGTCAGGCT	605
Db	674	TAAAGTTTTTTTAAGTGGCTCACTTGCCTTAAATATGCAAAATGATGCTGTCAGGCT	615
OY	606	TGATATTTCACATTCATGAGTGAAGTGTACAGAGCTCTTCCATATGAAGCTAATAT	665
Db	614	TGATATTTCACATTCATGAGTGAAGTGTACAGAGCTCTTCCATATGAAGCTAATAT	555
OY	666	TATTTTGGACCAAGAGAGCCCTGAATATGATTTCAACAATTAATATTCATGACACTTCTCT	725
Db	554	TATTTTGGACCAAGAGAGCCCTGAATATGATTTCAACAATTAATATTCATGACACTTCTCT	495
OY	726	GTGAGAGACTTTGGAAGAAATTTGGTCGTCGATTTAGTGAATGTGTGATATCGGTGTGGC	785
Db	494	GTGAGAGACTTTGGAAGAAATTTGGTCGTCGATTTAGTGAATGTGTGATATCGGTGTGGC	435
OY	786	ACTTGTTCAGATTAACCCAAAGAGATGCTTCTACTGTGATGAATTCAGTTTCTGCAATC	845
Db	434	ACTTGTTCAGATTAACCCAAAGAGATGCTTCTACTGTGATGAATTCAGTTTCTGCAATC	375
OY	846	ATTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTTCTACTCTTTTATATTT	905
Db	374	ATTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTTCTACTCTTTTATATTT	315
OY	906	ATGCTCTGGATGGTTCCTTAATATGACATTTTAAATAGTTTATAGTATACATTCGATATG	965
Db	314	ATGCTCTGGATGGTTCCTTAATATGACATTTTAAATAGTTTATAGTATACATTCGATATG	255
OY	966	AAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGATTTTCACACTGTTTTAAATCTA	1025
Db	254	AAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGATTTTCACACTGTTTTAAATCTA	195
OY	1026	GCATTTATTCATTTTGCCTTCATTCACAAATGGTTTCAATTTTTTTTAAAGTTAGTTAGAT	1085
Db	194	GCATTTATTCATTTTGCCTTCATTCACAAATGGTTTCAATTTTTTTTAAAGTTAGTTAGAT	135
OY	1086	ACTTTCTTCATAGTCACATTCCTCAACCCATTAATTTGGAATATTTGTGTGGCTTTTGT	1145
Db	134	ACTTTCTTCATAGTCACATTCCTCAACCCATTAATTTGGAATATTTGTGTGGCTTTTGT	75
OY	1146	TTTTTCTCTAGTATAGCATTTTAAAAAAATATAAAAAGCTACCAATCTTTGTACAAATTT	1205
Db	74	TTTTTCTCTAGTATAGCATTTTAAAAAAATATAAAAAGCTACCAATCTTTGTACAA - TW	16
OY	1206	GTAATGTTAGCAAT 1220	
Db	15	GTAAGKTTTAAAGAT 1	
RESULT 5			
LOCUS	AL551834	1201 bp	linear
DEFINITION	AL551834 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION	AL551834		
VERSION	AL551834.2		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1201)		
JOURNAL	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished		
	On Feb 15, 2001 this sequence version replaced gi:12890161.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 91006 EVRY cedex - France		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	Library was constructed by Life Technologies, a division of		
	Invitrogen. This sequence belongs to sequence cluster 4941.f For		

```

FEATURES
SOURCE
    more information about this cluster, see
    http://www.genoscope.cns.fr/
    cgi-bin/cluster/cgi1seq?CSODI061BA100plac1cluster=4941.f. Contact :
    Feng Liang Email : fliang@lifetech.com URL :
    http://fullengh.invitrogen.com/invitrogen Corporation 1600
    Faraday Avenue Genoscope sequence ID : CSODI061BA100pl.
    Location/Qualifiers
        1. 1201
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSODI061YA20"
            /issue_type="PLACENTA COT 25-NORMALIZED"
            /clone_1lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
    307 a      258 c      287 g      327 t      22 others
ORIGIN

```

Query Match	72.7%	Score 91.4/2	DB 9	Length 1201
Best Local Similarity	94.8%	Pred. No. 4.4e-142		
Matches	983	Conservative	5	Mismatches 40
			Indels	9
			Gaps	4
QY	45	CGGCGCTGGAGCGGGCGGAGCCAGACGCTGACACAGCTTCCTCTCTCTCGTCTCTCCGCGC	104	
DB	61	CGGAGTGGAGCGGGCGGGCGGNACAGACGTCGACCAAGTTCCTCTCTCGTCTCTCCGCGC	120	
QY	105	CTCCAGCTCCCGCGCTGCCCCGGGCGAGCCGGGAGCCATGCGACCCCAAGGCCCGCGCGCTCC	164	
DB	121	CTCCAGCTCCCGCGCTGCCCCGGGCGAGCCGGGAGCCCAAGCCCAAGGCCCGCGCGCTCC	180	
QY	165	CCGCGAGCGGCTCCGCGGCGCTCTGCTGCTCTGCTGCTGCGAGCTCCCGCGCGCTCCGAGC	224	
DB	181	CCGCGAGCGGCTCCGCGGCGCTCTGCTGCTCTGCTGCTGCGAGCTCCCGCGCGCTCCGAGC	240	
QY	225	GCTCTGTGAGATCCCCAGGGGAGCAAAAGGCGCAGCTCCGCGCAGAGGAGGTGGTGGAC	284	
DB	241	GCTCTGTGAGATCCCCAGGGGAGCAAAAGGCGCA - CTCGCGCAGAGGAGGTGGTGGAC	299	
QY	285	CTGTATATGGAATGTGCTTACAAAGGCGCAGCAGAGATGCTGTGCTCGAGAGCGGAGCCCT	344	
DB	300	CTGTATATGGAATGTGCTTACAAAGGCGCAGCAGAGATGCTGTGCTCGAGAGCGGAGCCCT	359	
QY	345	GGGCGCAATGTATTCGGGGTACACCTGGGAGTCCGAGTCCGGGATGGATTCAAAGAGAA	404	
DB	360	GGGCGCAATGTATTCGGGGTACACCTGGGATCCGAGTCCGGGATGGATTCAAAGAGAA	419	
QY	405	AAGGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCTGTGACACCACACTACAGCAGTGT	464	
DB	420	AAGGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCTGTGACACCACACTACAGCAGTGT	479	
QY	465	TCATGAGTTCATTTGATTTATGCGATACATCTTGGGAAAATTGCGGAGTTCATTTACA	524	
DB	480	TCATGAGTTCATTTGATTTATGCGATACATCTTGGGAAAATTGCGGAGTTCATTTACA	539	
QY	525	AAGATGCGCTCAAAATAGTGTCTAAGATTTTGTCACTGGGCTCACTTCGGCTAAATAGC	584	
DB	540	AAGATGCGCTCAAAATAGTGTCTAAGATTTTGTCACTGGGCTCACTTCGGCTAAATAGC	599	
QY	585	AGAATGCGATCTGTCAAGCTGTGGATTTTACATTCATTTGAGAGCGAATGTTCAAGACTT	644	
DB	600	AGAATGCGATCTGTCAAGCTGTGGATTTTACATTCATTTGAGAGCGAATGTTCAAGACTT	659	
QY	645	CTTCCCATTTGAAGCTATATTTATTTTGGACCAAGGAGCCCTGAATGAATTTCAACAATT	704	
DB	660	CTTCCCATTTGAAGCTATATTTATTTTGGACCAAGGAGCCCTGAATGAATTTCAACAATT	719	
QY	705	AATATTCATGCGACTTCTGTGTGGAGAGACTTGTGGAAGGAATGTGGTGGATTTAGTG	764	
DB	720	AATATTCATGCGACTTCTGTGTGGAGAGACTTGTGGAAGGAATGTGGTGGATTTAGTG	779	

QY 765 GATGTCCTATCTGGGTTGGACATCTTGTGATTAACCAAAAGAGATGCTTCTACTGA 824  
 DB 780 GAGTGTGCTATCTGGGTTGGACATCTTGTGATTAACCAAAAGAGATGCTTCTACTGA 839  
 QY 825 TGAATTCAGTTCCTGATCATATTAAGAAATACCAAAATTAATGCTTAAATTTCA 884  
 DB 840 TGAATTCAGTTCCTGATCATATTAAGAAATACCAAAATTAATGCTTAAATTTCA 899  
 QY 885 TTGCTACGCTCTTTTAAATGAGTTCGATTAAGTTCATTAATGATTTAAATTA 944  
 DB 900 TTGCTACGCTCTTTTAAATGAGTTCGATTAAGTTCATTAATGATTTAAATTA 959  
 QY 945 GTTATATATACATCTTAATGAAGAAAGCAATTAATGCTTAAATGATTTAAATTA 1004  
 DB 960 GTTATATATACATCTTAATGAAGAAAGCAATTAATGCTTAAATGATTTAAATTA 1015  
 QY 1005 TTCACTGCTTTTAAATGAGTTCGATTAAGTTCATTAATGATTTAAATTA 1064  
 DB 1016 ATTTTMCCTGCTTTTAAATGAGTTCGATTAAGTTCATTAATGATTTAAATTA 1071  
 QY 1065 TTTTCTTCTGCTGTTA 1081  
 DB 1072 TTTTCTGCTGCTGTTA 1088  
 RESULT 6  
 BX387691 1201 bp mRNA linear EST 08-MAY-2003  
 LOCUS BX387691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION clone CSOD1037YD19 5-PRIME, mRNA sequence.  
 ACCESSION BX387691  
 VERSION BX387691.1 GI:30461701  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4941.f For more information about this cluster, see  
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOA1037CB100P1&cluster=4941.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOA1037CB100P1.  
 location/Qualifiers  
 1. 1201  
 /organism="Homo sapiens"  
 /mol\_type="RNA"  
 /db\_xref="taxon:9606"  
 /clone="CSOD1037YD19"  
 /issue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NOTI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  
 BASE COUNT 286 a 257 c 274 g 306 t 78 others  
 ORIGIN  
 Query Match 68.5%; Score 861.6; DB 13; Length 1201;  
 Best Local Similarity 95.7%; Pred. NO. 2,4e-133;  
 Matches 915; Conservative 10; Mismatches 26; Indels 5; Gaps 4;  
 QY 45 CGGCTCGGAGCGCGGCGGAGCCAGACGCTGACCACTTCTCTCTCGGCTCTCTCGC 104

DB 57 CGGATCGGAGCGGGGGA -CAAGACGCTGACACGTTCTCTCTCTCTCTCTCTCTCT 115  
 QY 105 CTCAGCTCCGCGCTGCGCGGACGCGGAGCCATGAGACCCCGGCGCGCGCTCC 164  
 DB 116 CTCAGCTCCGCGCTGCGCGGACGCGGAGCCATGAGACCCCGGCGCGCTCC 175  
 QY 165 CCGAGCGGCTCCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 224  
 DB 176 CCGAGCGGCTCCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 235  
 QY 225 GCTCTGAGATCCCGAGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAC 284  
 DB 236 GCTCTGAGATCCCGAGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAC 294  
 QY 285 CTGATATATGGAATGCTTACCAAGGCGACAGAGAGTGCCTGTGAGAGCGGAGCT 344  
 DB 295 CTGATATATGGAATGCTTACCAAGGCGACAGAGAGTGCCTGTGAGAGCGGAGCT 354  
 QY 345 GGGGCCAATGTTATTCGGGTCACCTGGGATCCAGGTCGGGATGATTCAGAGAA 404  
 DB 355 GGGGCCAATGTTATTCGGGTCACCTGGGATCCAGGTCGGGATGATTCAGAGAA 414  
 QY 405 AAGGGGAATGCTGAGGAAAGCTTGGAGAGTCTGAGACCCCACTACAGACATGT 464  
 DB 415 AAGGGGAATGCTGAGGAAAGCTTGGAGAGTCTGAGACCCCACTACAGACATGT 474  
 QY 465 TCATGAGATCATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 524  
 DB 475 TCATGAGATCATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 534  
 QY 525 AAGATGCTCAATAGTGTCTAAGAGTTTGTTCAGTGGCTCCTCGCTAAATATGC 584  
 DB 535 AAGATGCTCAATAGTGTCTAAGAGTTTGTTCAGTGGCTCCTCGCTAAATATGC 594  
 QY 585 AGAATGATGCTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 644  
 DB 595 AGAATGATGCTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 654  
 QY 645 CTTCCTCAATGAGTAAATTTATTTGAGCAAGGAGCCCTGAAATGATTCACATTT 704  
 DB 655 CTTCCTCAATGAGTAAATTTATTTGAGCAAGGAGCCCTGAAATGATTCACATTT 714  
 QY 705 AATATTCATGACACTTCTCTGAGAGGACTTGTGAAGAAATGCTGTGATTAAGTG 764  
 DB 715 AATATTCATGACACTTCTCTGAGAGGACTTGTGAAGAAATGCTGTGATTAAGTG 774  
 QY 765 GATGTCCTATCTGGGTTGGACATCTTGTGATTAACCAAAAGAGATGCTTCTACTGA 824  
 DB 775 GATGTCCTATCTGGGTTGGACATCTTGTGATTAACCAAAAGAGATGCTTCTACTGA 834  
 QY 825 TGAATTCAGTTCCTGATCATATTAAGAAATACCAAAATTAATGCTTAAATTTCA 884  
 DB 835 TGAATTCAGTTCCTGATCATATTAAGAAATACCAAAATTAATGCTTAAATTTCA 894  
 QY 885 TTGCTACGCTCTTTTAAATGAGTTCGATTAAGTTCATTAATGATTTAAATTA 944  
 DB 895 TTGCTACGCTCTTTTAAATGAGTTCGATTAAGTTCATTAATGATTTAAATTA 953  
 QY 945 GTTATATATACATCTTAATGAAGAAAGCAATTAATGCTTAAATGATTTAAATTA 1000  
 DB 954 GTTATATATACATCTTAATGAAGAAAGCAATTAATGCTTAAATGATTTAAATTA 1007  
 RESULT 7  
 BX387690/c 1201 bp mRNA linear EST 08-MAY-2003  
 LOCUS BX387690 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION clone CSOD1037YD19 3-PRIME, mRNA sequence.  
 ACCESSION BX387690  
 VERSION BX387690.1 GI:30461700  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

REFERENCE	ADTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 1201)	L1,W.B., Gruber,C., Jessee,J. and Polays,D.	Full-length cDNA libraries and normalization	Unpublished
				Contact: Genoscope
				Genoscope - Centre National de Sequencage
				BP 191 91006 EVRY cedex - France
				Email: seqref@genoscope.cns.fr, Web : ww.genoscope.cns.fr
				Library was constructed by life technologies, a division of
				Invitrogen. This sequence belongs to sequence cluster 4941.f for
				more information about this cluster, see
				http://www.genoscope.cns.fr/
				cgl-bin/cluster.cgl?seq=CSOA1037CB10NP1&cluster=4941.f. Contact :
				Feng Liang Email : liangq@life.technet.com URL :
				http://fulllength.invitrogen.com/ invitrogen Corporation 1600
				Faraday Avenue Genoscope sequence ID : CSOA1037CB10NP1.
				Location/Qualifiers
				1. 1201
				/organism="Homo sapiens"
				/mol_type="mRNA"
				/db_xref="taxon:9606"
				/clone="CSOD1037YD19"
				/cissue_type="PLACENTA COT 25-NORMALIZED"
				/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
				/note="1st strand cDNA was primed with a NotI-oligo(dT)
				primer. Five prime end enriched, double-strand cDNA was
				digested with Not I and cloned into the Not I and EcoR V
				sites of the pCMVSPORT 6 vector. Library was normalized."
				BASE COUNT
				358 a 232 c 212 g 308 t 91 others
				ORIGIN
				Query Match
				Best Local Similarity 85.6%; Score 842.6; DB 13; Length 1201;
				Matches 946; Conservative 22; Mismatches 129; Indels 8; Gaps 4
QY	146	CCAGGCCCCC	CGCCCTCCCGCCAGCGGCTCCGCGGCTCCTGCTGCTCTGCTCTGCTCA	205
Db	1097	YCGVGTSC	CRAKGCGACCATSTACCCAGCGCCGCTCCCGTAGCGSTGCGGCTCTG	1033
QY	206	GCTGCCCG	CGCCCTGCGAGCGCTTGAGATCCCAAGGGAAGCAAAAGCGCAGCTCCG	265
Db	1037	CGCTCWC	GTSGCRAGCGCGCTTCBCCTTAKATCCCAAGGAAGCAAAAGCGCAG	978
QY	266	CAGAGGAG	GAGTGCGACTGTAAATGAGATGCTTACAAAGGGCCAGCAGAGGCTCC	325
Db	977	CCGCGC	AGCAGAGTGTSGTGACCTATATATGATGTGCT--ACAGGGCCAGCAKAGTCC	920
QY	326	TGTCGAG	ACGCGGAGCCCTGGGGCCCAATGTATTCGGGTACACCTGGGATCCAGGTGC	385
Db	919	TG--	--TGATACGGAGCCCTGGGCAATGGCATTCGGK--ACACCTGATCCAGGTGC	865
QY	386	GGATGGA	TTCACAGCAAAAGGGGGAATGCTGAGGAAAGCTTGAAGAGTCTCGAC	445
Db	864	GGAT	--GATTCACAGCAAAAGGGGGAATGCTGAGGAAAGCTTGAAGAGTCTCGAC	806
QY	446	ACCCAC	ACACAGAGGAGTTCATGGAGTTCATTTGAATATGAGCATAGATCTTGGGAAT	505
Db	805	ACCCMA	CTACAGCAGTGTTCATGGAGTTCATTTGAATATGAGCATAGATCTTGGGAAT	746
QY	506	TGCGAG	TGTACATTTACAAAGATGCGTTCAATAGTCTTAAGAGTTTGTTCAGTGG	565
Db	745	TGGGAG	TGTACATTTACAAAGATGCGTTCAATAGTCTTAAGAGTTTGTTCAGTGG	686
QY	566	CTCAGT	TGGCTAAATATGCAAAATGCATGCTGTACAGCGTTGGATTTACATTCATATG	625
Db	685	CTCAGT	TGGCTAAATATGCAAAATGCATGCTGTACAGCGTTGGATTTACATTCATATG	626
QY	626	AGCGAAT	TGTTCAGGAGCTTCCCATTTGAAGCTATATTTATTTGGACCAAGAAAGCC	685
Db	625	AGCGAAT	TGTTCAGGAGCTTCCCATTTGAAGCTATATTTATTTGGACCAAGAAAGCC	566

[illegible]

```

/db_xref="taxon:9606"
/clone_image="5476455"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(5). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
BASE COUNT      278 a      260 c      297 g      297 t
ORIGIN
Query Match      67.0%; Score 842.2; DB 12; Length 1132;
Best Local Similarity 96.1%; Pred. No. 4,1e-130;
Matches 895; Conservative 0; Mismatches 33; Indels 3; Gaps 3;
OY      52 GGACGGCGGGGAGCCAGACGCTGACACGCTTCCTCCTCCGCTCCGCTCAGC 111
      1 GGACGGCGGGGAGCCAGACGCTGACACGCTTCCTCCTCCGCTCCGCTCAGC 60
OY      112 TCCGCGCTGCCCGGCGGAGCCGATGCGAGCCCGGCGGCGCTCCGCGAGC 171
      61 TCCGCGCTGCCCGGCGGAGCCGATGCGAGCCCGGCGGCGCTCCGCGAGC 120
OY      172 GGCCTCCGCGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 231
      121 GGCCTCCGCGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 180
OY      232 AGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 291
      181 AGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
OY      292 ATGGAATGTGCTTCAAGGGCCAGCAGAGAGTGGCTGGCGAGGAGGAGGAGGAGG 351
      241 ATGGAATGTGCTTCAAGGGCCAGCAGAGAGTGGCTGGCGAGGAGGAGGAGGAGG 300
OY      352 ATGTTATTCGGGCTACACCTGGGATCCAGTCCGATGCGATGCGATGCGATGCG 411
      301 ATGTTATTCGGGCTACACCTGGGATCCAGTCCGATGCGATGCGATGCGATGCG 360
OY      412 AATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 471
      361 AATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
OY      472 GTTCATGAATTTATGAGATAGATCTTGGAATAATTTGCGAGTGTACATTTACAAGATGC 531
      421 GTTCATGAATTTATGAGATAGATCTTGGAATAATTTGCGAGTGTACATTTACAAGATGC 480
OY      532 GTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTCGGCTAAATATGCAAGATG 591
      481 GTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTCGGCTAAATATGCAAGATG 540
OY      592 CATGCTGTACGCTTGGTATTTTCAATTCATGAGCTGAATGTTTACAGAGCTTCCCA 651
      541 CATGCTGTACGCTTGGTATTTTCAATTCATGAGCTGAATGTTTACAGAGCTTCCCA 600
OY      652 TTGAAGCTAATTAATTTTGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 711
      601 TTGAAGCTAATTAATTTTGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
OY      712 ATCCGACTTCTCTGTGGAAGACTTTGTGAAGAAATTTGGTGTAGTATGATGTG 771
      661 ATCCGACTTCTCTGTGGAAGACTTTGTGAAGAAATTTGGTGTAGTATGATGTG 720
OY      772 CTATCTGGG-TTGGCACTTGTTCAGATTACCAAAAGAGATGCTTCTACTGATGAT 830
      721 CTATCTGGGTTGGCACTTGTTCAGATTACCAAAAGAGATGCTTCTACTGATGATGAT 780
OY      831 TCAGTTCTCGCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTGCT 890

```

```

|||||
Db      781 TCAGTTCTCGCATCATTTATGAAGAGCTACCCAAATATGCTTTAATTTTCAATTGCT 840
OY      891 ACCG-CTTTTATTAATGAGCTTGGAT-GGTCATTAATGACATTTAAATTAATGAT 948
      841 ACCGCTTTTATTAATGAGCTTGGATGAGTGTGATGATTAAGGACTTTTAAATTAATGAT 900
OY      949 ATGTTATCATCTGAATGAAAAAGCAAGCTTA 979
      901 TATGGAATTAACCTCGGAATGAAAAAGCAAA 931
Db
RESULT 9
BI763295
LOCUS
DEFINITION      903 bp mRNA linear EST 25-SEP-2001
603047656F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518069 5',
mRNA sequence.
BI763295
VERSION      BI763295.1 GI:15754873
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 903)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.lnl.gov
plate: LLM11469 row: 0 column: 14
High quality sequence stop: 875.
Location/Qualifiers
1. 903
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="518069"
/lab_host="DH10B"
/clone_id="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC library."
BASE COUNT      274 a      137 c      178 g      313 t
ORIGIN
Query Match      64.9%; Score 815.2; DB 12; Length 903;
Best Local Similarity 96.4%; Pred. No. 1.3e-125;
Matches 855; Conservative 0; Mismatches 29; Indels 3; Gaps 2;
OY      362 GGTACACCTGGGATCCAGTCCGATGATTTAAAGGAGGAGGAGGAGGAGGAGGAGG 421
      1 GGTACACCTGGGATCCAGTCCGATGATTTAAAGGAGGAGGAGGAGGAGGAGGAGG 60
OY      422 GGAAGCTTTGAGAGTCTGAGACACCACTACAGACAGTTCATGAGATCATGAA 481
      61 GGAAGCTTTGAGAGTCTGAGACACCACTACAGACAGTTCATGAGATCATGAA 120

```



Db 720 GAAGACTTTGTGAAGATTGGCTGAGATTAGGATGTTGCTATCTGGGTTGGCACT 779

QY 789 TGTTCAGATTACCCAAAAGAGATGCTTCTACTGGATGGAATTCAGTTTCGCATCAT 848

Db 780 TGTTCAGATTACCCAAAAGAGATGCTTCTACTGGATGGAATTCAGTTTCGCATCAT 839

QY 849 ATTGAAGACTACCCAAAATTAATGTTTAATTTTCATTTGCTACTCT 836

Db 840 ATTGAAGACTACCCAAAATTAATGTTTAATTTTCATTTGCTACTCT 887

RESULT 11

LOCUS B0425266 851 bp mRNA linear EST 23-MAY-2002

DEFINITION AGENCOURT\_7912803 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6150166

ACCESSION B0425266

VERSION B0425266.1 GI:21120581

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: LLM13484 row: f column: 23

FEATURES

source High quality sequence stop: 670.  
Location/Qualifiers  
1..851

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6150166"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_72"  
/note="Organ: Skin; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 186 a 224 c 258 g 183 t

ORIGIN

Query Match 58.88: Score 739.4: DB 13: Length 851:  
Best Local Similarity 99.18: Pred. No. 5e-113:  
Matches 754: Conservative 0: Mismatches 6: Indels 1: Gaps 1:

QY 6 GAGGCGGCGGGGTAAAGAGCGCATGTGACGCTGGCGGGCTCGAGAGCGGGCGAG 65

Db 36 GAGGCGGCGGGGTAAAGAGCGCATGTGACGCTGGCGGGCTCGAGAGCGGGCGAG 95

QY 66 CCAGAGCGTGAACACAGTTCCTCTCGGCTCTCGGCTCGAGCTCCGCGGCTGCCG 125

Db 96 CCAGAGCGTGAACACAGTTCCTCTCGGCTCTCGGCTCGAGCTCCGCGGCTGCCG 155

QY 126 CAGCGGGAGCCAGCAAGCAAGCCAGGCGCGGCGGCTCCGCGAGCGGCTCGCGGCTC 185

Db 156 CAGCGGGAGCCAGCAAGCAAGCCAGGCGCGGCGGCTCCGCGAGCGGCTCGCGGCTC 215

QY 186 CTGCTGCTCTGCTGCTGACAGTCCGCGCGCGTGAAGCGCTCTGAATCCCAAGGG 245

Db 216 CTGCTGCTCTGCTGCTGACAGTCCGCGCGGCTGAGCGCTCTGAGATCCCAAGGG 275

QY 246 AAGCAAAAGCGCACCTCCGCGAGAGAGGTGTGTGACCTGTATATGAATGCTTA 305

Db 276 AAGCAAAAGCGCACCTCCGCGAGAGAGGTGTGTGACCTGTATATGAATGCTTA 335

QY 306 CAAGGCGCAGAGAGTCTGTGTGTGACAGCGGAGCCCTGGGGCCATGTTATTCGGGT 365

Db 336 CAAGGCGCAGAGAGTCTGTGTGTGACAGCGGAGCCCTGGGGCCATGTTATTCGGGT 395

QY 366 ACACCTGGATCCAGTCCGCGGATGATTCAGAGAGAAAGGGGATGCTGAGGGA 425

Db 396 ACACCTGGATCCAGTCCGCGGATGATTCAGAGAGAAAGGGGATGCTGAGGGA 455

QY 426 AGCTTTGAGAGTCTGTGACACCCCAACATACAGAGTGTATGAGTTCAATTAAT 485

Db 456 AGCTTTGAGAGTCTGTGACACCCCAACATACAGAGTGTATGAGTTCAATTAAT 515

QY 486 GGCATAGATCTTTGGGAAATTCGCGAGTGTACATTTACAAAGATCCGTTCAATAGTCT 545

Db 516 GGCATAGATCTTTGGGAAATTCGCGAGTGTACATTTACAAAGATCCGTTCAATAGTCT 575

QY 546 CTAAGAGTTTGTTCAGTGGGCTCACTTGGCTAAATGACAGAAATGCATGCTGAGGT 605

Db 576 CTAAGAGTTTGTTCAGTGGGCTCACTTGGCTAAATGACAGAAATGCATGCTGAGGT 635

QY 606 TGTATATTCACATTCATGAGAGTGAATGTTGAGAGCTCTTCCATTAAGATTAAT 665

Db 636 TGTATATTCACATTCATGAGAGTGAATGTTGAGAGCTCTTCCATTAAGATTAAT 695

QY 666 TATTTTGACCAAGAGAGCCCTGAAATGATTCACATTAATTCATGCACTTCTCT 725

Db 696 TATTTTGACCAAGAGAGCCCTGAAATGATTCACATTAATTCATGCACTTCTCT 755

QY 726 GTGGAAGACCTTTGTC-AAGAAATGTCGTGATTAATG 765

Db 756 GTGGAAGACCTTTGTAAGAAATGTCGTGATTAATG 796

RESULT 12

LOCUS B0425098 922 bp mRNA linear EST 23-MAY-2002

DEFINITION AGENCOURT\_7902947 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6157844

ACCESSION B0425098

VERSION B0425098.1 GI:21120413

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: LLM13504 row: f column: 21

FEATURES

source High quality sequence stop: 714.  
Location/Qualifiers  
1..922

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6157844"  
/tissue\_type="melanotic melanoma"



```

/1ab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: PCMV-SPORE; site:1: NotI;
site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT      209 a      236 c      252 g      224 t      1 others
ORIGIN
Query Match      57.0%; Score 716.4; DB 13; Length 922;
Best Local Similarity 89.4%; Pred. No. 3.3e-109;
Matches 816; Conservative 0; Mismatches 92; Indels 5; Gaps 4;

OY 25 CGCATGATGACAGCTGCGGCGGCTCGGAGCGCGGAGCCAGACGAGTACAGCTTC 84
    |||||
DB 10 CGCATGATGACAGCTGCGGCGGCTCGGAGCGCGGAGCCAGACGAGTACAGCTTC 69
OY 85 CTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGG 144
    |||||
DB 70 CTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGG 129
OY 145 CCCAGGCGCGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCG 204
    |||||
DB 130 CCCAGGCGCGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCG 189
OY 205 AGCTGCGCGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCG 264
    |||||
DB 190 AGCTGCGCGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCG 249
OY 265 GGCAGAGGAGGTGTGACCTGTATTAATGGAATGTCTTCAAGGCCAGCAGAGTGC 324
    |||||
DB 250 GGCAGAGGAGGTGTGACCTGTATTAATGGAATGTCTTCAAGGCCAGCAGAGTGC 309
OY 325 CTGCTGAGAGCGGAGCGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCG 384
    |||||
DB 310 CTGCTGAGAGCGGAGCGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTCG 369
OY 385 GGGATGATTCAGAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTGAAGAGTCTGGA 444
    |||||
DB 370 GGGATGATTCAGAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTGAAGAGTCTGGA 429
OY 445 CACCAACTACAGAGCTGTCTCATGAGATTCATGGAATTTGCGATAGATCTTGGGAAA 504
    |||||
DB 430 CACCAACTACAGAGCTGTCTCATGAGATTCATGGAATTTGCGATAGATCTTGGGAAA 489
OY 505 TTGCGAGAGTGTACATTCAGAAAGATGCTTCAATAGTGTCTTAAAGAGTTTGTCAAGT 564
    |||||
DB 490 TTGCGAGAGTGTACATTCAGAAAGATGCTTCAATAGTGTCTTAAAGAGTTTGTCAAGT 549
OY 565 GCTGACTTGGCTAAAGAGAGAAATGATGTGAGCGTGTGATTTTCATTCATG 624
    |||||
DB 550 GCTGACTTGGCTAAAGAGAGAAATGATGTGAGCGTGTGATTTTCATTCATG 609
OY 625 GAGCTAATGTTGAGAGCTCTTCCATGAGTAAAGTAAATTTTATTTGAGCAAGAGAGCC 684
    |||||
DB 610 GAGCTAATGTTGAGAGCTCTTCCATGAGTAAAGTAAATTTTATTTGAGCAAGAGAGCC 669
OY 685 CTGAATGATTCAGAAATTAATATTCATGCACTT-CTTCTGAGAGAGCTTGTG-7A 742
    |||||
DB 670 CTGAATGATTCAGAAATTAATATTCATGCACTTCTTCTGAGAGAGCTTGTGAA 729
OY 743 AGGAATTTGTGCT-AGATTAAGTGAATTTGCT--TATCTGGGTTGGCACTTGTTCAGATTA 799
    |||||
DB 730 AGGAATTTGTGCT-AGATTAAGTGAATTTGCT--TATCTGGGTTGGCACTTGTTCAGATTA 789
OY 800 CCCAAAAGAGAGAGCTTCTGAGTGAATTCAGTTTCTGCACTATTTAAGAGACT 859
    |||||
DB 790 ACCCAAGAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 849
OY 860 ACCAAATTAATGCTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 919
    |||||
DB 850 TTGGAAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 909

```

```

OY 920 TTCCTTGAATGA 932
    |||||
DB 910 TTCCTTGAATGA 922

RESULT 13
BM915926
LOCUS
DEFINITION
AGENCOURT_6639781 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482196
5', mRNA sequence.
ACCESSION
BM915926
VERSION
BM915926.1 GI:19366305
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1037)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LICM2007 row: n column: 21
High quality sequence stop: 482.
Location/Qualifiers
1..1037
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5482196"
/tissue_type="amelanotic melanoma, cell line"
/1ab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: POTB; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using zap-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT      218 a      310 c      291 g      218 t
ORIGIN
Query Match      56.1%; Score 705.4; DB 12; Length 1037;
Best Local Similarity 91.7%; Pred. No. 2.2e-107;
Matches 791; Conservative 0; Mismatches 66; Indels 6; Gaps 4;

OY 53 GAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 112
    |||||
DB 1 GAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
OY 113 CCGGCGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 172
    |||||
DB 61 CCGGCGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
OY 173 GCTCCGCGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 232
    |||||
DB 121 GCTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
OY 233 GATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 292
    |||||
DB 181 GATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 293 TGGAGTGTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 352

```

```

Db      241 TGGAAATGCTTACACAGGCGCCAGCAGAGTGGCTGGTCAGACGGAGGCCCTGGGGCCAA 300
Qy      353 TGTATTCGGGGTACACCTGGGATCCAGGTGCGGATGATTCAAAGAGAAAGGGGGA 412
Db      301 TGGCATTCGGGGTACACCTGGGATCCAGGTGCGGATGATTCAAAGAGAAAGGGGGA 360
Qy      413 ATGTCTGAGGAAACCTTTGAGAGATCCCGACACCACCAACTCAAGCACTGTTATGAG 472
Db      361 ATGTCTGAGGAAACCTTTGAGAGATCCCGACACCACCAACTCAAGCACTGTTATGAG 420
Qy      473 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 532
Db      421 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Qy      533 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 592
Db      481 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Qy      593 ATGTCTGAGGAAACCTTTGAGAGATCCCGACACCACCAACTCAAGCACTGTTATGAG 652
Db      541 ATGTCTGAGGAAACCTTTGAGAGATCCCGACACCACCAACTCAAGCACTGTTATGAG 600
Qy      653 TGAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 711
Db      601 TGAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Qy      712 ATC-GCATTCTCTCTGTCGAGAGAGACTTTGTGAGAGAAATGTTGTCGATTAGTATG 770
Db      661 ATCGGACCTTCTCTGTCGAGAGAGACTTTGTGAGAGAAATGTTGTCGATTAGTATG 720
Qy      771 GCTATCTGGGTT--GGCACTTGTTCAGATTAATCCCAAGAGAGATCTTCTAC--TGAGAG 826
Db      721 GCTATCTGGGTTGGGAGCTTTGTCATTAATCCCAAGAGAGATCTTCTAC--TGAGAG 780
Qy      827 GAATTCAGTTTCTCTGTCGAGAGAGACTTTGTGAGAGAAATGTTGTCGATTAGTATG 886
Db      781 AATGTCGCGCTGTCGAGAGAGACTTTGTGAGAGAAATGTTGTCGATTAGTATG 840
Qy      887 TGTCTACCTCTTTTATTAATG 909
Db      841 TGGGACAGACTCTCTTTCGGAAGC 863

```

RESULT 14  
CA415410/c  
LOCUS CA415410 747 bp mRNA linear EST 07-NOV-2002  
DEFINITION UI-H-E20-daw-n-12-0-UI.s1 NCI\_CGAP Chl Homo sapiens cDNA clone  
ACCESSION UI-H-E20-daw-n-12-0-UI 3', mRNA sequence.  
VERSION CA415410  
KEYWORDS CA415410.1 GI:24778061  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 747)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
UNPUBLISHED  
CONTACT: Robert Strausberg, Ph.D.  
Tissue Procurement: Dr. Steven Gilelis/ Rush Presbyterian, Dept. of  
Orthopedics  
CNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 1-60, >AT-rich<low-complexity (matched complement)  
Seq primer: M13 FORWARD

```

FEATURES
    source POLYA=yes.
    Location/Qualifiers
        1..747
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="UI-H-E20-daw-n-12-0-UI"
            /tissue_type="Chondrosarcoma Grade II"
            /dev_stage="Adult"
            /lab_host="PHIOB (Life Technologies)"
            /clone_lib="NCI_CGAP-Ch1"
            /note="Organ: Left Pelvis; Vector: pRT3-Pac (Pharmacia)
            with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
            NCI_CGAP-Ch1 is a cDNA library containing the following
            tissue(s): Chondrosarcoma Grade II. The library was
            constructed according to Bonaldi, Lennon and Soares,
            Genome Research, 6:791-806, 1996. First strand cDNA
            synthesis was primed with an oligo-dT primer containing a
            Not I site. Double stranded cDNA was ligated to an EcoR I
            adaptor, digested with Not I, and cloned directionally
            into pRT3-Pac vector. The oligonucleotide used to prime
            the synthesis of first-strand cDNA contains a library tag
            sequence that is located between the Not I site and the
            (drr)18 tail. The sequence tag for this library is
            TAGTACGCT.
            TAG_LIB=UI-H-E20
            TAG_TISSUE=grade-2-chondrosarcoma
            TAG_SEQ=ATCTAATATG"
BASE COUNT 277 a 121 c 113 g 236 t
ORIGIN
Query Match 55.7%; Score 700.4; DB 14; Length 747;
Best Local Similarity 98.9%; Pred. No. 1.5e-106;
Matches 716; Conservative 0; Mismatch 6; Indels 2; Gaps 1;

```

534 TCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 593  
742 TCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 685  
594 TGTCTGAGCGTTGGTATTTACATTAATGAGAGCTGATGTCAGACCTCTTCCAT 653  
684 TGTCTGAGCGTTGGTATTTACATTAATGAGAGCTGATGTCAGACCTCTTCCAT 625  
654 GAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 713  
624 GAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 565  
714 GCGACTTCTCTGTCGAGAGAGACTTTGTGAGAGAAATGTTGTCGATTAGTATG 773  
564 GCGACTTCTCTGTCGAGAGAGACTTTGTGAGAGAAATGTTGTCGATTAGTATG 505  
774 ATCTGGTGGCAGCTTTGTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 833  
504 ATCTGGTGGCAGCTTTGTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 445  
834 GTTCTGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 893  
444 GTTCTGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 385  
894 TCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 953  
384 TCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 325  
954 TACATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1013  
324 TACATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 265  
1014 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1073  
264 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 205  
1074 GTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1133









QY	248	GC AAAAGGCGCAGCTCCGCGCAGAGGGAGGGTGGTGAACCTGTAATAATGAATGTCCTTACA	307
Db	251	GC AAAAGGCGCAGCTCCGCGCAGAGGGAGGGTGGTGAACCTGTAATAATGAATGTCCTTACA	310
QY	308	AGGCGCCAGCAGAGATGCTGCTGCTCGAGACGCGGAGCCCTGGGGCCCAATGTTATATCCGGGTAC	367
Db	311	AGGGCCAGCAGAGATGCTGCTGCTCGAGACGCGGAGCCCTGGGGCCCAATGTTATATCCGGGTAC	370
QY	368	ACCTGGGATCCCAAGGTCGGGATGATGATTC AAAAGAAAAGGGGAATGTCGTAGGCGAAAG	427
Db	371	ACCTGGGATCCCAAGGTCGGGATGATGATTC AAAAGAAAAGGGGAATGTCGTAGGCGAAAG	430
QY	428	CTTTAGAGAGTCTGTGACACCCAACTACAAAGCAGTGTATGAGTTCATTTGAATATAG	487
Db	431	CTTTAGAGAGTCTGTGACACCCAACTACAAAGCAGTGTATGAGTTCATTTGAATATAG	490
QY	488	CATGATCTTGGGAAAATTTCCGGAGTGTACATTTTACAAAAGATGCTTCAATAGTCTCT	547
Db	491	CATGATCTTGGGAAAATTTCCGGAGTGTACATTTTACAAAAGATGCTTCAATAGTCTCT	550
QY	548	AAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATTCACAAAATGCAATGCTGTACGGTTG	607
Db	551	AAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATTCACAAAATGCAATGCTGTACGGTTG	610
QY	608	GTATTTACATTCATATGAGAGCTGAATGTTCAGAGACCTCTCCCATTTGAAGCTTAATTTA	665
Db	611	GTATTTACATTCATATGAGAGCTGAATGTTCAGAGACCTCTCCCATTTGAAGCTTAATTTA	670
QY	668	TTTGGACCAAGAGAGCCCTGAAATGCAATTCACAAATTAATTCATGCGACCTTCTCTGT	727
Db	671	TTTGGACCAAGAGAGCCCTGAAATGCAATTCACAAATTAATTCATGCGACCTTCTCTGT	730
QY	728	GGAAGGACTTTTGGAAAGAAATTTGGTCGTGATTAAGGATTAAGGATTAATGCGGTTGGCAC	787
Db	731	GGAAGGACTTTTGGAAAGAAATTTGGTCGTGATTAAGGATTAAGGATTAATGCGGTTGGCAC	790
QY	788	TTGTTCAGATTAACCCAAAAGAGATGCTTCTACTGTGATGGAATTCAGTTTCTTCGCATCAT	847
Db	791	TTGTTCAGATTAACCCAAAAGAGATGCTTCTACTGTGATGGAATTCAGTTTCTTCGCATCAT	850
QY	848	TATTCAGAACTAACCAAAATTAATGCTTTAATTTTCATTTTGCATCTCTTTTATATAT	907
Db	851	TATTCAGAACTAACCAAAATTAATGCTTTAATTTTCATTTTGCATCTCTTTTATATAT	910
QY	908	GCCTTTGGATGCTTCACTTAATAATGACATTTTAAATTAATTAATGATATACATCGAATGAA	965
Db	911	GCCTTTGGATGCTTCACTTAATAATGACATTTTAAATTAATTAATGATATACATCGAATGAA	970
QY	968	AAGCAAAGCTAAATATGTTTACAGACACAAAGTGTGATTCACACTGTTTTAAATCTAGC	1022
Db	971	AAGCAAAGCTAAATATGTTTACAGACACAAAGTGTGATTCACACTGTTTTAAATCTAGC	1033
QY	1028	ATTATATCTATTGTCATCATCAAAAAGTGTTCCAATATTTTGTGTTGGTTAGAAATAC	108
Db	1031	ATTATATCTATTGTCATCATCAAAAAGTGTTCCAATATTTTGTGTTGGTTAGAAATAC	109
QY	1088	TTTCTTCATAGTCACATTCCTCAACACTTAATTTTGGAAATATGTTGTGTGCTTTGTTT	114
Db	1091	TTTCTTCATAGTCACATTCCTCAACACTTAATTTTGGAAATATGTTGTGTGCTTTGTTT	115
QY	1148	TTTCTCTTATGATATACATTTTAAAAAAATATPAAAAGCTACCAATCTTGTGTACAAATTTGT	120
Db	1151	TTTCTCTTATGATATACATTTTAAAAAAATATPAAAAGCTACCAATCTTGTGTACAAATTTGT	121
QY	1208	AAATGTTTAAAGATTTTATATGCTTAATGCTTAATAATTAATAATTTTCCAAACA	1257
Db	1211	AAATGTTTAAAGATTTTATATGCTTAATAATTAATAATTTTCCAAACA	1260

```

GENERAL INFORMATION:
  APPLICANT: Rosen et al
  TITLE OF INVENTION: 98 Human Secreted Proteins
  FILE REFERENCE: P2031P1
  CURRENT APPLICATION NUMBER: US/09/489, 847
  CURRENT FILING DATE: 2000-01-24
  EARLIER APPLICATION NUMBER: Pct/US99/17130
  EARLIER FILING DATE: 1999-07-29
  EARLIER APPLICATION NUMBER: 60/094, 657
  EARLIER FILING DATE: 1998-07-30
  EARLIER APPLICATION NUMBER: 60/095, 486
  EARLIER FILING DATE: 1998-08-05
  EARLIER APPLICATION NUMBER: 60/096, 319
  EARLIER FILING DATE: 1998-08-12
  EARLIER APPLICATION NUMBER: 60/095, 454
  EARLIER FILING DATE: 1998-08-06
  EARLIER APPLICATION NUMBER: 60/095, 455
  EARLIER FILING DATE: 1998-08-06
  NUMBER OF SEQ ID NOS: 376
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 124
  LENGTH: 1286
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
    NAME/KEY: SITE
    LOCATION: (1284)
    OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-124

```

Query Match	97.3%	Score 1232.8;	DB 4;	length 1286;
Best Local Similarity	99.7%	Pred. No. 2.4e-271;		
Matches 1246; Conservative	0;	Mismatches 2;	Indels 2;	Gaps 2;

[illegible]



US-09-205-258-125

Query Match 95.2%; Score 1197; DB 4; Length 1288;  
Best Local Similarity 99.3%; Pred. No. 2e-255;  
Matches 1242; Conservative 2; Mismatches 2; Indels 5; Gaps 4;

```
OY 8 GGGCGGGGGGGAAGGCGCATATGACAGCTGGGGGCGCTCGAGAGCGGCGGAGCC 67
DB 1 GGGCGGGGGGGAAGGCGCATATGACAGCTGGGGGCGCTCGAGAGCGGCGGAGCC 59
OY 68 AGAGCTGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
DB 60 AGAGCTGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
OY 128 GCGGGGAGCAGTGGAGCCCAAGGGCCCGCGCTCGCCGCAAGCGGCTCGCGGCGCTCT 187
DB 120 GCGGGGAGCAGTGGAGCCCAAGGGCCCGCGCTCGCCGCAAGCGGCTCGCGGCGCTCT 179
OY 188 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
DB 180 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
OY 248 GCAAAAGGCGAGCTCCGCGAGAGGAGTGGTGAGCTGATATATGGAATGCTTACA 307
DB 240 GCAAAAGGCGCA--TCCGCGAGAGGAGTGGTGAGCTGATATATGGAATGCTTACA 297
OY 308 AGGGCGAGCAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
DB 298 AGGGCGAGCAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
OY 368 ACCTGGAGTCCAGGCTGGGATGGATGCAAGGAGAGAGAGGAGAGTCTGAGGAGAG 427
DB 358 ACCTGGAGTCCAGGCTGGGATGGATGCAAGGAGAGAGAGGAGAGTCTGAGGAGAG 417
OY 428 CTTTGAGAGTCTGCGACACCACTACAGAGTGTTCATGATGATGATGATGATGATG 487
DB 418 CTTTGAGAGTCTGCGACACCACTACAGAGTGTTCATGATGATGATGATGATGATG 477
OY 488 CATAGATTTGGGAGAAATGCGGAGTGTACATTTACAAGATGCTGCTGCTGCTGCT 547
DB 478 CATAGATTTGGGAGAAATGCGGAGTGTACATTTACAAGATGCTGCTGCTGCTGCT 537
OY 548 AAGGTTTGTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
DB 538 AAGGTTTGTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
OY 608 GTATTTACATTCATGAGCTGATGATGCTGAGACCTCTCCCATGGAAGTATATTTA 667
DB 598 GTATTTACATTCATGAGCTGATGATGCTGAGACCTCTCCCATGGAAGTATATTTA 657
OY 668 TTTGGACCAAGAAAGCCCTGAATGATGATGATGATGATGATGATGATGATGATG 727
DB 658 TTTGGACCAAGAAAGCCCTGAATGATGATGATGATGATGATGATGATGATGATG 717
OY 728 GGAAGGAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 787
DB 718 GGAAGGAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 777
OY 788 TTGTTACATTCACCAAGAGAGATGCTTACTGATGATGATGATGATGATGATGATG 847
DB 778 TTGTTACATTCACCAAGAGAGATGCTTACTGATGATGATGATGATGATGATGATG 837
OY 848 TATGAGAGATACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 907
DB 838 TATGAGAGATACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 897
OY 908 GCTTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
DB 898 GCTTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
OY 968 AAGCAAGGCTAAATATGTTTACAGACCAAGTGTGATGATGATGATGATGATGATG 1027
DB 958 AAGCAAGGCTAAATATGTTTACAGACCAAGTGTGATGATGATGATGATGATGATG 1016
```

```
OY 1028 ATTATTCATTTTGTCTCATCAAAAGTGTTCATATTTTGTAGTGTAGAAATAC 1087
DB 1017 ATTATTCATTTTGTCTCATCAAAAGTGTTCATATTTTGTAGTGTAGAAATAC 1076
OY 1088 TTTCTTCATGACATTCCTCTCAACCTATATTTT--GGAATATGTTGTGCTTTGTT 1146
DB 1077 TTTCTTCATGACATTCCTCTCAACCTATATTTTGGGAATATGTTGTGCTTTGTT 1136
OY 1147 TTTCTTCATGACATTTTAAAAAATATTAACCTCAATCTTGTACAAATTTG 1206
DB 1137 TTTCTTCATGACATTTTAAAAAATATTAACCTCAATCTTGTACAAATTTG 1196
OY 1207 TAAATGTAAAGATTTTAAAAAATATTAACCTCAATCTTGTACAAATTTG 1257
DB 1197 TAAATGTAAAGATTTTAAAAAATATTAACCTCAATCTTGTACAAATTTG 1247
```

## RESULT 4

US-09-222-575-63/c  
; Sequence 63, Application US/09222575  
; Patent No. 6387697  
; GENERAL INFORMATION:  
; APPLICANT: Yudiu, Jiang  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jianshun  
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer  
; FILE REFERENCE: 210121.470  
; CURRENT APPLICATION NUMBER: US/09/222.575  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Human  
US-09-222-575-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 2.5e-147;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
OY 516 ACATTTCAAAAGATGCGTTCAAAATAGTCTCAAGAGTTTGTTCAGTGGCTCACTTGG 575
DB 683 ACATTTCAAAAGATGCGTTCAAAATAGTCTCAAGAGTTTGTTCAGTGGCTCACTTGG 624
OY 576 CTAAATGCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
DB 623 CTAAATGCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
OY 636 TCAGAGCTCTCCCATGAGCTATATATTTATTTGACCAAGAGCCCGAATGAT 695
DB 563 TCAGAGCTCTCTCCCATGAGCTATATATTTATTTGACCAAGAGCCCGAATGAT 504
OY 696 TCAACATTAATATTCATGCGACTTCTCTGTTGGAAGACTTTGGAAGATTTGCT 755
DB 503 TCAACATTAATATTCATGCGACTTCTCTGTTGGAAGACTTTGGAAGATTTGCT 444
OY 756 GGATTTAGGAGATGTTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
DB 443 GGATTTAGGAGATGTTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
OY 816 TCTACTGATGGAATTCAGTTTCTGCGATCATATTTGAAGAATACCAAAATTAATGCT 875
DB 383 TCTACTGATGGAATTCAGTTTCTGCGATCATATTTGAAGAATACCAAAATTAATGCT 324
OY 876 TAAATTCATTTGCTACCTCTTTTATATATGCTTGAAGTGTGCTCAATTAATGAT 935
DB 323 TAAATTCATTTGCTACCTCTTTTATATATGCTTGAAGTGTGCTCAATTAATGAT 264
OY 936 TTTAAATTAAGTTTATGATACATCTGAATGAAAAGCAAGCTAAATATGTTTACAGACA 995
```

```

DB      263 TTTAAATTAAGTTATATATACATCTCAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA 204
      996 AAGTGTATTTACACACTGTTTAAATACATGATTTATCTTTGCTTCATCAAAAGTG 1055
      203 AAGTGTATTTACACACTGTTTAAATACATGATTTATCTTTGCTTCATCAAAAGTG 144
      1056 GTTTCATATTTTATTTAGTGTAGAAATCTTTCTCATCTCAACCT 1115
      143 GTTTCATATTTTATTTAGTGTAGAAATCTTTCTCATCTCAACCT 84
      1116 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCAATTTTAAAAA 1175
      83 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCAATTTTAAAAA 24
      1176 ATATAAAGCTACCAATCTTTGT 1198
      23 ATATAAAGCTACCAATCTTTGT 1

```

## RESULT 5

```

US-09-389-681-63/C
; Sequence 63, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqun, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389, 681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-63

```

```

Query Match      54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 2.5e-147;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

      516 ACATTACAAAGATGCGTCAAAATAGTCTAGAGTTTGTTCAGTGGCTCACTTCGG 575
      683 ACATTACAAAGATGCGTCAAAATAGTCTAGAGTTTGTTCAGTGGCTCACTTCGG 624
      576 CTAAATGCGAAGATGCTGTGTCAGCGTGTGATTTACATTCATGAGCTGAATGT 635
      623 CTAAATGCGAAGATGCTGTGTCAGCGTGTGATTTACATTCATGAGCTGAATGT 564
      636 TCAGGACCTCTCCCTTGAAGCTATTAATTTGAGCCAGGAAGCCCTGAATGAAT 695
      563 TCAGGACCTCTCCCTTGAAGCTATTAATTTGAGCCAGGAAGCCCTGAATGAAT 504
      696 TCACAAATTAATTAATGATGCACTTCTGTGGAAGCACTTTGAAGAAATTTGCTGT 755
      503 TCACAAATTAATTAATGATGCACTTCTGTGGAAGCACTTTGAAGAAATTTGCTGT 444
      756 GGATTAAGTGAATGTTGCTATCTGTGTCACATTTGTCAGATTAACCAAAAGAGATGCT 815
      443 GGATTAAGTGAATGTTGCTATCTGTGTCACATTTGTCAGATTAACCAAAAGAGATGCT 384
      816 TCTACGATGATGATTCATTTCTGCAATCATTATGAAGAACTACCAAAATTAATGCTT 875
      383 TCTACGATGATGATTCATTTCTGCAATCATTATGAAGAACTACCAAAATTAATGCTT 324
      876 TAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAAGATGCTCACTTAATGACAT 935
      323 TAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAAGATGCTCACTTAATGACAT 264

```

```

      936 TTTAAATTAAGTTATATATACATCTCAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA 995
      263 TTTAAATTAAGTTATATATACATCTCAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA 204
      996 AAGTGTATTTACACACTGTTTAAATACATGATTTATCTTTGCTTCATCAAAAGTG 1055
      203 AAGTGTATTTACACACTGTTTAAATACATGATTTATCTTTGCTTCATCAAAAGTG 144
      1056 GTTTCATATTTTATTTAGTGTAGAAATCTTTCTCATCTCAACCT 1115
      143 GTTTCATATTTTATTTAGTGTAGAAATCTTTCTCATCTCAACCT 84
      1116 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCAATTTTAAAAA 1175
      83 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCAATTTTAAAAA 24
      1176 ATATAAAGCTACCAATCTTTGT 1198
      23 ATATAAAGCTACCAATCTTTGT 1

```

## RESULT 6

```

US-09-620-405B-63/C
; Sequence 63, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.47008
; CURRENT APPLICATION NUMBER: US/09/620, 405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-63

```

```

Query Match      54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 2.5e-147;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

      516 ACATTACAAAGATGCGTCAAAATAGTCTAGAGTTTGTTCAGTGGCTCACTTCGG 575
      683 ACATTACAAAGATGCGTCAAAATAGTCTAGAGTTTGTTCAGTGGCTCACTTCGG 624
      576 CTAAATGCGAAGATGCTGTGTCAGCGTGTGATTTACATTCATGAGCTGAATGT 635
      623 CTAAATGCGAAGATGCTGTGTCAGCGTGTGATTTACATTCATGAGCTGAATGT 564
      636 TCAGGACCTCTCCCTTGAAGCTATTAATTTGAGCCAGGAAGCCCTGAATGAAT 695
      563 TCAGGACCTCTCCCTTGAAGCTATTAATTTGAGCCAGGAAGCCCTGAATGAAT 504
      696 TCACAAATTAATTAATGATGCACTTCTGTGGAAGCACTTTGAAGAAATTTGCTGT 755
      503 TCACAAATTAATTAATGATGCACTTCTGTGGAAGCACTTTGAAGAAATTTGCTGT 444
      756 GGATTAAGTGAATGTTGCTATCTGTGTCACATTTGTCAGATTAACCAAAAGAGATGCT 815
      443 GGATTAAGTGAATGTTGCTATCTGTGTCACATTTGTCAGATTAACCAAAAGAGATGCT 384
      816 TCTACGATGATGATTCATTTCTGCAATCATTATGAAGAACTACCAAAATTAATGCTT 875
      383 TCTACGATGATGATTCATTTCTGCAATCATTATGAAGAACTACCAAAATTAATGCTT 324

```









```
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc_feature
LOCATION: 17555..20674
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTGTA or TTTTGT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777
OTHER INFORMATION: 10-349-216 : deletion of CTG
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 8926
```

OTHER INFORMATION: 10-349-368 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 12171  
OTHER INFORMATION: 10-350-72 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 12429  
OTHER INFORMATION: 10-350-332 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 13341  
OTHER INFORMATION: 10-507-170 : polymorphic base A or G  
NAME/KEY: allele  
LOCATION: 13492  
OTHER INFORMATION: 10-507-321 : polymorphic base A or C  
NAME/KEY: allele  
LOCATION: 13524  
OTHER INFORMATION: 10-507-353 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 13535

Query Match 4.5%; Score 56.8; DB 4; Length 20674;  
Best local similarity 46.3%; Pred. No. 0.0026;  
Matches 187; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 845 CATATGAGACACCAAAATTAATGCTTAATTTGCTACCTCTTTTAT 904  
DB 11062 CTTTTTATAGCTAAGGAAATATTTAATTTAATTTAATTTAATTTAA 11121  
QY 905 TATGCTTGAAAGCTTCAATTAATGACATTTTAATTAATTAATTAATTAAT 964  
DB 11122 TATTAATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTAAT 11181  
QY 965 GAAAGCAAGCTAATATATGTTACAGACCAAGTGTGATTCACATGTTTAAATCT 1024  
DB 11182 AAAATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11241  
QY 1025 AACATTAATTCATTTCTTCAATCAAAAGTGTGATTTAATTTTGTGTTAGAA 1084  
DB 11242 TTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11301  
QY 1085 TACTTCTCATAGTACATTCCTCAACCTAATTTGAATGTTGTGCTTTTG 1144  
DB 11302 TAAATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11361  
QY 1145 TTTTTCCTAGTATAGATTTTAAAAAATTAATTAATTAATTTGATACAT 1204  
DB 11362 TATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11421  
QY 1205 TGTAAATGTTAAGATTTTATATCTGTTAATTAATTAATTAATTAATTAAT 1248  
DB 11422 AATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTAATTAAT 11465

RESULT 11  
US-09-370-838-153/C  
Sequence 153, Application US/09370838  
Patent No. 6444425  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Roadoh  
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.475c1  
CURRENT APPLICATION NUMBER: US/09/370,838  
CURRENT FILING DATE: 1999-08-09  
EARLIER APPLICATION NUMBER: US 09/285,333  
EARLIER FILING DATE: 1999-04-02  
NUMBER OF SEQ ID NOS: 289  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 153  
LENGTH: 2109  
TYPE: DNA

ORGANISM: Homo sapien  
US-09-370-838-153

Query Match 4.4%; Score 55.2; DB 4; Length 2109;  
Best local similarity 51.2%; Pred. No. 0.0023;  
Matches 129; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 6 GAGGCGCGGGGTGAAGGCGCATTTGATCAGCTCGCGGCGGCGGCGGAG 65  
DB 1140 GAGGCGCGCGGGGTGCGTCCGCTCCGCGGCGGCGGCGGCGGCGGCGG 1081  
QY 66 CCAGACGCTGACACCTTCTCTCGGCTCTCTCCGCTCCGCTCCGCTCCG 125  
DB 1080 CGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1021  
QY 126 CAGCGGCGGAGCATATGAGACCCGCGCGCGCGCGCGCGCGCGCGCGCG 185  
DB 1020 CG 961  
QY 186 CTGCT 245  
DB 960 CAGCGGCG 901  
QY 246 AGCGAAGAGCG 257  
DB 900 CAGCGAGAGCGG 889

RESULT 12  
US-08-817-926-27  
Sequence 27, Application US/08817926  
Patent No. 6001590  
GENERAL INFORMATION:  
APPLICANT: Kameda, Toshihiro  
APPLICANT: Suda, Hisako  
APPLICANT: Tamai, Yukio  
APPLICANT: Iwamatsu, Akihito  
APPLICANT: Kato, No. 6001590uo  
APPLICANT: Sakai, Yasuyoshi  
TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINII  
TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,926  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/02597  
FILING DATE: 12-SEP-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 234133/1995  
FILING DATE: 12-SEP-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 42536/1996  
FILING DATE: 29-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 081356/0112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300



```

; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
;
; TELETYPE: 706141
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(3056..3226, 3325..3453, 3539..3700, 4582
; LOCATION: ..5574)
; US-08-378-313-26

```

Query Match 4.2%; Score 52.8; DB 3; Length 7244;  
 Best Local Similarity 58.1%; Pred. No. 0.014;  
 Matches 93; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

```

QY 1092 TTCATAGTCACATCTCTCAACCTATAATTGGAAATATTGTGTCCTTTGTTTTC 1151
DB 6813 TTTAACTAGATGAATCAAAAGATAATTAATTTGATGATTTTATAATGATCTTT 6872
QY 1152 TCTTAGTATAGCATTTTAAAAAATATAAGCTACCAATCTTTACATTTGTAAT 1211
DB 6873 TTATCATATTGACATGTAGAAAAATTAATTAATTAATTAATTAATTAATTAAT 6932
QY 1212 GTTAAGAAATTTTATATCTGTAAATAAATAATTAATTT 1251
DB 6933 ATTAAATTTTATTATTAATAATTAATGAATATTTT 6972

```

RESULT 15  
 US-09-056-075-1/C  
 Sequence 1, Application US/09056075  
 Patent No. 5955368  
 GENERAL INFORMATION:  
 APPLICANT: Johnson, Eric A.  
 APPLICANT: Bradshaw, Marile  
 APPLICANT: Rood, Julian  
 TITLE OF INVENTION: Expression System for Clostridium  
 TITLE OF INVENTION: Species  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quarles & Brady  
 STREET: 1 South Plinckney Street  
 CITY: Madison  
 STATE: WI  
 COUNTRY: US  
 ZIP: 53701-2113

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
; OTHER INFORMATION: plasmid RP4"
; US-09-056-075-1

```

Query Match 4.1%; Score 52; DB 2; Length 6243;  
 Best Local Similarity 45.7%; Pred. No. 0.02;  
 Matches 181; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

```

QY 850 TTGAAGACTACAAAATAATGCTTTAATTTTCATTGCTACCTCTTTTATATGTC 909
DB 1488 TTTATTAAGGCTCTTTTATTTCTTTCTTCAAGATATATATATATATATATAT 1429
QY 910 CTGGAATGGTTCATTAATGACATTTTAATTAATGATATGATACATCTGAATGAAA 969
DB 1428 TTTTCAACTTTAATATATATATTTTATTTTATTTTATTTTATTTTATTTT 1369
QY 970 GCAAGCTAATATGTTTACGACCAAGTGATTTTCACACTGTTTAAATCTAGCAT 1029
DB 1368 TTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1309
QY 1030 TATTCATTTTGCCTCAATCAAAAGCTTTCAATTTTATTTTATTTTATTTTATTT 1089
DB 1308 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1249
QY 1090 TCTTCATAGCACATCTCTCAACCTATAATTTGGAATATTGTGTCCTTTGTTT 1149
DB 1248 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1189
QY 1150 TCTCTAGATATACATTTTAAAAAATATAAAGCTACCAATCTTTGATCAATTTGTA 1209
DB 1188 CCGCATTTTTCGCTTGATATATAGGATCTTTGACCTGTTCTTTTGGGGAGG 1129
QY 1210 ATGTTAAGAAATTTTATATCTGTTAAATAAATAA 1245
DB 1128 TTGTAAGATTAATTTTACTTTAGTAGTCGAA 1093

```

Search completed: August 20, 2003, 15:56:33  
 Job time : 92 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 13:48:04 ; Search time 309 Seconds

(without alignments)  
9145.443 Million cell updates/sec

Title: US-09-938-418-2

Perfect score: 1257  
Sequence: 1 ggagagagggcgcgcggtga.....ataaaattttcccaaca 1257

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_MA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	100.0	1257	10	US-09-938-418-2
2	1257	100.0	1257	11	US-09-946-374-430
3	1257	100.0	1257	12	US-10-015-387A-430
4	1257	100.0	1257	12	US-10-063-735-121
5	1257	100.0	1257	12	US-10-006-130A-430
6	1257	100.0	1257	12	US-10-199-672-365
7	1257	100.0	1257	12	US-10-006-172A-430
8	1257	100.0	1257	12	US-10-187-749-365
9	1257	100.0	1257	12	US-10-194-457-365
10	1257	100.0	1257	13	US-10-006-867-121
11	1257	100.0	1257	13	US-10-052-586-365
12	1257	100.0	1257	13	US-10-063-547-121
13	1257	100.0	1257	14	US-10-174-590-365
14	1257	100.0	1257	14	US-10-176-758-365
15	1257	100.0	1257	14	US-10-175-737-365
16	1257	100.0	1257	14	US-10-063-616-121

17	1257	100.0	1257	14	US-10-173-706-365	Sequence 365, App
18	1257	100.0	1257	14	US-10-175-738-365	Sequence 365, App
19	1257	100.0	1257	14	US-10-175-752-365	Sequence 365, App
20	1257	100.0	1257	14	US-10-176-488-365	Sequence 365, App
21	1257	100.0	1257	14	US-10-176-757-365	Sequence 365, App
22	1257	100.0	1257	14	US-10-176-913-365	Sequence 365, App
23	1257	100.0	1257	14	US-10-180-552-365	Sequence 365, App
24	1257	100.0	1257	14	US-10-180-557-365	Sequence 365, App
25	1257	100.0	1257	14	US-10-063-502-121	Sequence 121, App
26	1257	100.0	1257	14	US-10-173-700-365	Sequence 365, App
27	1257	100.0	1257	14	US-10-174-572-365	Sequence 365, App
28	1257	100.0	1257	14	US-10-174-579-365	Sequence 365, App
29	1257	100.0	1257	14	US-10-174-582-365	Sequence 365, App
30	1257	100.0	1257	14	US-10-174-588-365	Sequence 365, App
31	1257	100.0	1257	14	US-10-175-739-365	Sequence 365, App
32	1257	100.0	1257	14	US-10-175-740-365	Sequence 365, App
33	1257	100.0	1257	14	US-10-175-743-365	Sequence 365, App
34	1257	100.0	1257	14	US-10-176-488-365	Sequence 365, App
35	1257	100.0	1257	14	US-10-176-492-365	Sequence 365, App
36	1257	100.0	1257	14	US-10-176-747-365	Sequence 365, App
37	1257	100.0	1257	14	US-10-176-750-365	Sequence 365, App
38	1257	100.0	1257	14	US-10-176-985-365	Sequence 365, App
39	1257	100.0	1257	14	US-10-176-987-365	Sequence 365, App
40	1257	100.0	1257	14	US-10-176-992-365	Sequence 365, App
41	1257	100.0	1257	14	US-10-176-993-365	Sequence 365, App
42	1257	100.0	1257	14	US-10-184-658-365	Sequence 365, App
43	1257	100.0	1257	14	US-10-176-991-365	Sequence 365, App
44	1257	100.0	1257	14	US-10-173-695-365	Sequence 365, App
45	1257	100.0	1257	14	US-10-173-697-365	Sequence 365, App

#### ALIGNMENTS

RESULT 1  
US-09-938-418-2  
Sequence 2, Application US/09938418  
Patent No. US20020161199A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Gurney, Austin L.  
APPLICANT: Polakis, Paul  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Wu, Thomas D.  
APPLICANT: Zhang, Gemin  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR  
FILE REFERENCE: P5009R1  
CURRENT APPLICATION NUMBER: US/09/938,418  
CURRENT FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: 60/081,071  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: 60/085,697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/097,022  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/101,922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/103,679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: 1999-06-02  
PRIOR APPLICATION NUMBER: PCT/US99/20111  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US00/04342  
PRIOR FILING DATE: 2000-02-18





[illegible]

```
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103633
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103678
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807
```

```
Query Match      100.0%; Score 1257; DB 11; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2,3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGAAGAGAGCGCGGGGTGAAAGCGCATGTGACAGCTCGGCGGCGCTCGAGCGCGG 60
DB 1 GGAGAGAGCGCGGGGTGAAAGCGCATGTGACAGCTCGGCGGCGCTCGAGCGCGG 60
QY CGGAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB CGGAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 61 CGGAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCGCGGAGCGCATGTGACAGCTCGGCGGCGCTCGAGCGCGCTCGGCG 180
DB 121 CCCGCGAGCGCGGAGCGCATGTGACAGCTCGGCGGCGCTCGAGCGCGCTCGGCG 180
QY 181 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGAAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 AGGGAAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 GCTTACAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
DB 301 GCTTACAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 361 CGGGAAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 361 CGGGAAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 421 GGGGAAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 421 GGGGAAGCGCGAGCGCTGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 481 ATTATGCGATGATCTTGGGAAATTCGAGAGTGTACATTACAAAGATGCTTCAATA 540
DB 481 ATTATGCGATGATCTTGGGAAATTCGAGAGTGTACATTACAAAGATGCTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTCTAGTGTCTACTTGGCTCAATAATGAGAAATGCATGCTGTC 600
DB 541 GTGCTCTAAGAGTTTGTCTAGTGTCTACTTGGCTCAATAATGAGAAATGCATGCTGTC 600
```

```
QY 601 AGCGTTGATATTCAATTCAGAGTGAATGTTTCAGAGCGCTCTCCATTCAGAGTGA 660
DB 601 AGCGTTGATATTCAATTCAGAGTGAATGTTTCAGAGCGCTCTCCATTCAGAGTGA 660
QY 661 TAAATTTATTTGAGCAAGAGCGCTGAAAGCAATTCAGAGTGAATTCAGAGTGA 720
DB 661 TAAATTTATTTGAGCAAGAGCGCTGAAAGCAATTCAGAGTGAATTCAGAGTGA 720
QY 721 CTCTGTGGAAGAGTCTTGTGAGAGTGAATGTTTCAGAGTGAATTCAGAGTGA 780
DB 721 CTCTGTGGAAGAGTCTTGTGAGAGTGAATGTTTCAGAGTGAATTCAGAGTGA 780
QY 781 TTGGCAGCTTGTTCAGATTCACCAAGAGAGTGTTCAGAGTGAATTCAGAGTGA 840
DB 781 TTGGCAGCTTGTTCAGATTCACCAAGAGAGTGTTCAGAGTGAATTCAGAGTGA 840
QY 841 GCATCATTTATGAAAGTACCAAGAGTGAATTCAGAGTGAATTCAGAGTGAATTC 900
DB 841 GCATCATTTATGAAAGTACCAAGAGTGAATTCAGAGTGAATTCAGAGTGAATTC 900
QY 901 TTATTTATGCGTGAAGTGTTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 960
DB 901 TTATTTATGCGTGAAGTGTTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 960
QY 961 GATGAAAGAGCAAGTGAATTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 1020
DB 961 GATGAAAGAGCAAGTGAATTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 1020
QY 1021 ATCTAGCATTTATGAAAGTGTTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 1080
DB 1021 ATCTAGCATTTATGAAAGTGTTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 1080
QY 1081 AGAATTTATTTCTCTCAATTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 1140
DB 1081 AGAATTTATTTCTCTCAATTCAGATTCACCAAGAGTGAATTCAGAGTGAATTC 1140
QY 1141 TTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
DB 1141 TTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1201 AATTTGTAATGTTAAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1257
DB 1201 AATTTGTAATGTTAAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1257

RESULT 3
US-10-015-387A-430
; Sequence 430. Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
; LENGTH: 1257
```

```
TYPE: DNA
ORGANISM: Homo Sapien
US-10-015-387A-430

Query Match      100.0%; Score 1257; DB 12; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACGCTGGCGGCGCTCGAGCGCGG 60
DB 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACGCTGGCGGCGCTCGAGCGCGG 60
QY 61 CGAGACGACGCTGACACGCTTCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 CGAGACGACGCTGACACGCTTCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 CCCGGAGCGCGGAGCGCATGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180
DB 121 CCCGGAGCGCGGAGCGCATGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180
QY 181 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AGGGAGAGCAAAAGCGCGACGCTCCGCGCAGAGGAGGAGTGCTGATTAATGAGATGT 300
DB 241 AGGGAGAGCAAAAGCGCGACGCTCCGCGCAGAGGAGGAGTGCTGATTAATGAGATGT 300
QY 301 GCTTACAAAGGCGCAGAGAGTCCGCTGCTGAGAGCGCGCGCTGGGGCGCATTTATTC 360
DB 301 GCTTACAAAGGCGCAGAGAGTCCGCTGCTGAGAGCGCGCGCTGGGGCGCATTTATTC 360
QY 361 CGGATACACCTGAGATCCGAGGTCGAGATGATTCGAGAGAGAGAGAGAGAGAGTCTGA 420
DB 361 CGGATACACCTGAGATCCGAGGTCGAGATGATTCGAGAGAGAGAGAGAGAGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGAGTCTGAGACACCCACTACAGCAGTTCATGAGTTCATGA 480
DB 421 GGGAAAGCTTTGAGAGAGTCTGAGACACCCACTACAGCAGTTCATGAGTTCATGA 480
QY 481 ATTATGCGATATGCTGGGAAATTTGGGAGTGTACATTTCCAAAGAGCGCTCAATAA 540
DB 481 ATTATGCGATATGCTGGGAAATTTGGGAGTGTACATTTCCAAAGAGCGCTCAATAA 540
QY 541 GTGCTCTAGAGCTTTGTTCACTGCTCACTTCGCGCTAAATGACAGAAATGATGCTGTC 600
DB 541 GTGCTCTAGAGCTTTGTTCACTGCTCACTTCGCGCTAAATGACAGAAATGATGCTGTC 600
QY 601 AGCGTTGGTATTTCAATTCATGAGAGTGAATGTTTCAGAGACCTCTCCCATTTGAAGCTA 660
DB 601 AGCGTTGGTATTTCAATTCATGAGAGTGAATGTTTCAGAGACCTCTCCCATTTGAAGCTA 660
QY 661 TAATTAATTTGGAGAGAGCGCTGAATGAATTCATTAATTAATTCATTCGACAT 720
DB 661 TAATTAATTTGGAGAGAGCGCTGAATGAATTCATTAATTAATTCATTCGACAT 720
QY 721 CTTCGTGAGAGAGCTTTGTAAGAAATTTGCTGATGATGATGATGATGATGATGATG 780
DB 721 CTTCGTGAGAGAGCTTTGTAAGAAATTTGCTGATGATGATGATGATGATGATGATG 780
QY 781 TTGGGACATTTGTCAGATTAACCAAAAGAGATGCTTCTAGTGAATTTAGATTTTC 840
DB 781 TTGGGACATTTGTCAGATTAACCAAAAGAGATGCTTCTAGTGAATTTAGATTTTC 840
QY 841 GCATCATTTATGAGAGAGTACCAAAATTAATGCTTAATTTCAATTTGCTACCTTTT 900
DB 841 GCATCATTTATGAGAGAGTACCAAAATTAATGCTTAATTTCAATTTGCTACCTTTT 900
QY 901 TTATTAATGCTTTGAGATGCTTCAATTAATGATGATGATGATGATGATGATGATGATG 960
DB 901 TTATTAATGCTTTGAGATGCTTCAATTAATGATGATGATGATGATGATGATGATGATG 960
QY 961 GAATGAGAGAGAGAGAGTGAATGTTTACAGACCAAAAGTGTGATTTTCACTGTTTAA 1020
```

```
DB 961 GAATGAGAGAGAGAGTGAATGTTTACAGACCAAAAGTGTGATTTTCACTGTTTAA 1020
QY 1021 ATCTGACATTAATTCATTTGCTTCATCAATCAAAAGTGTTCATATTTTATTTAGTTGCT 1080
DB 1021 ATCTGACATTAATTCATTTGCTTCATCAATCAAAAGTGTTCATATTTTATTTAGTTGCT 1080
QY 1081 AGAATACCTTCTTCATAGTACATTTCTCAACCTTTAATTTGGAATATTTGTTGCTCT 1140
DB 1081 AGAATACCTTCTTCATAGTACATTTCTCAACCTTTAATTTGGAATATTTGTTGCTCT 1140
QY 1141 TTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
DB 1141 TTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1257
DB 1201 AATTTGTAATGTTAAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1257

RESULT 4
US-10-063-735-121
; Sequence 121, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLETIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-735-121

Query Match      100.0%; Score 1257; DB 12; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACGCTGGCGGCGCTCGAGCGCGG 60
DB 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACGCTGGCGGCGCTCGAGCGCGG 60
QY 61 CGAGACGACGCTGACACGCTTCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 CGAGACGACGCTGACACGCTTCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 CCCGGAGCGCGGAGCGCATGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180
DB 121 CCCGGAGCGCGGAGCGCATGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180
QY 181 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AGGGAGAGCAAAAGCGCGACGCTCCGCGCAGAGGAGGAGTGCTGATTAATGAGATGT 300
DB 241 AGGGAGAGCAAAAGCGCGACGCTCCGCGCAGAGGAGGAGTGCTGATTAATGAGATGT 300
QY 301 GCTTACAAAGGCGCAGAGAGTCCGCTGCTGAGAGCGCGCGCTGGGGCGCATTTATTC 360
```

Db 301 GCTTACAAGGCCAGAGAGTGCCTGTGAGACGGAGGCCCTGGGCCCAATGTATTC 360  
QY 361 CGGGTACACCTGGGATCCAGGTGGAGTATTCAGAGAGAGAGAGAGAGAGATGTCTGA 420  
Db 361 CGGGTACACCTGGGATCCAGGTGGAGTATTCAGAGAGAGAGAGAGAGAGATGTCTGA 420  
QY 421 GGGAAAGCTTTGAGAGATCCCTGGACACCCAACTACAGAGAGTGTTCATGGAGTTCATGA 480  
Db 421 GGGAAAGCTTTGAGAGATCCCTGGACACCCAACTACAGAGAGTGTTCATGGAGTTCATGA 480  
QY 481 ATTATGCGATAGATCTGGGAGAGAGATCCAGAGTGTTCATTCAGAGAGAGTGTTCATGA 540  
Db 481 ATTATGCGATAGATCTGGGAGAGAGATCCAGAGTGTTCATTCAGAGAGAGTGTTCATGA 540  
QY 541 GTGCTTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 GTGCTTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 601 AGCGTTGGTATTTACATTCATGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTCAG 660  
Db 601 AGCGTTGGTATTTACATTCATGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTCAG 660  
QY 661 TAATTTATTTGAG 720  
Db 661 TAATTTATTTGAG 720  
QY 721 CTCTGTGAG 780  
Db 721 CTCTGTGAG 780  
QY 781 TTGGCATTGTTCAGATTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
Db 781 TTGGCATTGTTCAGATTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 841 GCATCATTTATGAG 900  
Db 841 GCATCATTTATGAG 900  
QY 901 TTATTTAGGCTTGGAG 960  
Db 901 TTATTTAGGCTTGGAG 960  
QY 961 GAATGAAG 1020  
Db 961 GAATGAAG 1020  
QY 1021 ATCTAGCATTTATGAG 1080  
Db 1021 ATCTAGCATTTATGAG 1080  
QY 1081 AGAATACTTCTTATGAG 1140  
Db 1081 AGAATACTTCTTATGAG 1140  
QY 1141 TTGCTTTTCTCTAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1200  
Db 1141 TTGCTTTTCTCTAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1200  
QY 1201 AATTTGTAATGTTAG 1257  
Db 1201 AATTTGTAATGTTAG 1257

RESULT 5  
US-10-006-130A-430  
; Sequence 430, Application US/10006130A  
; Publication No. US20030148375A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan J.  
; APPLICANT: Ferrara, Napoleone

APPLICANT: Pong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C7  
CURRENT FILING DATE: 2002-03-19  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 430  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-006-130A-430  
Query Match 100.0%; Score 1257; DB 12; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,3e-281; Indels 0; Gaps 0;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAG 60  
Db 1 GGAG 60  
QY 61 CGGAG 120  
Db 61 CGGAG 120  
QY 121 CCGGAG 180  
Db 121 CCGGAG 180  
QY 181 GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 241 AGGGAG 300  
Db 241 AGGGAG 300  
QY 301 GCTTACAAGGCCAG 360  
Db 301 GCTTACAAGGCCAG 360  
QY 361 CGGGTACACCTGGGATCCAGGTGGAGTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
Db 361 CGGGTACACCTGGGATCCAGGTGGAGTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 421 GGGAAAGCTTTGAGAGATCCCTGGACACCCAACTACAGAGAGTGTTCATGGAGTTCATGA 480  
Db 421 GGGAAAGCTTTGAGAGATCCCTGGACACCCAACTACAGAGAGTGTTCATGGAGTTCATGA 480  
QY 481 ATTATGCGATAGATCTGGGAGAGAGATCCAGAGTGTTCATTCAGAGAGAGTGTTCATGA 540  
Db 481 ATTATGCGATAGATCTGGGAGAGAGATCCAGAGTGTTCATTCAGAGAGAGTGTTCATGA 540  
QY 541 GTGCTTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 GTGCTTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 601 AGCGTTGGTATTTACATTCATGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTCAG 660  
Db 601 AGCGTTGGTATTTACATTCATGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTCAG 660  
QY 661 TAATTTATTTGAG 720  
Db 661 TAATTTATTTGAG 720









QY	841	GCATCATTTATGAGAACTACCAAAATTAAGCTTAAATTTTCATTTGCTCACTCTTTT	900
Db	841	GCATCATTTATGAGAACTACCAAAATTAAGCTTAAATTTTCATTTGCTCACTCTTTT	900
QY	901	TTATATAGCCTTGGAAATGCTTCACTTAAATGACATTTTAAATAGTTATGTATACATCT	960
Db	901	TTATATAGCCTTGGAAATGCTTCACTTAAATGACATTTTAAATAGTTATGTATACATCT	960
QY	961	GAATGAAGAAAGCAAGCTTAATATATTTTACAGACCAAAAGTGTGATTTTCACATGTTTTTA	1020
Db	961	GAATGAAGAAAGCAAGCTTAATATATTTTACAGACCAAAAGTGTGATTTTCACATGTTTTTA	1020
QY	1021	ATCTAGCATTTATTCATTTTGGCTTCAATCAAAAGTGGTTCAATATTTTATTTAGTGGTT	1080
Db	1021	ATCTAGCATTTATTCATTTTGGCTTCAATCAAAAGTGGTTCAATATTTTATTTAGTGGTT	1080
QY	1081	AGAACTACTTTCCTCATAGTCACATTTCTCTCAACCTATATTTGGAATATTTGTGTGCT	1140
Db	1081	AGAACTACTTTCCTCATAGTCACATTTCTCTCAACCTATATTTGGAATATTTGTGTGCT	1140
QY	1141	TTTGTGTTTTTCTCTTAGTATAGCAATTTTAAAAAATATAAAGCTACCAATCTTTGTAC	1200
Db	1141	TTTGTGTTTTTCTCTTAGTATAGCAATTTTAAAAAATATAAAGCTACCAATCTTTGTAC	1200
QY	1201	AATTTGTAAATGTAAAGAAATTTTAAAAATATCTGTAAATAAAAAATTAATTTCCAAACA	1257
Db	1201	AATTTGTAAATGTAAAGAAATTTTAAAAATATCTGTAAATAAAAAATTAATTTCCAAACA	1257

RESULT 8  
US-10-187-749-365  
Sequence 365, Application US/10187749  
Publication No. US2003015036A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gunney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C1  
CURRENT APPLICATION NUMBER: US/10/187,749  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: US/10/052,586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Remaining Prior Application data removed - See File Wrapper or PAM.  
NUMBER OF SEQ ID NOS: 612

[illegible]



QY 961 GAATGAAAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACACTGTTTTAA 1020  
DB 961 GAATGAAAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACACTGTTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTGCTTCATTCACAAAGTGTGTTCAATTTTGTAGTGGTT 1080  
DB 1021 ATCTAGCATTTATTCATTTGCTTCATTCACAAAGTGTGTTCAATTTTGTAGTGGTT 1080  
QY 1081 AAGATCTTTCTTCATAGTACATTTCTCAACCTTAATTTGGAATTTGTGTGCT 1140  
DB 1081 AAGATCTTTCTTCATAGTACATTTCTCAACCTTAATTTGGAATTTGTGTGCT 1140  
QY 1141 TTTGTTTCTTCTAGTATGATTTTAAAAAATPAAAAAGTACCAATCTTTGTAC 1200  
DB 1141 TTTGTTTCTTCTAGTATGATTTTAAAAAATPAAAAAGTACCAATCTTTGTAC 1200  
QY 1201 AATTTGTAATGTAGTAATTTTATATCTGTAATPAAAAATTTATTTCCAA 1257  
DB 1201 AATTTGTAATGTAGTAATTTTATATCTGTAATPAAAAATTTATTTCCAA 1257

RESULT 9

US-10-194-457-365  
Sequence 365, Application US/10194457  
Publication No. US20030153037A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Guirney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C296  
CURRENT APPLICATION NUMBER: US/10/194,457  
PRIOR FILING DATE: 2002-07-11  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-194-457-365

Query Match 100.0%; Score 1257; DB 12; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,3e-281;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAGAGAGCGCGCGGGTAAAGCGCATTTGATGACGTGGCGCGGCTCGAGCGCG 60  
DB 1 GGAGAGAGCGCGCGGGTAAAGCGCATTTGATGACGTGGCGCGGCTCGAGCGCG 60  
QY 61 CGAGGCGAAGCGTGCACACGTTCTCTCTGCGGTCTCTCGGCTCGAGCTCCGGCTG 120  
DB 61 CGAGGCGAAGCGTGCACACGTTCTCTCTGCGGTCTCTCGGCTCGAGCTCCGGCTG 120  
QY 121 CCGGCGAGCGGGAGCGATCGGACCCGAGGCGCGCGCGCTCCCGGAGCGGCTCGGG 180  
DB 121 CCGGCGAGCGGGAGCGATCGGACCCGAGGCGCGCGCGCTCCCGGAGCGGCTCGGG 180  
QY 181 GCGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GCGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 AGGCGAAGCAAAAGCGCGACGCTCCGCGAGAGGAGGTGCTGATTAATGAAATG 300  
DB 241 AGGCGAAGCAAAAGCGCGACGCTCCGCGAGAGGAGGTGCTGATTAATGAAATG 300  
QY 301 GCTTACAGGCGCAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 301 GCTTACAGGCGCAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 361 CGGCTACACCTGGGATCCGAGGCTGGATGATTCAAAGAGAAAGGGGAGATGCTGA 420  
DB 361 CGGCTACACCTGGGATCCGAGGCTGGATGATTCAAAGAGAAAGGGGAGATGCTGA 420  
QY 421 GGGAAAGCTTTGAGAGGCTCTGAGACACCACTACAGAGGTTTCATGAGTTCAATGA 480  
DB 421 GGGAAAGCTTTGAGAGGCTCTGAGACACCACTACAGAGGTTTCATGAGTTCAATGA 480  
QY 481 ATTATGCAATGATCTGGGAAATATGCGAGGCTGATTTCAAGATGCGTCAAA 540  
DB 481 ATTATGCAATGATCTGGGAAATATGCGAGGCTGATTTCAAGATGCGTCAAA 540  
QY 541 GTGCTTAAGAGTTTGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 541 GTGCTTAAGAGTTTGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 601 AGCGTTGATTTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 660  
DB 601 AGCGTTGATTTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 660  
QY 661 TAATTAATTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 720  
DB 661 TAATTAATTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 720  
QY 721 CTTCGTGAGAGACTTTGTGAAGAAATGAGTGTGATTTAGTGTGATTTAGTGTG 780  
DB 721 CTTCGTGAGAGACTTTGTGAAGAAATGAGTGTGATTTAGTGTGATTTAGTGTG 780  
QY 781 TTGGCACTGTTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 840  
DB 781 TTGGCACTGTTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 840  
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAATTTTATTTTATTTTATTTT 900  
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAATTTTATTTTATTTTATTTT 900  
QY 901 TTAATTTGCTTGAATGCTTCACTTAATGCAATTTTAATTAATTTTATTTTATTTT 960  
DB 901 TTAATTTGCTTGAATGCTTCACTTAATGCAATTTTAATTAATTTTATTTTATTTT 960  
QY 961 GAATGAAAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACACTGTTTTAA 1020  
DB 961 GAATGAAAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACACTGTTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTGCTTCATTCACAAAGTGTGTTCAATTTTGTAGTGGTT 1080  
DB 1021 ATCTAGCATTTATTCATTTGCTTCATTCACAAAGTGTGTTCAATTTTGTAGTGGTT 1080

OY 1081 AGAATCTTCTCATAGTCACATTCCTCAACCTATATTTGGAATTTGTGTGCTT 1140  
|||||  
Db 1081 AGAATCTTCTCATAGTCACATTCCTCAACCTATATTTGGAATTTGTGTGCTT 1140  
OY 1141 TTGCTTTTCTCTAGTATGCAATTTTAAAAAATTAACCTACCAATCTTTGTAC 1200  
|||||  
Db 1141 TTGCTTTTCTCTAGTATGCAATTTTAAAAAATTAACCTACCAATCTTTGTAC 1200  
OY 1201 AATTTGTAATGTAAGATTTTATATCTGTAAATATAATTTTCCACA 1257  
|||||  
Db 1201 AATTTGTAATGTAAGATTTTATATCTGTAAATATAATTTTCCACA 1257  
RESULT 10  
US-10-006-867-121  
Sequence 121, Application US/10006867  
Publication No. US20020119130A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gutney, Austin L.  
APPLICANT: Watanabe, Colin K.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/006, 867  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/063435  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/064215  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090688  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091628  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/096012  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096757  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096949  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/096959  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/097954  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097971  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097979  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105881  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106030



QY 1081 AGAATCTCTTCATAGTCACATCTCTCAACCTATATATTTGGAATATGTTGTGCT 1140  
1141 TTTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAACTACCATCTTTGTAC 1200  
1141 TTTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAACTACCATCTTTGTAC 1200  
QY 1201 AATTGTAAATGTTAAGATTTTATATCTGTAAATATAATTTTCCACA 1257  
1201 AATTGTAAATGTTAAGATTTTATATCTGTAAATATAATTTTCCACA 1257  
Db 1201 AATTGTAAATGTTAAGATTTTATATCTGTAAATATAATTTTCCACA 1257

RESULT 11  
US-10-052-586-365  
Sequence 365, Application US/10052586  
Publication No. US20020127584A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gunney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OR INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C1  
CURRENT APPLICATION NUMBER: US/10/052,586  
PRIOR APPLICATION NUMBER: 2002-01-15  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063564  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063734  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063870  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066120  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066466  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066772  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069335  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069425  
PRIOR FILING DATE: 1997-12-12

PRIOR APPLICATION NUMBER: 60/069870  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/068017  
PRIOR FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086023

PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/086486  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087098  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087208  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088722  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089090  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1257; DB 13; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,3e-281;

Matches 1257;		Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	GGAGAGAGGCGCGGGGTGAAGGCCCATTTGATGACGCTCGCGCGGCTCGAGAGCGG	60						
Db	1	GGAGAGAGGCGCGGGGTGAAGGCCCATTTGATGACGCTCGCGCGGCTCGAGAGCGG	60						
QY	61	CGAGGCGAGAGCGTGACACAGTTCCTCTCGGTCTCTCCGCTCCAGACTCGGCGTG	120						
Db	61	CGAGGCGAGAGCGTGACACAGTTCCTCTCGGTCTCTCCGCTCCAGACTCGGCGTG	120						
QY	121	CCCGGACGCGGGAGCCATGCGACCCAGGCGCCCGCGCTCCCGGACGCGCTCGCG	180						
Db	121	CCCGGACGCGGGAGCCATGCGACCCAGGCGCCCGCGCTCCCGGACGCGCTCGCG	180						
QY	181	GCCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240						
Db	181	GCCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240						
QY	241	AGGGAGAGCAAAAGGCGAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAATGT	300						
Db	241	AGGGAGAGCAAAAGGCGAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAATGT	300						
QY	301	GCTTACAGGCGCCAGCAGAGTCTGCTGCGAGCGGAGCCTGGGCGCAATGTTATTC	360						
Db	301	GCTTACAGGCGCCAGCAGAGTCTGCTGCGAGCGGAGCCTGGGCGCAATGTTATTC	360						
QY	361	CGGGTACCTGGGATCCAGGTCGGGATGATGATTAAGAGAGAGAGGAGGATGCTGA	420						
Db	361	CGGGTACCTGGGATCCAGGTCGGGATGATGATTAAGAGAGAGAGGAGGATGCTGA	420						
QY	421	GGGAAAGCTTTGAGAGTCCCTGAGCACCCAGTACAGAGTGTGATGAGTTCATTTGA	480						
Db	421	GGGAAAGCTTTGAGAGTCCCTGAGCACCCAGTACAGAGTGTGATGAGTTCATTTGA	480						
QY	481	ATTATGCGATAGTCTTGGGAAATTCGGAGTGTACATTTACAAAGATCGTTCAATA	540						
Db	481	ATTATGCGATAGTCTTGGGAAATTCGGAGTGTACATTTACAAAGATCGTTCAATA	540						
QY	541	GTCCTTAAGAGTGTGTCAGTGGCTACTGGCTTAATAATGCAAAATGCAATGCTGTC	600						
Db	541	GTCCTTAAGAGTGTGTCAGTGGCTACTGGCTTAATAATGCAAAATGCAATGCTGTC	600						
QY	601	AGCGTGTGATTTACATTCATGAGCTGATGTCAGAGCTCTTCCCATTTGAAGCTA	660						
Db	601	AGCGTGTGATTTACATTCATGAGCTGATGTCAGAGCTCTTCCCATTTGAAGCTA	660						
QY	661	TAAATTTATTTGACCAAGAGAGCCCTGAATTAATTAATTAATTAATTAATTAAT	720						
Db	661	TAAATTTATTTGACCAAGAGAGCCCTGAATTAATTAATTAATTAATTAATTAAT	720						
QY	721	CTTCGTGAGAGCTTGTGAAGAAATGTCGTCGATTAAGTATGATGATGATGATG	780						
Db	721	CTTCGTGAGAGCTTGTGAAGAAATGTCGTCGATTAAGTATGATGATGATGATG	780						
QY	781	TTGGCACTTGTTCAGATTAACCCAAAGAGATCTCTAGTGAATGATGATGATGATG	840						
Db	781	TTGGCACTTGTTCAGATTAACCCAAAGAGATCTCTAGTGAATGATGATGATGATG	840						
QY	841	GCATCAATTAATGAAGACTACCAAAATTAATTAATTAATTAATTAATTAATTAAT	900						
Db	841	GCATCAATTAATGAAGACTACCAAAATTAATTAATTAATTAATTAATTAATTAAT	900						
QY	901	TTATTTGCTTGGATGATGCTTCAATTAATTAATTAATTAATTAATTAATTAATTA	960						
Db	901	TTATTTGCTTGGATGATGCTTCAATTAATTAATTAATTAATTAATTAATTAATTA	960						
QY	961	GAATGAAGAGCAAGCTAATATGTTTACAGACCAAGTGTGATTTACACAGTGTTTA	1020						
Db	961	GAATGAAGAGCAAGCTAATATGTTTACAGACCAAGTGTGATTTACACAGTGTTTA	1020						
QY	1021	ATCTAGCATTAATTAATTTGCTTCAATCAAAAGTGTTCAAATTAATTTTATGTTGT	1080						
Db	1021	ATCTAGCATTAATTAATTTGCTTCAATCAAAAGTGTTCAAATTAATTTTATGTTGT	1080						

QY 1081 AGAATCTTCTTCATAGTACATCTCTCAACCTATAATTTGGAAATATGTTGGTCT 1140  
DB 1081 AGAATCTTCTTCATAGTACATCTCTCAACCTATAATTTGGAAATATGTTGGTCT 1140  
QY 1141 TTTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAGCTTACCATCTTTGAC 1200  
DB 1141 TTTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAGCTTACCATCTTTGAC 1200  
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATAAATTTATTTCCACA 1257  
DB 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATAAATTTATTTCCACA 1257

RESULT 12  
US-10-063-547-121  
; Sequence 121, Application US/10063547  
; Publication No. US20020182638A1  
; GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 121  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-547-121

Query Match 100.0%; Score 1257; DB 13; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,3e-281;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGAGCGCGCGGTGAAAAAGCGCATTTATGACGCTCGGCGGCTCGGAGCGGG 60  
DB 1 GGAAGAGAGCGCGCGGTGAAAAAGCGCATTTATGACGCTCGGCGGCTCGGAGCGGG 60  
QY 61 CGAGCGCGAGCGCTGACCGAGTCTCTCGGTCTCGGCTCGGCTCGGCTCGGCTCGGCTG 120  
DB 61 CGAGCGCGAGCGCTGACCGAGTCTCTCGGTCTCGGCTCGGCTCGGCTCGGCTCGGCTG 120  
QY 121 CCCGCGACCGCGGAGCCATGCGACCCCGAGGCGCCCGCCCGCCCGCGCGCTCGGCTG 180  
DB 121 CCCGCGACCGCGGAGCCATGCGACCCCGAGGCGCCCGCCCGCCCGCGCGCTCGGCTG 180  
QY 181 GCTTCCTGCTGCTCTGCTGCTGCAAGCTGCGCGCGCGCTCGAGCGCTCTGATGCCA 240  
DB 181 GCTTCCTGCTGCTCTGCTGCTGCAAGCTGCGCGCGCGCTCGAGCGCTCTGATGCCA 240  
QY 241 AGGGGAACCAAAAGCGAGCTCCGGCAGAGGAGGTGTGAGCTGTATATGGAATGT 300  
DB 241 AGGGGAACCAAAAGCGAGCTCCGGCAGAGGAGGTGTGAGCTGTATATGGAATGT 300  
QY 301 GCTTACAAAGGCGCAGCAGAGTGCCTGCTGCGAGAGCGGAGCCCTTGAGCTTATTC 360  
DB 301 GCTTACAAAGGCGCAGCAGAGTGCCTGCTGCGAGAGCGGAGCCCTTGAGCTTATTC 360  
QY 361 CGGGTACACCTGGAGATCCAGGTGCGGATGATTCAAAGGAGAAAAAGGGGAATGTCTGA 420  
DB 361 CGGGTACACCTGGAGATCCAGGTGCGGATGATTCAAAGGAGAAAAAGGGGAATGTCTGA 420

QY 421 GGGAAAGCTTTAGAGAGTCTCGGACACCCAACTACAGCAGTTCATGAGTCAATGCA 480  
DB 421 GGGAAAGCTTTAGAGAGTCTCGGACACCCAACTACAGCAGTTCATGAGTCAATGCA 480  
QY 481 AATTAGCATAGATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGTGGCTCAATA 540  
DB 481 AATTAGCATAGATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGTGGCTCAATA 540  
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACCTGCGCTAAATATGAGAAATCATAGCTGC 600  
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACCTGCGCTAAATATGAGAAATCATAGCTGC 600  
QY 601 AGCGTGGTATTTACATTCATTAAGAGCTGAATGTTCAGAGACCTCTCCATTTGAAGCTA 660  
DB 601 AGCGTGGTATTTACATTCATTAAGAGCTGAATGTTCAGAGACCTCTCCATTTGAAGCTA 660  
QY 661 TAAATTTATTTGAGCAAGAGCCCTGAATGAATTCAAATTAATTTATGAGCACTT 720  
DB 661 TAAATTTATTTGAGCAAGAGCCCTGAATGAATTCAAATTAATTTATGAGCACTT 720  
QY 721 CTTCGTGGAAGAGCTTTGTGAAGAAATTTGGTGTGATTTAGTGGATGTTGCTATCTGGG 780  
DB 721 CTTCGTGGAAGAGCTTTGTGAAGAAATTTGGTGTGATTTAGTGGATGTTGCTATCTGGG 780  
QY 781 TTGGCAGCTTTGTCAGATTACCCAAAGAGATGCTTCTACAGATGAGAAATTCAGTTCTC 840  
DB 781 TTGGCAGCTTTGTCAGATTACCCAAAGAGATGCTTCTACAGATGAGAAATTCAGTTCTC 840  
QY 841 GCATCATTAATTTGAAGAACTACCAAAATTAATGCTTTAATTTCAATTTCTACCTTTT 900  
DB 841 GCATCATTAATTTGAAGAACTACCAAAATTAATGCTTTAATTTCAATTTCTACCTTTT 900  
QY 901 TTAATATGCTTTGGAATGTTCACTTAATGATTAATGATTAATTAATTAATTAATTAAT 960  
DB 901 TTAATATGCTTTGGAATGTTCACTTAATGATTAATGATTAATTAATTAATTAATTAAT 960  
QY 961 GAATGAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTTAA 1020  
DB 961 GAATGAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGTGTTCATTAATTTTATGAGTGT 1080  
DB 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGTGTTCATTAATTTTATGAGTGT 1080  
QY 1081 AGAATCTTCTTCATAGTACATCTCTCAACCTATAATTTGGAATATGTTGGTCT 1140  
DB 1081 AGAATCTTCTTCATAGTACATCTCTCAACCTATAATTTGGAATATGTTGGTCT 1140  
QY 1141 TTTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAGCTTACCAATCTTTGAC 1200  
DB 1141 TTTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAGCTTACCAATCTTTGAC 1200  
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATAAATTTATTTCCACA 1257  
DB 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATAAATTTATTTCCACA 1257

RESULT 13  
US-10-174-590-365  
; Sequence 365, Application US/10174590  
; Publication No. US20030008352A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

```

: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C42
: CURRENT APPLICATION NUMBER: US/10/174,590
: CURRENT FILING DATE: 2002-06-18
: Prior application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 365
: LENGTH: 1257
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-174-590-365

```

```

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACAGCTGCGGGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACAGCTGCGGGCGCTCGAGGCGCG 60
QY 61 CGAGAGCAGACGCGTGCACAGTTCCTCTCGGTGCTCCGCGCTCCAGCTCCGGGCTG 120
DB 61 CGAGAGCAGACGCGTGCACAGTTCCTCTCGGTGCTCCGCGCTCCAGCTCCGGGCTG 120
QY 121 CCCGGAGCGCGGGAGCCATGCGACCCAGAGGCGCGCGCTCCCGCAGCGGCTCCGCG 180
DB 121 CCCGGAGCGCGGGAGCCATGCGACCCAGAGGCGCGCGCTCCCGCAGCGGCTCCGCG 180
QY 181 GCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GCTTACAAAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GCTTACAAAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ATTATGAGCATATGATCTTGGAGAAATTCGAGAGTGTACATTTACAAAGATGCGTTCAATA 540
DB 481 ATTATGAGCATATGATCTTGGAGAAATTCGAGAGTGTACATTTACAAAGATGCGTTCAATA 540
QY 541 GTCGCTCTAAGAGATTTTGTTCAGTGGCTCCTCGGCTTAATAATGACAGAAATGCACTGCTG 600
DB 541 GTCGCTCTAAGAGATTTTGTTCAGTGGCTCCTCGGCTTAATAATGACAGAAATGCACTGCTG 600
QY 601 AGCGTGTGATTTTCAATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 AGCGTGTGATTTTCAATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TAATTTATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TAATTTATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTTTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CTTTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

```

```

QY 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TTTATTTGCGTGGAGATGCTGCTTAAATGACATTTTAAATGAGTTATGATATCATCT 960
DB 901 TTTATTTGCGTGGAGATGCTGCTTAAATGACATTTTAAATGAGTTATGATATCATCT 960
QY 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 ATCTAGCATTTATCATTTTGTCTTCAATCAATGAGTTTCAATATTTTGTGTTGTT 1080
DB 1021 ATCTAGCATTTATCATTTTGTCTTCAATCAATGAGTTTCAATATTTTGTGTTGTT 1080
QY 1081 AGAATATCTTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 AGAATATCTTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 TTTGTTTTTCTCTTGTATGATGATTTTAAATATTAATTAATTAATTAATTAATTAAT 1200
DB 1141 TTTGTTTTTCTCTTGTATGATGATTTTAAATATTAATTAATTAATTAATTAATTAAT 1200
QY 1201 AATTGTAAATGTTAAGAAATTTTAAATATCTGTTAAATTAATTAATTAATTAATTAAT 1257
DB 1201 AATTGTAAATGTTAAGAAATTTTAAATATCTGTTAAATTAATTAATTAATTAATTAAT 1257

```

```

RESULT 14
US-10-176-758-365
Sequence 365, Application US/10176758
Publication No. US20030008353A1
GENERAL INFORMATION:

```

```

: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jilan
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Goddard, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Collin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C104
: CURRENT APPLICATION NUMBER: US/10/176,758
: CURRENT FILING DATE: 2002-06-21
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 365
: LENGTH: 1257
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-176-758-365

```

```

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACAGCTGCGGGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGGGGTGAAGAGCGCATTTGATGACAGCTGCGGGCGCTCGAGGCGCG 60
QY 61 CGAGAGCAGACGCGTGCACAGTTCCTCTCGGTGCTCCGCGCTCCAGCTCCGGGCTG 120
DB 61 CGAGAGCAGACGCGTGCACAGTTCCTCTCGGTGCTCCGCGCTCCAGCTCCGGGCTG 120
QY 121 CCCGGAGCGCGGGAGCCATGCGACCCAGAGGCGCGCGCTCCCGCAGCGGCTCCGCG 180
DB 121 CCCGGAGCGCGGGAGCCATGCGACCCAGAGGCGCGCGCTCCCGCAGCGGCTCCGCG 180

```







```
OY 601 ACCGTTGGTATTTACATTCAAATGAGCTGAAATGTTTCAGACCTCTTCCATTGAAGCTA 660
|||||
DB 601 ACCGTTGGTATTTACATTCAAATGAGCTGAAATGTTTCAGACCTCTTCCATTGAAGCTA 660
|||||
OY 661 TAATTTATTTGAGCAGAGAGACCCCGGAATGATTCACCAATTAATATTCATCGACATT 720
|||||
DB 661 TAATTTATTTGAGCAGAGAGACCCCGGAATGATTCACCAATTAATATTCATCGACATT 720
|||||
OY 721 CTTCGTGAGAGACTTTTGAAGAAATGTTGCTGATTAAGTATGATGTTGCTATCTGGG 780
|||||
DB 721 CTTCGTGAGAGACTTTTGAAGAAATGTTGCTGATTAAGTATGATGTTGCTATCTGGG 780
|||||
OY 781 TTGGCAGCTGTTCAGATTCACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840
|||||
DB 781 TTGGCAGCTGTTCAGATTCACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840
|||||
OY 841 GCATCATTTTGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
|||||
DB 841 GCATCATTTTGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
|||||
OY 901 TTATTATGCTTGAATGTTTCACTTAATGACATTTTAATAGTTTATGATATACATCT 960
|||||
DB 901 TTATTATGCTTGAATGTTTCACTTAATGACATTTTAATAGTTTATGATATACATCT 960
|||||
OY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTTACACTGTTTTTAA 1020
|||||
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTTACACTGTTTTTAA 1020
|||||
OY 1021 ATCTAGCATTTATTCATTTTGCCTTCATCAATCAAAAAGTGTTCAATATTTTATGTTGTT 1080
|||||
DB 1021 ATCTAGCATTTATTCATTTTGCCTTCATCAATCAAAAAGTGTTCAATATTTTATGTTGTT 1080
|||||
OY 1081 AGAATACCTTCTTCATAGTACATCTCTCAACCTATATTTGAATATTTGTTGTTGCT 1140
|||||
DB 1081 AGAATACCTTCTTCATAGTACATCTCTCAACCTATATTTGAATATTTGTTGTTGCT 1140
|||||
OY 1141 TTTGTTTTTCTCTAGTATACATTTTAAAAAATATATAAAGCTACCAATCTTTGTAC 1200
|||||
DB 1141 TTTGTTTTTCTCTAGTATACATTTTAAAAAATATATAAAGCTACCAATCTTTGTAC 1200
|||||
OY 1201 AATTTGTAAGTGAAGATTTTATTTATCTGTTAATATAAATTAATTTCCACACA 1257
|||||
DB 1201 AATTTGTAAGTGAAGATTTTATTTATCTGTTAATATAAATTAATTTCCACACA 1257
|||||
```

Search completed: August 20, 2003, 16:01:55  
Job time : 314 secs

**THIS PAGE BLANK (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 12:28:07 ; Search time 4236 Seconds  
(without alignments)  
9723.603 Million cell updates/sec

Title: US-09-938-418-2

Perfect score: 1257  
Sequence: 1 ggaagagagcgcgcggtga.....aataaattattccaca 1257

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/2/pna/PCRTUS\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/PCRTUS\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq.\*  
8: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq.\*  
9: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq.\*  
10: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq.\*  
11: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq.\*  
12: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq.\*  
13: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq.\*  
14: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq.\*  
15: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq.\*  
16: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq.\*  
17: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq.\*  
18: /cgn2\_6/ptodata/2/pna/US093\_COMB.seq.\*  
19: /cgn2\_6/ptodata/2/pna/US093A\_COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US093B\_COMB.seq.\*  
21: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq.\*  
22: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq.\*  
23: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq.\*  
24: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq.\*  
25: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq.\*  
26: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq.\*  
27: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq.\*  
29: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq.\*  
30: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq.\*  
31: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq.\*  
32: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq.\*  
33: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq.\*  
34: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq.\*  
35: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq.\*  
36: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US098D\_COMB.seq.\*  
38: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq.\*  
39: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq.\*  
40: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq.\*  
41: /cgn2\_6/ptodata/2/pna/US099E\_COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq.\*

44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq.\*  
45: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq.\*  
46: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq.\*  
47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq.\*  
48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq.\*  
49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq.\*  
50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq.\*  
51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq.\*  
52: /cgn2\_6/ptodata/2/pna/US104A\_COMB.seq.\*  
53: /cgn2\_6/ptodata/2/pna/US104B\_COMB.seq.\*  
54: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq.\*  
55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq.\*  
56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq.\*  
57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq.\*  
58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq.\*  
59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq.\*  
60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq.\*  
61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq.\*  
62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq.\*  
63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq.\*  
64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq.\*  
65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq.\*  
66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq.\*  
67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq.\*  
68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq.\*  
69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq.\*  
70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq.\*  
71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq.\*  
72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq.\*  
74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq.\*  
75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq.\*  
76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq.\*  
77: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq.\*  
78: /cgn2\_6/ptodata/2/pna/US6023A\_COMB.seq.\*  
79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq.\*  
80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq.\*  
81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq.\*  
82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq.\*  
83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq.\*  
84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq.\*  
85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq.\*  
86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq.\*  
87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq.\*  
88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq.\*  
89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq.\*  
90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*  
91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq.\*  
92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq.\*  
93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq.\*  
94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq.\*  
95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq.\*  
96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq.\*  
97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq.\*  
98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq.\*  
99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq.\*  
100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq.\*  
101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq.\*  
102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1257	100.0	39	US-09-938-418-2	Sequence 2, Appl1
2	1257	100.0	40	US-09-946-374-430	Sequence 430, App
3	1257	100.0	44	US-10-006-041A-430	Sequence 430, App
4	1257	100.0	44	US-10-006-063A-430	Sequence 430, App

5	1257	100.0	1257	44	US-10-006-116A-430	Sequence 430, App
6	1257	100.0	1257	44	US-10-006-117A-430	Sequence 430, App
7	1257	100.0	1257	44	US-10-006-130A-430	Sequence 430, App
8	1257	100.0	1257	44	US-10-006-172A-430	Sequence 430, App
9	1257	100.0	1257	44	US-10-006-485A-430	Sequence 430, App
10	1257	100.0	1257	44	US-10-006-746A-430	Sequence 430, App
11	1257	100.0	1257	44	US-10-006-768A-430	Sequence 430, App
12	1257	100.0	1257	44	US-10-006-818A-430	Sequence 430, App
13	1257	100.0	1257	44	US-10-006-856A-430	Sequence 430, App
14	1257	100.0	1257	44	US-10-006-867-121	Sequence 430, App
15	1257	100.0	1257	44	US-10-007-194A-430	Sequence 430, App
16	1257	100.0	1257	44	US-10-007-236A-430	Sequence 430, App
17	1257	100.0	1257	44	US-10-011-671A-430	Sequence 430, App
18	1257	100.0	1257	44	US-10-011-692A-430	Sequence 430, App
19	1257	100.0	1257	44	US-10-011-795A-430	Sequence 430, App
20	1257	100.0	1257	44	US-10-011-795B-430	Sequence 430, App
21	1257	100.0	1257	44	US-10-011-833A-430	Sequence 430, App
22	1257	100.0	1257	44	US-10-012-064A-430	Sequence 430, App
23	1257	100.0	1257	44	US-10-012-101B-430	Sequence 430, App
24	1257	100.0	1257	44	US-10-012-121A-430	Sequence 430, App
25	1257	100.0	1257	44	US-10-012-137A-430	Sequence 430, App
26	1257	100.0	1257	44	US-10-012-149A-430	Sequence 430, App
27	1257	100.0	1257	44	US-10-012-231A-430	Sequence 430, App
28	1257	100.0	1257	44	US-10-012-237A-430	Sequence 430, App
29	1257	100.0	1257	44	US-10-012-752A-430	Sequence 430, App
30	1257	100.0	1257	44	US-10-012-753A-430	Sequence 430, App
31	1257	100.0	1257	44	US-10-012-754A-430	Sequence 430, App
32	1257	100.0	1257	44	US-10-012-755A-430	Sequence 430, App
33	1257	100.0	1257	44	US-10-013-430A-430	Sequence 430, App
34	1257	100.0	1257	44	US-10-013-906A-430	Sequence 430, App
35	1257	100.0	1257	44	US-10-013-907A-430	Sequence 430, App
36	1257	100.0	1257	44	US-10-013-909A-430	Sequence 430, App
37	1257	100.0	1257	44	US-10-013-910A-430	Sequence 430, App
38	1257	100.0	1257	44	US-10-013-911A-430	Sequence 430, App
39	1257	100.0	1257	44	US-10-013-912A-430	Sequence 430, App
40	1257	100.0	1257	44	US-10-013-913A-430	Sequence 430, App
41	1257	100.0	1257	44	US-10-013-915A-430	Sequence 430, App
42	1257	100.0	1257	44	US-10-015-385A-430	Sequence 430, App
43	1257	100.0	1257	44	US-10-015-386A-430	Sequence 430, App
44	1257	100.0	1257	44	US-10-015-387A-430	Sequence 430, App
45	1257	100.0	1257	44	US-10-015-388A-430	Sequence 430, App

## ALIGNMENTS

RESULT 1

US-09-938-418-2

Sequence 2, Application US/09938418

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Gurney, Austin L.

APPLICANT: Polakis, Paul

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Wu, Thomas D.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TITLE OF INVENTION: TREATMENT OF TUMOR

FILE REFERENCE: P5009R1

CURRENT APPLICATION NUMBER: US/09/938,418

PRIOR APPLICATION NUMBER: 60/081,071

PRIOR FILING DATE: 1998-04-07

PRIOR APPLICATION NUMBER: 60/085,697

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/097,022

PRIOR FILING DATE: 1998-08-18

PRIOR APPLICATION NUMBER: 60/101,922

PRIOR FILING DATE: 1998-09-24

PRIOR APPLICATION NUMBER: 60/103,679

QY	1	GGAGAGAGCGCGGGGTGAAGGCGATTGATGAGCTGCGGGGCGCTCGAGCGCGG	60	PRIOR FILING DATE: 1998-10-08	PCT/US99/05028
DB	1	GGAGAGAGCGCGGGGTGAAGGCGATTGATGAGCTGCGGGGCGCTCGAGCGCGG	60	PRIOR FILING DATE: 1999-03-08	PCT/US99/12252
QY	61	CGAGCGCGAGCGCTGACCGCTTCCTCCTCGCTGCTCCGCTCCGAGCTCGCGCTG	120	PRIOR FILING DATE: 1999-06-02	PCT/US99/20111
DB	61	CGAGCGCGAGCGCTGACCGCTTCCTCCTCGCTGCTCCGCTCCGAGCTCGCGCTG	120	PRIOR FILING DATE: 1999-09-01	PCT/US99/28565
QY	121	CCCGGACCGCGGAGCCATGAGCCCGAGGCGCGCGCTCCCGGAGGCGCTCGCGG	180	PRIOR FILING DATE: 1999-12-02	PCT/US00/04342
DB	121	CCCGGACCGCGGAGCCATGAGCCCGAGGCGCGCGCTCCCGGAGGCGCTCGCGG	180	PRIOR FILING DATE: 2000-02-18	PCT/US00/04341
QY	181	GCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240	PRIOR FILING DATE: 2000-02-18	PCT/US00/04341
DB	181	GCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240	PRIOR FILING DATE: 2000-03-02	PCT/US00/05841
QY	241	AGGGGAGCAAAAGGCGAGCTCCGCGAGAGAGAGCTGAGCTGATATATGGAATGT	300	PRIOR FILING DATE: 2000-03-02	PCT/US00/08439
DB	241	AGGGGAGCAAAAGGCGAGCTCCGCGAGAGAGAGCTGAGCTGATATATGGAATGT	300	PRIOR FILING DATE: 2000-03-30	PCT/US00/14042
QY	301	GCTTACAAAGGCGCAGAGAGTGCCTGCTGAGAGGAGGAGGCTGAGGCAATGTATTC	360	PRIOR FILING DATE: 2000-05-22	PCT/US00/23328
DB	301	GCTTACAAAGGCGCAGAGAGTGCCTGCTGAGAGGAGGAGGCTGAGGCAATGTATTC	360	PRIOR FILING DATE: 2000-08-24	PCT/US00/32678
QY	361	CGGTACACCTGGGATCCCAAGTGGGATGATTCAAAGGAGGAGGAGGAGTGTCTGA	420	PRIOR FILING DATE: 2000-12-01	PCT/US01/06520
DB	361	CGGTACACCTGGGATCCCAAGTGGGATGATTCAAAGGAGGAGGAGGAGTGTCTGA	420	PRIOR FILING DATE: 2001-02-28	PCT/US01/17800
QY	421	GGGAAGCTTTGAGAGAGTCTGAGACACCAACTACAGAGTTCATGAGTTCATTTGA	480	PRIOR FILING DATE: 2001-06-01	PCT/US01/19692
				PRIOR FILING DATE: 2001-06-20	PCT/US01/21066
				PRIOR FILING DATE: 2001-06-29	PCT/US01/21735
				PRIOR FILING DATE: 2001-07-09	
				NUMBER OF SEQ ID NOS: 10	
				SEQ ID NO 2	
				LENGTH: 1257	
				TYPE: DNA	
				ORGANISM: Homo Sapien	
				US-09-938-418-2	

Query Match 100.0%; Score 1257; DB 39; Length 1257;

Best Local Similarity 100.0%; Pred. No. 2; 7e-230; Indels 0; Gaps 0;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315

PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807  
PRIOR FILING DATE: 1998-10-27

Query Match 100.0%; Score 1257; DB 40; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,7e-230;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGGGGTGAAGGCGCATTTGATGACGCTCGCGGCGCTCGAGCGCG 60  
DB 1 GGAGAGAGCGCGGGGTGAAGGCGCATTTGATGACGCTCGCGGCGCTCGAGCGCG 60  
QY 61 CGGAGCCAGACGCTGACACGCTTCTCTCCGCTCTCCGCTCGAGCTCGCGCTG 120  
DB 61 CGGAGCCAGACGCTGACACGCTTCTCTCCGCTCTCCGCTCGAGCTCGCGCTG 120  
QY 121 CCCGAGACCGCGGAGCATGCGACCCAGAGGCGCCGCGCTCCCGCAGCGGCTCGCG 180  
DB 121 CCCGAGACCGCGGAGCATGCGACCCAGAGGCGCCGCGCTCCCGCAGCGGCTCGCG 180  
QY 181 GCTCTGCTGCTCTCTGCTGCTGACGCTGCCGCGCGCTGAGATCCCA 240  
DB 181 GCTCTGCTGCTCTCTGCTGCTGACGCTGCCGCGCGCTGAGATCCCA 240  
QY 241 AGGGGAAGCAAAAGCGGAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGAAATGT 300  
DB 241 AGGGGAAGCAAAAGCGGAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGAAATGT 300  
QY 301 GCTTCAAGGCGCAGAGAGTGCCTGTGAGAGGAGGAGCCCTGGGGCCAAATGTATTC 360  
DB 301 GCTTCAAGGCGCAGAGAGTGCCTGTGAGAGGAGGAGCCCTGGGGCCAAATGTATTC 360  
QY 361 CGGGTACACCTGGGATCCAGGTGCGGATGATTAAGGAGGAGGAGGAGGAGGAGGAGG 420  
DB 361 CGGGTACACCTGGGATCCAGGTGCGGATGATTAAGGAGGAGGAGGAGGAGGAGGAGG 420  
QY 421 GGGAAAGCTTTGAGGAGTCTCTGACACCACTTCAAGCAGTGTTCATGAGATTTCATG 480

```

Db      421 GGGAAAGCTTGGAGAGTCTGGACACCCAACTACAGAGTGCATGAGCTTCATTTGA 480
OY      481 ATTATGGCATATGATCTTGGGAAAAATTCGGAGCTGTACATTTTCAAAAGATGCTTCAAATA 540
Db      481 ATTATGGCATATGATCTTGGGAAAAATTCGGAGCTGTACATTTTCAAAAGATGCTTCAAATA 540
OY      541 GTGCTCTAAGAGTCTTGTTCAGTGGCTCACTTGGCTAAATATGCAAAAATGCAATGCTGTC 600
Db      541 GTGCTCTAAGAGTCTTGTTCAGTGGCTCACTTGGCTAAATATGCAAAAATGCAATGCTGTC 600
OY      601 AGCGTTGGATTTTGCATTCATTCATGAGAGCTGATTTTCAGAGCTCTCTCCCATTTGAAGCTA 660
Db      601 AGCGTTGGATTTTGCATTCATTCATGAGAGCTGATTTTCAGAGCTCTCTCCCATTTGAAGCTA 660
OY      661 TAATTTATTTGGACCAAGAGACCTCGAAATATGATTCACATTTATATTCATTCGCACTT 720
Db      661 TAATTTATTTGGACCAAGAGACCTCGAAATATGATTCACATTTATATTCATTCGCACTT 720
OY      721 CTTCGTGGAGAGACTTGTGTGAAGAAATTTGTGTGATTTAGTGAATGTTCATCTGAGG 780
Db      721 CTTCGTGGAGAGACTTGTGTGAAGAAATTTGTGTGATTTAGTGAATGTTCATCTGAGG 780
OY      781 TTGGGACTTTGTTCACATTTACCCAAAAGAGATGCTTTTACTGATGGAATTCAGTTCTC 840
Db      781 TTGGGACTTTGTTCACATTTACCCAAAAGAGATGCTTTTACTGATGGAATTCAGTTCTC 840
OY      841 GCATCATTTATGGAAGACTTACCAAAATTAATGCTTTATTTTCATTTGCTACCTCTTTT 900
Db      841 GCATCATTTATGGAAGACTTACCAAAATTAATGCTTTATTTTCATTTGCTACCTCTTTT 900
OY      901 TTATTTATGCTTGAATGATGTCCTTAAATGATTCATTTTAAATAGTTTATGTATACACT 960
Db      901 TTATTTATGCTTGAATGATGTCCTTAAATGATTCATTTTAAATAGTTTATGTATACACT 960
OY      961 GAATGAAAAGCAAACTAAATATGTTTACAGACCAAGTGTATTCACACGTTTTTAA 1020
Db      961 GAATGAAAAGCAAACTAAATATGTTTACAGACCAAGTGTATTCACACGTTTTTAA 1020
OY      1021 ATCTGACATTTATTCATTTTGTCTTCATCAAAAAGTGTTCATTTTATTTTATGTTGCT 1080
Db      1021 ATCTGACATTTATTCATTTTGTCTTCATCAAAAAGTGTTCATTTTATTTTATGTTGCT 1080
OY      1081 AGAATACCTTCTTCATTCATTCATCTCTCAACCTATATTTTGAATATTTGTTGGCTC 1140
Db      1081 AGAATACCTTCTTCATTCATTCATCTCTCAACCTATATTTTGAATATTTGTTGGCTC 1140
OY      1141 TTGTTTTTCTCTAGTATATGCAATTTTAAAAAATATATAAGCTACCAATCTTTGTAC 1200
Db      1141 TTGTTTTTCTCTAGTATATGCAATTTTAAAAAATATATAAGCTACCAATCTTTGTAC 1200
OY      1201 AATTTGTAATGTTAAGATTTTATTTTATCTGTTAAATAAATTTATTTCCACACA 1257
Db      1201 AATTTGTAATGTTAAGATTTTATTTTATCTGTTAAATAAATTTATTTCCACACA 1257

```

RESULT 3  
US-10-006-041A-430

; Sequence 430, Application us/10006041A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botsstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geo, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James

```

; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC8  
; CURRENT APPLICATION NUMBER: US/10/006,041A  
; CURRENT FILING DATE: 2001-12-06  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 430  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-006-041A-430  
  
Query Match      100.0%; Score 1257; DB 44; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,7e+230;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY      1  GGAGAGAGCGCGCGCGTGAAGGCGCATTTGATGACAGCTCGGCGGCTCGAGCGCG 60  
Db      1  GGAGAGAGCGCGCGCGGTGAAGGCGCATTTGATGACAGCTCGGCGGCTCGAGCGCGG 60  
OY      61  CGAGAGCAGACGCTGACACAGCTTCTCTCTGCTGCTCTCTCGGCTCCAGCTCCGCGCTG 120  
Db      61  CGAGAGCAGACGCTGACACAGCTTCTCTCTGCTGCTCTCTCGGCTCCAGCTCCGCGCTG 120  
OY      121  CCGGAGAGCGGAGAGCAATGACCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db      121  CCGGAGAGCGGAGAGCAATGACCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
OY      181  GCCTCCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Db      181  GCCTCCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
OY      241  AGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGAGTGTGACCTGTTAATGCAATGT 300  
Db      241  AGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGAGTGTGACCTGTTAATGCAATGT 300  
OY      301  GCTTACAAAGGCGCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Db      301  GCTTACAAAGGCGCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
OY      361  CGGCTACACCTGGGATCCAGGTCCGGATGATTCACAAAGAGGGAATGTCTGA 420  
Db      361  CGGCTACACCTGGGATCCAGGTCCGGATGATTCACAAAGAGGGAATGTCTGA 420  
OY      421  GGGAAAGCTTTAGAGAGTCTCTGACACCCCACTACAAAGAGGTTTATGATTA 480  
Db      421  GGGAAAGCTTTAGAGAGTCTCTGACACCCCACTACAAAGAGGTTTATGATTA 480  
OY      481  ATTATGGCATATGATCTTGGGAAAAATTCGGAGCTGTACATTTTCAAAAGATGCTTCAAATA 540  
Db      481  ATTATGGCATATGATCTTGGGAAAAATTCGGAGCTGTACATTTTCAAAAGATGCTTCAAATA 540  
OY      541  GTGCTCTAAGAGTCTTGTTCAGTGGCTCACTTGGCTAAATATGCAAAAATGCAATGCTGTC 600  
Db      541  GTGCTCTAAGAGTCTTGTTCAGTGGCTCACTTGGCTAAATATGCAAAAATGCAATGCTGTC 600  
OY      601  AGCGTTGGATTTTGCATTCATTCATGAGAGCTGATTTTCAGAGCTCTCTCCCATTTGAAGCTA 660  
Db      601  AGCGTTGGATTTTGCATTCATTCATGAGAGCTGATTTTCAGAGCTCTCTCCCATTTGAAGCTA 660  
OY      661  TAATTTATTTGGACCAAGAGACCTCGAAATATGATTCACATTTATATTCATTCGCACTT 720  
Db      661  TAATTTATTTGGACCAAGAGACCTCGAAATATGATTCACATTTATATTCATTCGCACTT 720  
OY      721  CTTCGTGGAGAGACTTGTGTGAAGAAATTTGTGTGATTTAGTGAATGTTCATCTGAGG 780  
Db      721  CTTCGTGGAGAGACTTGTGTGAAGAAATTTGTGTGATTTAGTGAATGTTCATCTGAGG 780  
OY      781  TTGGGACTTTGTTCACATTTACCCAAAAGAGATGCTTTTACTGATGGAATTCAGTTCTC 840  
Db      781  TTGGGACTTTGTTCACATTTACCCAAAAGAGATGCTTTTACTGATGGAATTCAGTTCTC 840

```





Db 1201 AATTGTAATGTAAGATAATTTTATATCTGTAATTAATAATTTATTCACACA 1257

RESULT 5  
US-10-006-116A-430  
Sequence 430, Application US/10006116A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1c15  
CURRENT FILING DATE: 2001-12-16  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099556  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15

PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570

1	PRIOR FILING DATE: 1998-09-30
2	PRIOR APPLICATION NUMBER: 60/102571
3	PRIOR FILING DATE: 1998-09-30
4	PRIOR APPLICATION NUMBER: 60/102664
5	PRIOR FILING DATE: 1998-10-01
6	PRIOR APPLICATION NUMBER: 60/102687
7	PRIOR FILING DATE: 1998-10-01
8	PRIOR APPLICATION NUMBER: 60/102965
9	PRIOR FILING DATE: 1998-10-02
10	PRIOR APPLICATION NUMBER: 60/103258
11	PRIOR FILING DATE: 1998-10-06
12	PRIOR APPLICATION NUMBER: 60/103314
13	PRIOR FILING DATE: 1998-10-07
14	PRIOR APPLICATION NUMBER: 60/103315
15	PRIOR FILING DATE: 1998-10-07
16	PRIOR APPLICATION NUMBER: 60/103328
17	PRIOR FILING DATE: 1998-10-07
18	PRIOR APPLICATION NUMBER: 60/103395
19	PRIOR FILING DATE: 1998-10-07
20	PRIOR APPLICATION NUMBER: 60/103396
21	PRIOR FILING DATE: 1998-10-07
22	PRIOR APPLICATION NUMBER: 60/103401
23	PRIOR FILING DATE: 1998-10-07
24	PRIOR APPLICATION NUMBER: 60/103449
25	PRIOR FILING DATE: 1998-10-06
26	PRIOR APPLICATION NUMBER: 60/103633
27	PRIOR FILING DATE: 1998-10-08
28	PRIOR APPLICATION NUMBER: 60/103678
29	PRIOR FILING DATE: 1998-10-08
30	PRIOR APPLICATION NUMBER: 60/103679
31	PRIOR FILING DATE: 1998-10-08
32	PRIOR APPLICATION NUMBER: 60/103711
33	PRIOR FILING DATE: 1998-10-08
34	PRIOR APPLICATION NUMBER: 60/104257
35	PRIOR FILING DATE: 1998-10-14
36	PRIOR APPLICATION NUMBER: 60/104987
37	PRIOR FILING DATE: 1998-10-20
38	PRIOR APPLICATION NUMBER: 60/105000
39	PRIOR FILING DATE: 1998-10-20
40	PRIOR APPLICATION NUMBER: 60/105002
41	PRIOR FILING DATE: 1998-10-20
42	PRIOR APPLICATION NUMBER: 60/105104
43	PRIOR FILING DATE: 1998-10-21
44	PRIOR APPLICATION NUMBER: 60/105169
45	PRIOR FILING DATE: 1998-10-22
46	PRIOR APPLICATION NUMBER: 60/105266
47	PRIOR FILING DATE: 1998-10-22
48	PRIOR APPLICATION NUMBER: 60/105653
49	PRIOR FILING DATE: 1998-10-26
50	PRIOR APPLICATION NUMBER: 60/105694
51	PRIOR FILING DATE: 1998-10-26
52	PRIOR APPLICATION NUMBER: 60/105807
53	PRIOR FILING DATE: 1998-10-27
54	PRIOR APPLICATION NUMBER: 60/105881
55	PRIOR FILING DATE: 1998-10-27
56	PRIOR APPLICATION NUMBER: 60/105882
57	PRIOR FILING DATE: 1998-10-27
58	PRIOR APPLICATION NUMBER: 60/106023
59	PRIOR FILING DATE: 1998-10-28
60	PRIOR APPLICATION NUMBER: 60/106029

Query Match	100.0%	Score 1257	DB 44	Length 1257
Best Local Similarity	100.0%	Pred. No. 2.7e-230		
Matches 1257; Conservative	0	Mismatches	0	Gaps 0

Qy	Dy	Qy	Dy
1	1	61	61
GGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	GGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG
60	60	120	120
CGGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	CGGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG
1	1	61	61
GGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	GGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG
60	60	120	120
GGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	GGAGAGAGCGCGCGGGTGAAGAGGCGCATTTGATGCGACGCTGGGGGGGGCGCTCGGAGAGCGGG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG	CGGAGACCGAGCGCTATCAACGTTCTCTCTCTGCTGCTCTCTCGGCTCCAGACTCCGCGCTG

OY	121	CCCGGACGCCGGAGGCATGGGAGACCCCGAGGCCCTCCCGAGGCGTCGGC	180
OY	121	CCCGGACGCCGGAGGCATGGGAGACCCCGAGGCCCTCCCGAGGCGTCGGC	180
Db	121	CCCGGACGCCGGAGGCATGGGAGACCCCGAGGCCCTCCCGAGGCGTCGGC	180
OY	181	GCTCTCTGCTCTCTCTGCTCTGCAAGCTGCCCGGCGCTCGAGCGCTCTGAGATCCCA	240
Db	181	GCTCTCTGCTCTCTCTGCTCTGCAAGCTGCCCGGCGCTCGAGCGCTCTGAGATCCCA	240
OY	241	AGGGGAAAGCAAAGGCGCAGCTCCGGCAGAGGGAGGTGTGACCTGTATTAATGGAATGT	300
Db	241	AGGGGAAAGCAAAGGCGCAGCTCCGGCAGAGGGAGGTGTGACCTGTATTAATGGAATGT	300
OY	301	GCTTACAAAGGCGCAGCAGAGTGGCTGGTGCAGACGGGAGGCCCTGGGGCCAAATGTATTC	360
Db	301	GCTTACAAAGGCGCAGCAGAGTGGCTGGTGCAGACGGGAGGCCCTGGGGCCAAATGTATTC	360
OY	361	CGGGTACACCTCGGAGTCCGAGTCCGAGTGGGATTCMAAGSAGAAAAGGGGAAATGTCTGA	420
Db	361	CGGGTACACCTCGGAGTCCGAGTGGGATTCMAAGSAGAAAAGGGGAAATGTCTGA	420
OY	421	GGGAAAGCTTTGAGAGAGTCTTGAGACCCCAACTCMAGCAGTGTTCATGAGTTCAATGA	480
Db	421	GGGAAAGCTTTGAGAGAGTCTTGAGACCCCAACTCMAGCAGTGTTCATGAGTTCAATGA	480
OY	481	ATTATAGCATATCTTGGGAAATTTGCGGAGTGTACATTATACAAAGATGGCTCAATA	540
Db	481	ATTATAGCATATCTTGGGAAATTTGCGGAGTGTACATTATACAAAGATGGCTCAATA	540
OY	541	GTGCTCTAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGCGAAGAAATGCATGCTGTC	600
Db	541	GTGCTCTAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGCGAAGAAATGCATGCTGTC	600
OY	601	AGCGTTGGTATTTACATTTCAATGAGCTGATGTTTCAGAGCTCTTCCATTTGAAGCTA	660
Db	601	AGCGTTGGTATTTACATTTCAATGAGCTGATGTTTCAGAGCTCTTCCATTTGAAGCTA	660
OY	661	TAAATTTAATTTGGACCAAGSAGGCCCTGAAATGCAATTCACAAATTAATTTTCATGCGACTT	720
Db	661	TAAATTTAATTTGGACCAAGSAGGCCCTGAAATGCAATTCACAAATTAATTTTCATGCGACTT	720
OY	721	CTTCTGTGGAGGACTTTGTGAAGAAATTTGGTGTGATTTAGTGGATTTGCTATCTGCGG	780
Db	721	CTTCTGTGGAGGACTTTGTGAAGAAATTTGGTGTGATTTAGTGGATTTGCTATCTGCGG	780
OY	781	TTGGCAGCTTGTTCAGATTACCCAAAAGSAGATGCTTCTACTGAGTGAATTCAGTTTCTC	840
Db	781	TTGGCAGCTTGTTCAGATTACCCAAAAGSAGATGCTTCTACTGAGTGAATTCAGTTTCTC	840
OY	841	GCATCATTTATGGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACGCTTTT	900
Db	841	GCATCATTTATGGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACGCTTTT	900
OY	901	TTATTTATGCGCTGGAAATGCTCACTTAATGACATTTTAAATGAATTAATGATATACACT	960
Db	901	TTATTTATGCGCTGGAAATGCTCACTTAATGACATTTTAAATGAATTAATGATATACACT	960
OY	961	GAAATGAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTTCACACTGTTTTAA	1020
Db	961	GAAATGAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTTCACACTGTTTTAA	1020
OY	1021	ATCTAGCATTTATCAATTTTCTTCAATCAAAAGGTTCAAATATTTTATTAATGATGCT	1080
Db	1021	ATCTAGCATTTATCAATTTTCTTCAATCAAAAGGTTCAAATATTTTATTAATGATGCT	1080
OY	1081	AGAAATCTTCTTCAATGATGCAATCTCTCAACCTATTAATTTGGAAATTTGTGTGGCTT	1140
Db	1081	AGAAATCTTCTTCAATGATGCAATCTCTCAACCTATTAATTTGGAAATTTGTGTGGCTT	1140
OY	1141	TTTGTGTTTTCTCTTAGATATGACATTTTAAAAAAATTAAGACCTACCAATCTTTGTATC	1200
Db	1141	TTTGTGTTTTCTCTTAGATATGACATTTTAAAAAAATTAAGACCTACCAATCTTTGTATC	1200
OY	1201	AATTTGTATATGTTAAGAAATTTTTTTTATATCTGTTAAATTAATAATTAATTTTCAACA	1257

Db 1201 AATTGTAAATGTAAAGAAATTTTATATCTGTTAAATAAAAAATATTTCACACA 1257

RESULT 6  
US-10-006-117A-430  
; Sequence 430, Application US/10006117A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC13  
; CURRENT APPLICATION NUMBER: US/10/006,117A  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 430  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-006-117A-430

Query Match 100.0%; Score 1257; DB 44; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2.7e-230;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGAGAGAGCGCGCGGTGAAGGCGCATGTGATGACGCTGGGGCGGCGCTCGAGAGCGGG 60  
1 GGAGAGAGCGCGCGGTGAAGGCGCATGTGATGACGCTGGGGCGGCGCTCGAGAGCGGG 60  
QY 61 CGGAGCAGACGCTGACACGCTTCCTCTGCGGTCCTCCGCTCCGCTCCGCTCCGCTG 120  
61 CGGAGCAGACGCTGACACGCTTCCTCTGCGGTCCTCCGCTCCGCTCCGCTCCGCTG 120  
Db 61 CGGAGCAGACGCTGACACGCTTCCTCTGCGGTCCTCCGCTCCGCTCCGCTCCGCTG 120  
QY 121 CCGGCGAGCGGAGCGCATGCGACCCGAGGCGCGCGCTCCGCTCCGCTCCGCTCCG 180  
121 CCGGCGAGCGGAGCGCATGCGACCCGAGGCGCGCGCGCTCCGCTCCGCTCCGCTCCG 180  
Db 121 CCGGCGAGCGGAGCGCATGCGACCCGAGGCGCGCGCGCTCCGCTCCGCTCCGCTCCG 180  
QY 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 241 AGGCGAAGCAAAAGCGCAGCTCCGCGCAGAGGAGGTGCTGACCTGTATTAATGAATG 300  
241 AGGCGAAGCAAAAGCGCAGCTCCGCGCAGAGGAGGTGCTGACCTGTATTAATGAATG 300  
Db 241 AGGCGAAGCAAAAGCGCAGCTCCGCGCAGAGGAGGTGCTGACCTGTATTAATGAATG 300  
QY 301 GCTTACAAAGGCGCAGAGAGTGCTGCGAGAGCGGAGCCCTGGGCGCAATGTATTC 360  
301 GCTTACAAAGGCGCAGAGAGTGCTGCGAGAGCGGAGCCCTGGGCGCAATGTATTC 360  
Db 301 GCTTACAAAGGCGCAGAGAGTGCTGCGAGAGCGGAGCCCTGGGCGCAATGTATTC 360  
QY 361 CGGCTACACCTGGGAGTCCAGTCCGAGATGATTCAAAAGAGAAAGGGGGAATGCTCA 420  
361 CGGCTACACCTGGGAGTCCAGTCCGAGATGATTCAAAAGAGAAAGGGGGAATGCTCA 420  
Db 361 CGGCTACACCTGGGAGTCCAGTCCGAGATGATTCAAAAGAGAAAGGGGGAATGCTCA 420  
QY 421 GGGAAAGCTTTGAGAGTCTCTGAGACCACTACAAAGAGTGTTCATGAGTTCATTA 480  
421 GGGAAAGCTTTGAGAGTCTCTGAGACCACTACAAAGAGTGTTCATGAGTTCATTA 480  
Db 421 GGGAAAGCTTTGAGAGTCTCTGAGACCACTACAAAGAGTGTTCATGAGTTCATTA 480  
QY 481 AATTATGATAGATCTTGAGAAATTCGAGAGTGTATTAATTAACAAAGATGCGTTCAATA 540  
481 AATTATGATAGATCTTGAGAAATTCGAGAGTGTATTAATTAACAAAGATGCGTTCAATA 540

Db 481 AATTATGATAGATCTTGAGAAATTCGAGAGTGTATTAATTAACAAAGATGCGTTCAATA 540  
481 AATTATGATAGATCTTGAGAAATTCGAGAGTGTATTAATTAACAAAGATGCGTTCAATA 540

QY 541 GTGCTCTAAGAGTCTTGTTCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
541 GTGCTCTAAGAGTCTTGTTCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 GTGCTCTAAGAGTCTTGTTCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 601 AGCGTGTATTTACATTCATCAATGAGTGAATGTTGAGAGTCTGCTGCTGCTGCTGCTG 660  
601 AGCGTGTATTTACATTCATCAATGAGTGAATGTTGAGAGTCTGCTGCTGCTGCTGCTG 660  
Db 601 AGCGTGTATTTACATTCATCAATGAGTGAATGTTGAGAGTCTGCTGCTGCTGCTGCTG 660  
QY 661 TAAATTTATTTGACCAAGAGAGCGCTGAAATGATTCACAAATTAATTAATTCATGCA 720  
661 TAAATTTATTTGACCAAGAGAGCGCTGAAATGATTCACAAATTAATTAATTCATGCA 720  
Db 661 TAAATTTATTTGACCAAGAGAGCGCTGAAATGATTCACAAATTAATTAATTCATGCA 720  
QY 721 CTTCTGTGAGAGACTTGTGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
721 CTTCTGTGAGAGACTTGTGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 721 CTTCTGTGAGAGACTTGTGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
QY 781 TTGGCAGCTTGTTCAGATTAACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840  
781 TTGGCAGCTTGTTCAGATTAACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840  
Db 781 TTGGCAGCTTGTTCAGATTAACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840  
QY 841 GCATCATTTATGGAAGACTACCAAAATTAATGCTTAAATTTTCAATTCCTGCTGCTG 900  
841 GCATCATTTATGGAAGACTACCAAAATTAATGCTTAAATTTTCAATTCCTGCTGCTG 900  
Db 841 GCATCATTTATGGAAGACTACCAAAATTAATGCTTAAATTTTCAATTCCTGCTGCTG 900  
QY 901 TTAATTTGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
901 TTAATTTGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 TTAATTTGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 GAATGAAAGCAAGCTAATATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
961 GAATGAAAGCAAGCTAATATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
Db 961 GAATGAAAGCAAGCTAATATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
QY 1021 ATCTACATTTATTCATTTTGTCTCAATCAAAAGTGTTCATATTTTAAATTTTAA 1080  
1021 ATCTACATTTATTCATTTTGTCTCAATCAAAAGTGTTCATATTTTAAATTTTAA 1080  
Db 1021 ATCTACATTTATTCATTTTGTCTCAATCAAAAGTGTTCATATTTTAAATTTTAA 1080  
QY 1081 AGAATCTTCTTCATAGACATCTGCTCAACCTTAATTTGGAATTTGCTGCTGCTG 1140  
1081 AGAATCTTCTTCATAGACATCTGCTCAACCTTAATTTGGAATTTGCTGCTGCTGCTG 1140  
Db 1081 AGAATCTTCTTCATAGACATCTGCTCAACCTTAATTTGGAATTTGCTGCTGCTGCTG 1140  
QY 1141 TTTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
1141 TTTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
Db 1141 TTTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
QY 1201 AATTGTAAATGTAAAGAAATTTTATATCTGTTAAATAAAAAATATTTCACACA 1257  
1201 AATTGTAAATGTAAAGAAATTTTATATCTGTTAAATAAAAAATATTTCACACA 1257  
Db 1201 AATTGTAAATGTAAAGAAATTTTATATCTGTTAAATAAAAAATATTTCACACA 1257

RESULT 7  
US-10-006-130A-430  
; Sequence 430, Application US/10006130A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC7

```
;; CURRENT APPLICATION NUMBER: US/10/006.130A
;; CURRENT FILING DATE: 2002-03-19
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 430
;; LENGTH: 1257
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-006-130A-430

Query Match      100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACAGCCCTCGGGCGCTCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACAGCCCTCGGGCGCTCGAGCGCG 60
QY 61 CGGAGCCAGAGCGCTGACACGCTCTCTCCGCTGCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCCAGAGCGCTGACACGCTCTCTCCGCTGCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGAGCCGCGGAGCCATGCGACCCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCTCT 180
DB 121 CCCGAGCCGCGGAGCCATGCGACCCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 GCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 AGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 GCTTACAAAGGCGCAGAGAGTGGCTGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 GCTTACAAAGGCGCAGAGAGTGGCTGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 CGGCTACACCTGGAGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 420
DB 361 CGGCTACACCTGGAGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 420
QY 421 GGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAG 480
DB 421 GGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAG 480
QY 481 ATTATGCAATGATCTTGGAGAAATGGAGAGTGTACATTATTAACAAGATGGCTTCAATA 540
DB 481 ATTATGCAATGATCTTGGAGAAATGGAGAGTGTACATTATTAACAAGATGGCTTCAATA 540
QY 541 GTGCTTAAGAGTTTGTCAAGTGGCTCACTTGGCTTAATAATGCAAGAAATGCATGCTGC 600
DB 541 GTGCTTAAGAGTTTGTCAAGTGGCTCACTTGGCTTAATAATGCAAGAAATGCATGCTGC 600
QY 601 AGGCTGTGTAATTCATCAATGAGAGTGAATGTTCAGAGCCCTTCCCTTGAAGCTA 660
DB 601 AGGCTGTGTAATTCATCAATGAGAGTGAATGTTCAGAGCCCTTCCCTTGAAGCTA 660
QY 661 TAATTTATTTGAGCAAGAGCCCTGAATGAATTAACAATTAATTAATTAATTAATTAAT 720
DB 661 TAATTTATTTGAGCAAGAGCCCTGAATGAATTAACAATTAATTAATTAATTAATTAAT 720
QY 721 CTCTGTGGAAGAGCTTGTGAAGAAATGGTGTGATTAAGTGAGTGTGCTATCTGCGG 780
DB 721 CTCTGTGGAAGAGCTTGTGAAGAAATGGTGTGATTAAGTGAGTGTGCTATCTGCGG 780
QY 781 TTGGCACTTTGTCAGATTACCAAAAGAGATGCTTCTACAGATGGAATTCAGTTCTC 840
DB 781 TTGGCACTTTGTCAGATTACCAAAAGAGATGCTTCTACAGATGGAATTCAGTTCTC 840
QY 841 GCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
DB 841 GCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
```

```
QY 901 TTATATGCTTGGAGATGTTCACTTAATGACATTTTAATTAAGTTATGATACATCT 960
DB 901 TTATATGCTTGGAGATGTTCACTTAATGACATTTTAATTAAGTTATGATACATCT 960
QY 961 GATGAAAGCAAGCTTAATATGTTTACAGACCAAGCTGATTTCACTGTTTAA 1020
DB 961 GATGAAAGCAAGCTTAATATGTTTACAGACCAAGCTGATTTCACTGTTTAA 1020
QY 1021 ATCTAGCATTTATATTTGCTTCATCAATGAAGGTTTCAATATTTTCTAGTGGTT 1080
DB 1021 ATCTAGCATTTATCTTTGCTTCATCAATGAAGGTTTCAATATTTTCTAGTGGTT 1080
QY 1081 AGAATACCTTCTTCATACATCTCTCTCAACCTATATATTTGAATTTGTTGCT 1140
DB 1081 AGAATACCTTCTTCATACATCTCTCTCAACCTATATATTTGAATTTGTTGCT 1140
QY 1141 TTGTTTTTCTCTTATATGATTTTAAATTAATTAAGTACCAATCTTTGAC 1200
DB 1141 TTGTTTTTCTCTTATATGATTTTAAATTAATTAAGTACCAATCTTTGAC 1200
QY 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAATTAATTAATTTTCCAA 1257
DB 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAATTAATTAATTTTCCAA 1257

RESULT 8
US-10-006-172A-430
Sequence 430. Application US/10006172A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C11
CURRENT APPLICATION NUMBER: US/10/006.172A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
```



```

; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106029

Query Match      100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACAGCTTGGCGGCGTGGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACAGCTTGGCGGCGTGGAGCGCG 60
QY 61 CGGAGCGAGAGCGTGCAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAGAGCGTGCAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGCGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCT 180
DB 121 CCGGCGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCT 180
QY 181 GCGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGAGAGCGAGAGCGCGAGTCTCGGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 241 AGGGAGAGCGAGAGCGCGAGTCTCGGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 301 GCTTACAGAGGCGCGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
DB 301 GCTTACAGAGGCGCGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 361 CGGGTACACCTGGGATCCGAGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CGGGTACACCTGGGATCCGAGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAGAGCTTGAAGAGTCTGAGACACCACTCAAGCAGTGTTCATGAGTTCATGA 480
DB 421 GGGAGAGCTTGAAGAGTCTGAGACACCACTCAAGCAGTGTTCATGAGTTCATGA 480
QY 481 ATTATGCGATAGATCTTGGGAGAGTGGGAGTGTATTCATTCAGAGAGTGTTCAGTA 540
DB 481 ATTATGCGATAGATCTTGGGAGAGTGGGAGTGTATTCATTCAGAGAGTGTTCAGTA 540
QY 541 GTGCTCTAGAGTCTTGTCTAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
DB 541 GTGCTCTAGAGTCTTGTCTAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
QY 601 AGCGTGTATTTACATTCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 660
DB 601 AGCGTGTATTTACATTCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 660
QY 661 TAATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TAATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TTGCGACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TTGCGACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GCATCATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCATCATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

```

```

QY 901 TTATTTATGCTTGGAGATGTTCACTTAATGACATTTTAATAGTTATGATACATCT 960
DB 901 TTATTTATGCTTGGAGATGTTCACTTAATGACATTTTAATAGTTATGATACATCT 960
QY 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGTTCATTTATTTTATTTTATTTGTT 1080
DB 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGTTCATTTATTTTATTTTATTTGTT 1080
QY 1081 AGAATCTTTCTTCATGTCATCTCTCAACCTATTAATTTGGAATTTGTGTGTCT 1140
DB 1081 AGAATCTTTCTTCATGTCATCTCTCAACCTATTAATTTGGAATTTGTGTGTCT 1140
QY 1141 TTGTTTCTCTCTTATGATTTTATTTTAAATATTAAGTCTCAATCTTTTATC 1200
DB 1141 TTGTTTCTCTCTTATGATTTTATTTTAAATATTAAGTCTCAATCTTTTATC 1200
QY 1201 AATTTGTAATTTGTAAGATTTTATTTATATCTGTAAATTTAAATTTTTCACAA 1257
DB 1201 AATTTGTAATTTGTAAGATTTTATTTATATCTGTAAATTTAAATTTTTCACAA 1257

RESULT 9
US-10-006-485A-430
; Sequence 430, Application US/10006485A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC9
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09

```

[illegible]



PRIOR APPLICATION NUMBER: 60/105807  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: 60/105881  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: 60/105882  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: 60/106023  
 PRIOR FILING DATE: 1998-10-28  
 PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 1257; DB 44; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 2,7e+230;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAGGCGCATTTGATGAGCGCTCGGCGCTCGAGCGCGG 60  
 DB 1 GGAGAGAGCGCGCGGTGAAGGCGCATTTGATGAGCGCTCGGCGCTCGAGCGCGG 60  
 QY 61 CGGAGCGCGAGCGCGGTGAGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTG 120  
 DB 61 CGGAGCGCGAGCGCGGTGAGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTG 120  
 QY 121 CCCGCGAGCGCGAGCGCATTTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 DB 121 CCCGCGAGCGCGAGCGCATTTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 QY 121 CCCGCGAGCGCGAGCGCATTTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 DB 121 CCCGCGAGCGCGAGCGCATTTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 QY 181 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 DB 181 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 241 AGGAGAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
 DB 241 AGGAGAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
 QY 301 GCTTACAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 DB 301 GCTTACAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 QY 301 GCTTACAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 DB 301 GCTTACAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 QY 361 CGGCTACAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
 DB 361 CGGCTACAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
 QY 421 GGGAGAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 DB 421 GGGAGAGCGCGAGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 QY 481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCTTCAATA 540  
 DB 481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCTTCAATA 540  
 QY 541 GTGCTGTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 DB 541 GTGCTGTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 QY 601 AGGCTGTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 DB 601 AGGCTGTAAGAGTTTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 661 TAAATTTTGGAGCAAGAGAGCGCTGAAATGATTAACAAATTAATTTATGCACTT 720  
 DB 661 TAAATTTTGGAGCAAGAGAGCGCTGAAATGATTAACAAATTAATTTATGCACTT 720  
 QY 721 CTCTGTGGAAGAGCTTGTGGAAGAAATGCTGTGATTAAGTGAAGTTTCTATCTGG 780  
 DB 721 CTCTGTGGAAGAGCTTGTGGAAGAAATGCTGTGATTAAGTGAAGTTTCTATCTGG 780  
 QY 781 TTGGCACTTTGTTCAGATTTACCAAGAGAGTGTCTTACAGATGAGTAATTCAGTTTCTC 840  
 DB 781 TTGGCACTTTGTTCAGATTTACCAAGAGAGTGTCTTACAGATGAGTAATTCAGTTTCTC 840  
 QY 841 GCATCATTTATGAGAGACTACCAAAATTAATGCTTTATTTTCAATTTGCTACCTTTT 900  
 DB 841 GCATCATTTATGAGAGACTACCAAAATTAATGCTTTATTTTCAATTTGCTACCTTTT 900

QY 901 TTATATGCGTGGAGTGTGCTACTTAATGACATTTTAATTAAGTTATGATACATCT 960  
 DB 901 TTATATGCGTGGAGTGTGCTACTTAATGACATTTTAATTAAGTTATGATACATCT 960  
 QY 961 GATGAGAGCAAGAGTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTAA 1020  
 DB 961 GATGAGAGCAAGAGTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTAA 1020  
 QY 1021 ATCTAGCATTTATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 DB 1021 ATCTAGCATTTATGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 QY 1081 AGAATACCTTTCTCATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 DB 1081 AGAATACCTTTCTCATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 1141 TTGTTTTTCTGCTGATTTGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1200  
 DB 1141 TTGTTTTTCTGCTGATTTGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1200  
 QY 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTTAAATTAATTAATTAATTAATTA 1257  
 DB 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTTAAATTAATTAATTAATTAATTA 1257

RESULT 10  
 US-10-006-746A-430

Sequence 430, Application US/10006746A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan I.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillard, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2830P1C5

CURRENT APPLICATION NUMBER: US/10/006,746A

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 60/098716

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098723

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098749

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098750

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098803

PRIOR FILING DATE: 1998-09-02

PRIOR APPLICATION NUMBER: 60/098821

PRIOR FILING DATE: 1998-09-02

PRIOR APPLICATION NUMBER: 60/098843

PRIOR FILING DATE: 1998-09-02

PRIOR APPLICATION NUMBER: 60/099536

PRIOR FILING DATE: 1998-09-09

PRIOR APPLICATION NUMBER: 60/099596

PRIOR FILING DATE: 1998-09-09

PRIOR APPLICATION NUMBER: 60/099598

PRIOR FILING DATE: 1998-09-09

PRIOR APPLICATION NUMBER: 60/099602

PRIOR FILING DATE: 1998-09-09

PRIOR APPLICATION NUMBER: 60/099642

PRIOR FILING DATE: 1998-09-09



1	PRIOR APPLICATION NUMBER: 60/099741
2	PRIOR FILING DATE: 1998-09-10
3	PRIOR APPLICATION NUMBER: 60/099754
4	PRIOR FILING DATE: 1998-09-10
5	PRIOR APPLICATION NUMBER: 60/099763
6	PRIOR FILING DATE: 1998-09-10
7	PRIOR APPLICATION NUMBER: 60/099792
8	PRIOR FILING DATE: 1998-09-10
9	PRIOR APPLICATION NUMBER: 60/099816
10	PRIOR FILING DATE: 1998-09-10
11	PRIOR APPLICATION NUMBER: 60/100385
12	PRIOR FILING DATE: 1998-09-15
13	PRIOR APPLICATION NUMBER: 60/100388
14	PRIOR FILING DATE: 1998-09-15
15	PRIOR APPLICATION NUMBER: 60/100390
16	PRIOR FILING DATE: 1998-09-15
17	PRIOR APPLICATION NUMBER: 60/100584
18	PRIOR FILING DATE: 1998-09-16
19	PRIOR APPLICATION NUMBER: 60/100627
20	PRIOR FILING DATE: 1998-09-16
21	PRIOR APPLICATION NUMBER: 60/100661
22	PRIOR FILING DATE: 1998-09-16
23	PRIOR APPLICATION NUMBER: 60/100662
24	PRIOR FILING DATE: 1998-09-16
25	PRIOR APPLICATION NUMBER: 60/100664
26	PRIOR FILING DATE: 1998-09-16
27	PRIOR APPLICATION NUMBER: 60/100683
28	PRIOR FILING DATE: 1998-09-17
29	PRIOR APPLICATION NUMBER: 60/100684
30	PRIOR FILING DATE: 1998-09-17
31	PRIOR APPLICATION NUMBER: 60/100710
32	PRIOR FILING DATE: 1998-09-17
33	PRIOR APPLICATION NUMBER: 60/100711
34	PRIOR FILING DATE: 1998-09-17
35	PRIOR APPLICATION NUMBER: 60/100848
36	PRIOR FILING DATE: 1998-09-18
37	PRIOR APPLICATION NUMBER: 60/100849
38	PRIOR FILING DATE: 1998-09-18
39	PRIOR APPLICATION NUMBER: 60/100919
40	PRIOR FILING DATE: 1998-09-17
41	PRIOR APPLICATION NUMBER: 60/100930
42	PRIOR FILING DATE: 1998-09-17
43	PRIOR APPLICATION NUMBER: 60/101014
44	PRIOR FILING DATE: 1998-09-18
45	PRIOR APPLICATION NUMBER: 60/101068
46	PRIOR FILING DATE: 1998-09-18
47	PRIOR APPLICATION NUMBER: 60/101071
48	PRIOR FILING DATE: 1998-09-18
49	PRIOR APPLICATION NUMBER: 60/101279
50	PRIOR FILING DATE: 1998-09-22
51	PRIOR APPLICATION NUMBER: 60/101471
52	PRIOR FILING DATE: 1998-09-23
53	PRIOR APPLICATION NUMBER: 60/101472
54	PRIOR FILING DATE: 1998-09-23
55	PRIOR APPLICATION NUMBER: 60/101474
56	PRIOR FILING DATE: 1998-09-23
57	PRIOR APPLICATION NUMBER: 60/101475
58	PRIOR FILING DATE: 1998-09-23
59	PRIOR APPLICATION NUMBER: 60/101476
60	PRIOR FILING DATE: 1998-09-23
61	PRIOR APPLICATION NUMBER: 60/101477
62	PRIOR FILING DATE: 1998-09-23
63	PRIOR APPLICATION NUMBER: 60/101479
64	PRIOR FILING DATE: 1998-09-23
65	PRIOR APPLICATION NUMBER: 60/101738
66	PRIOR FILING DATE: 1998-09-24
67	PRIOR APPLICATION NUMBER: 60/101741

1	PRIOR FILING DATE: 1998-09-24
2	PRIOR APPLICATION NUMBER: 60/101743
3	PRIOR FILING DATE: 1998-09-24
4	PRIOR APPLICATION NUMBER: 60/101915
5	PRIOR FILING DATE: 1998-09-24
6	PRIOR APPLICATION NUMBER: 60/101918
7	PRIOR FILING DATE: 1998-09-24
8	PRIOR APPLICATION NUMBER: 60/102207
9	PRIOR FILING DATE: 1998-09-29
10	PRIOR APPLICATION NUMBER: 60/102240
11	PRIOR FILING DATE: 1998-09-29
12	PRIOR APPLICATION NUMBER: 60/102307
13	PRIOR FILING DATE: 1998-09-29
14	PRIOR APPLICATION NUMBER: 60/102480
15	PRIOR FILING DATE: 1998-09-30
16	PRIOR APPLICATION NUMBER: 60/102487
17	PRIOR FILING DATE: 1998-09-30
18	PRIOR APPLICATION NUMBER: 60/102571
19	PRIOR FILING DATE: 1998-09-30
20	PRIOR APPLICATION NUMBER: 60/102684
21	PRIOR FILING DATE: 1998-10-01
22	PRIOR APPLICATION NUMBER: 60/102687
23	PRIOR FILING DATE: 1998-10-01
24	PRIOR APPLICATION NUMBER: 60/102965
25	PRIOR FILING DATE: 1998-10-02
26	PRIOR APPLICATION NUMBER: 60/103258
27	PRIOR FILING DATE: 1998-10-06
28	PRIOR APPLICATION NUMBER: 60/103314
29	PRIOR FILING DATE: 1998-10-07
30	PRIOR APPLICATION NUMBER: 60/103315
31	PRIOR FILING DATE: 1998-10-07
32	PRIOR APPLICATION NUMBER: 60/103328
33	PRIOR FILING DATE: 1998-10-07
34	PRIOR APPLICATION NUMBER: 60/103395
35	PRIOR FILING DATE: 1998-10-07
36	PRIOR APPLICATION NUMBER: 60/103396
37	PRIOR FILING DATE: 1998-10-07
38	PRIOR APPLICATION NUMBER: 60/103401
39	PRIOR FILING DATE: 1998-10-07
40	PRIOR APPLICATION NUMBER: 60/103449
41	PRIOR FILING DATE: 1998-10-06
42	PRIOR APPLICATION NUMBER: 60/103633
43	PRIOR FILING DATE: 1998-10-08
44	PRIOR APPLICATION NUMBER: 60/103678
45	PRIOR FILING DATE: 1998-10-08
46	PRIOR APPLICATION NUMBER: 60/103679
47	PRIOR FILING DATE: 1998-10-08
48	PRIOR APPLICATION NUMBER: 60/103711
49	PRIOR FILING DATE: 1998-10-08
50	PRIOR APPLICATION NUMBER: 60/104257
51	PRIOR FILING DATE: 1998-10-14
52	PRIOR APPLICATION NUMBER: 60/104987
53	PRIOR FILING DATE: 1998-10-20
54	PRIOR APPLICATION NUMBER: 60/105000
55	PRIOR FILING DATE: 1998-10-20
56	PRIOR APPLICATION NUMBER: 60/105002
57	PRIOR FILING DATE: 1998-10-20
58	PRIOR APPLICATION NUMBER: 60/105104
59	PRIOR FILING DATE: 1998-10-21
60	PRIOR APPLICATION NUMBER: 60/105169
61	PRIOR FILING DATE: 1998-10-22
62	PRIOR APPLICATION NUMBER: 60/105266
63	PRIOR FILING DATE: 1998-10-22
64	PRIOR APPLICATION NUMBER: 60/105693
65	PRIOR FILING DATE: 1998-10-26
66	PRIOR APPLICATION NUMBER: 60/105694
67	PRIOR FILING DATE: 1998-10-26

```

: PRIOR APPLICATION NUMBER: 60/105807
: PRIOR FILING DATE: 1998-10-27
: PRIOR APPLICATION NUMBER: 60/105881
: PRIOR FILING DATE: 1998-10-27
: PRIOR APPLICATION NUMBER: 60/105882
: PRIOR FILING DATE: 1998-10-27
: PRIOR APPLICATION NUMBER: 60/106023
: PRIOR FILING DATE: 1998-10-28
: PRIOR APPLICATION NUMBER: 60/106029

Query Match      100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGGCGCGCGGTGAAAGCGCATGATGACAGCTGCGCGGCTCGAGCGCGG 60
DB 1 GGAGAGAGGCGCGCGGTGAAAGCGCATGATGACAGCTGCGCGGCTCGAGCGCGG 60
QY 61 CGGAGCGAGAGCGTGCACAGCTTCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAGAGCGTGCACAGCTTCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCGCGGAGCGCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCCGCGAGCGCGGAGCGCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGAGAGCGAGAGAGCGAGCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 AGGAGAGCGAGAGAGAGCGAGCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GCTTACAGAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GCTTACAGAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CGGCTACAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CGGCTACAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAGAGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GGGAGAGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ATTATGCGATAGATCTTGGGAAATTCGAGAGTGTACATTTACAAAGATGCTCA 540
DB 481 ATTATGCGATAGATCTTGGGAAATTCGAGAGTGTACATTTACAAAGATGCTCA 540
QY 541 GTGCTTAAGAGTTTGTTCAGTGTGCTACCTCGGCTAAATTCGAGAGAGAG 600
DB 541 GTGCTTAAGAGTTTGTTCAGTGTGCTACCTCGGCTAAATTCGAGAGAGAG 600
QY 601 AGCGTTGATATTCACATTCATGAGCTGATGATGAGAGAGAGAGAGAGAGAG 660
DB 601 AGCGTTGATATTCACATTCATGAGCTGATGATGAGAGAGAGAGAGAGAGAG 660
QY 661 TAATTTATTTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TAATTTATTTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TTGGCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 TTGGCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

```

```

QY 901 TTATTTATGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 TTATTTATGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 ATCTAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATCTAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AGAATTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AGAATTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 TTGTTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TTGTTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 AATTTGTAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
DB 1201 AATTTGTAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257

```

```

RESULT 11
US-10-006-768A-430
: Sequence 430, Application US/10006768A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan I.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2830P1C10
: CURRENT APPLICATION NUMBER: US/10/006,768A
: NUMBER OF SEQ ID NOS: 477
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 430
: LENGTH: 1257
: TYPE: DNA
: ORGANISM: Homo sapien
US-10-006-768A-430

```

```

Query Match      100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGGCGCGCGGTGAAAGCGCATGATGACAGCTGCGCGGCTCGAGCGCG 60
DB 1 GGAGAGAGGCGCGCGGTGAAAGCGCATGATGACAGCTGCGCGGCTCGAGCGCG 60
QY 61 CGGAGCGAGAGCGTGCACAGCTTCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAGAGCGTGCACAGCTTCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCGCGGAGCGCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCCGCGAGCGCGGAGCGCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

```



Db 541 GTGCTTAAGAGTTTGTTCAGTGCTCCTTCGGCTAAATGCAAGAAATGCATGCTGTC 600  
 QY 601 AGCGTGTGATTTACATTCATGAGCTGATGTTGTCAGAGCTTCCTCCATTGAGCTA 660  
 Db 601 AGCGTGTGATTTACATTCATGAGCTGATGTTGTCAGAGCTTCCTCCATTGAGCTA 660  
 QY 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGATTCACAAATTAATTTATGCTGCT 720  
 Db 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGATTCACAAATTAATTTATGCTGCT 720  
 QY 721 CTCTGTGGAAGAGCTTTGTGAGAAATGCTGATGATGATGATGATGATGATGATGAT 780  
 Db 721 CTCTGTGGAAGAGCTTTGTGAGAAATGCTGATGATGATGATGATGATGATGATGAT 780  
 QY 781 TTGGCACTTTGTCAGATTAACCAAAAGAGATGCTTCTACTGATGATGATGATGATGAT 840  
 Db 781 TTGGCACTTTGTCAGATTAACCAAAAGAGATGCTTCTACTGATGATGATGATGATGAT 840  
 QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTGCTGCTTT 900  
 Db 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTGCTGCTTT 900  
 QY 901 TTATTTATGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 Db 901 TTATTTATGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 QY 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGCTGATTTACAGCTGTTTAA 1020  
 Db 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGCTGATTTACAGCTGTTTAA 1020  
 QY 1021 ATTCAGCTATTTATGCTTGTCTCAATCAAGCTGCTCAATATTTTATGATGCTT 1080  
 Db 1021 ATTCAGCTATTTATGCTTGTCTCAATCAAGCTGCTCAATATTTTATGATGCTT 1080  
 QY 1081 AGAATACTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Db 1081 AGAATACTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1141 TTGCTTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 Db 1141 TTGCTTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 QY 1201 AATTTGTAATGTAAGATTTTCTTATCTGTTAATTAATTAATTTTCCAAACA 1257  
 Db 1201 AATTTGTAATGTAAGATTTTCTTATCTGTTAATTAATTAATTTTCCAAACA 1257  
 RESULT 13  
 US-10-006-856A-430  
 : Sequence 430. Application US/10006856A  
 : GENERAL INFORMATION:  
 : APPLICANT: Baker, Kevin P.  
 : APPLICANT: Botstein, David  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Eaton, Dan L.  
 : APPLICANT: Ferrara, Napoleone  
 : APPLICANT: Fong, Sherman  
 : APPLICANT: Gao, Wei-Qiang  
 : APPLICANT: Goddard, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Grimaldi, Christopher J.  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Hillan, Kenneth J.  
 : APPLICANT: Pan, James  
 : APPLICANT: Paoni, Nicholas F.  
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 : TITLE OF INVENTION: Acids Encoding the Same  
 : FILE REFERENCE: P2830P1C14  
 : CURRENT APPLICATION NUMBER: US/10/006, 856A  
 : NUMBER OF SEQ ID NOS: 477  
 : Prior Application removed - See File Wrapper or Palm  
 : SEQ ID NO 430

; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-006-856A-430  
 Query Match 100.0%; Score 1257; DB 44; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-230;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAGAGAGGCGGGGGAAGGCGCATTCATGATGATGATGATGATGATGATGATGATGATGAT 60  
 Db 1 GGAGAGAGGCGGGGGAAGGCGCATTCATGATGATGATGATGATGATGATGATGATGATGAT 60  
 QY 61 CGAGAGCAGAGCTGACACAGCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 Db 61 CGAGAGCAGAGCTGACACAGCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 121 CCGGCAAGCCGGGAGCCATGCGACCCGAGGCGCCGCGCTCCCGCAGCGCTCGCGC 180  
 Db 121 CCGGCAAGCCGGGAGCCATGCGACCCGAGGCGCCGCGCTCCCGCAGCGCTCGCGC 180  
 QY 181 GCTCTCTGCT 240  
 Db 181 GCTCTCTGCT 240  
 QY 241 AGGGAAGCAAGAGCGCAGCTCCGCAAGAGAGGTGAGCTGTATATGAAATGT 300  
 Db 241 AGGGAAGCAAGAGCGCAGCTCCGCAAGAGAGGTGAGCTGTATATGAAATGT 300  
 QY 301 GCTTACAAAGGCGCAGAGAGTGGCTGTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 Db 301 GCTTACAAAGGCGCAGAGAGTGGCTGTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 361 CGGCTACACCTCGGAGTCCAGTGGAGTGGATGATTCAAAGGAAAGGAGGAAATGTGTA 420  
 Db 361 CGGCTACACCTCGGAGTCCAGTGGAGTGGATGATTCAAAGGAAAGGAGGAAATGTGTA 420  
 QY 421 GGGAAAGCTTTGAGAGAGTCTGACACCCAACTACAAAGCAGTGTTCATGAGTCAATGA 480  
 Db 421 GGGAAAGCTTTGAGAGAGTCTGACACCCAACTACAAAGCAGTGTTCATGAGTCAATGA 480  
 QY 481 AATTAAGCATGATCTTGGGAAATGCGGAGTGTACATTTACAAAGATGCTCAATA 540  
 Db 481 AATTAAGCATGATCTTGGGAAATGCGGAGTGTACATTTACAAAGATGCTCAATA 540  
 QY 541 GTGCTTAAGAGTTTGTTCAGTGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 Db 541 GTGCTTAAGAGTTTGTTCAGTGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 QY 601 AGCGTGTGATTTACATTCATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 Db 601 AGCGTGTGATTTACATTCATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGATTCACAAATTAATTTATGCTGCTGCT 720  
 Db 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGATTCACAAATTAATTTATGCTGCTGCT 720  
 QY 721 CTCTGTGGAAGAGCTTTGTGAGAAATGCTGATGATGATGATGATGATGATGATGATGATGAT 780  
 Db 721 CTCTGTGGAAGAGCTTTGTGAGAAATGCTGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 781 TTGGCACTTTGTCAGATTAACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGAT 840  
 Db 781 TTGGCACTTTGTCAGATTAACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGAT 840  
 QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTGCTGCTTT 900  
 Db 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTGCTGCTTT 900  
 QY 901 TTATTTATGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 Db 901 TTATTTATGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
QY 1021 ACTTACCATTTATTCATTTGCTTCATTCACAAAGTGTTCATATTTTGTGTGTT 1080  
DB 1021 ACTTACCATTTATTCATTTGCTTCATTCACAAAGTGTTCATATTTTGTGTGTT 1080  
QY 1081 AGAATACCTTCTTCATAGTCACATTCCTCAACCTTAATTTGGAATATGTTGTGCT 1140  
DB 1081 AGAATACCTTCTTCATAGTCACATTCCTCAACCTTAATTTGGAATATGTTGTGCT 1140  
QY 1141 TTGTGTTTTCTCTTGATAGCATTTTAAAAAATATTAAGTACCAATCTTGTAC 1200  
DB 1141 TTGTGTTTTCTCTTGATAGCATTTTAAAAAATATTAAGTACCAATCTTGTAC 1200  
QY 1201 AATTTGTAATGTTAGAAATTTTATATCTGTAATTAATTAATTTATTTCCACA 1257  
DB 1201 AATTTGTAATGTTAGAAATTTTATATCTGTAATTAATTAATTTATTTCCACA 1257

RESULT 14  
US-10-006-867-121  
Sequence 121, Application US/10006867  
GENERAL INFORMATION:  
APPLICANT: Baton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William J.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/006,867  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/063435  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/064215  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090688  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091628  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/096012  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096757  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096949  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/096959  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/097954  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097971  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097979  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000

PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/1705002
PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/105884
PRIOR FILING DATE:	1998-10-27
PRIOR APPLICATION NUMBER:	60/106030
PRIOR FILING DATE:	1998-10-28
PRIOR APPLICATION NUMBER:	60/106464
PRIOR FILING DATE:	1998-10-30
PRIOR APPLICATION NUMBER:	60/106856
PRIOR FILING DATE:	1998-11-03
PRIOR APPLICATION NUMBER:	60/108807
PRIOR FILING DATE:	1998-11-17
PRIOR APPLICATION NUMBER:	60/112419
PRIOR FILING DATE:	1998-12-15
PRIOR APPLICATION NUMBER:	60/112422
PRIOR FILING DATE:	1998-12-15
PRIOR APPLICATION NUMBER:	60/112854
PRIOR FILING DATE:	1998-12-16
PRIOR APPLICATION NUMBER:	60/113300
PRIOR FILING DATE:	1998-12-22
PRIOR APPLICATION NUMBER:	60/113408
PRIOR FILING DATE:	1998-12-22
PRIOR APPLICATION NUMBER:	60/113430
PRIOR FILING DATE:	1998-12-23
PRIOR APPLICATION NUMBER:	60/113621
PRIOR FILING DATE:	1998-12-23
PRIOR APPLICATION NUMBER:	60/114223
PRIOR FILING DATE:	1998-12-30
PRIOR APPLICATION NUMBER:	60/115614
PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/116527
PRIOR FILING DATE:	1999-01-20
PRIOR APPLICATION NUMBER:	60/116843
PRIOR FILING DATE:	1999-01-22
PRIOR APPLICATION NUMBER:	60/119285
PRIOR FILING DATE:	1999-02-09
PRIOR APPLICATION NUMBER:	60/119287
PRIOR FILING DATE:	1999-02-09
PRIOR APPLICATION NUMBER:	60/119525
PRIOR FILING DATE:	1999-02-10
PRIOR APPLICATION NUMBER:	60/119549
PRIOR FILING DATE:	1999-02-10
PRIOR APPLICATION NUMBER:	60/120014
PRIOR FILING DATE:	1999-02-11
PRIOR APPLICATION NUMBER:	60/129122
PRIOR FILING DATE:	1999-04-13
PRIOR APPLICATION NUMBER:	60/129674
PRIOR FILING DATE:	1999-04-16
PRIOR APPLICATION NUMBER:	60/131291
PRIOR FILING DATE:	1999-04-27
PRIOR APPLICATION NUMBER:	60/138387
PRIOR FILING DATE:	1999-06-09
PRIOR APPLICATION NUMBER:	60/144791
PRIOR FILING DATE:	1999-07-20
PRIOR APPLICATION NUMBER:	60/169495
PRIOR FILING DATE:	1999-12-07
PRIOR APPLICATION NUMBER:	60/1175481
PRIOR FILING DATE:	2000-01-11
PRIOR APPLICATION NUMBER:	60/191007
PRIOR FILING DATE:	2000-03-21
PRIOR APPLICATION NUMBER:	60/199397
PRIOR FILING DATE:	2000-04-25
PRIOR APPLICATION NUMBER:	09/380139
PRIOR FILING DATE:	1998-08-25
PRIOR APPLICATION NUMBER:	09/311832
PRIOR FILING DATE:	1999-05-14
PRIOR APPLICATION NUMBER:	09/380137
PRIOR FILING DATE:	1999-08-25

; PRIOR APPLICATION NUMBER: 09/380138									
; PRIOR FILING DATE: 1999-08-25									
; PRIOR APPLICATION NUMBER: 09/780142									
; PRIOR FILING DATE: 1999-08-25									
Query Match									
Best Local Similarity 100.0%; Score 1257; DB 44; Length 1257;									
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0									
QY	1	GGAGAGAGCGCGCGGGGTGAAAAGGCGCATATGACGCTTGCGGGCGCTTGAGACGGCGG	60						
DB	1	GGAGAGAGCGCGCGGGGTGAAAAGGCGCATATGAGGCTTGCGGGCGCTTGAGACGGCGG	60						
QY	61	CGAGCGACAGCGGTGACACAGTTCCTCTCTGCTCGCTCCGCTCCAGCTCCGCGTG	120						
DB	61	CGAGCGACAGCGGTGACACAGTTCCTCTCTGCTCGCTCCGCTCCAGCTCCGCGTG	120						
QY	121	CCCGGACGCCGGGAGCCATGCGACCCCGAGGCCCGCGCTCCCGACGCGCTCCGCG	180						
DB	121	CCCGGAGCGCGGGAGCCATGCGACCCCGAGGCCCGCGCTCCCGACGCGCTCCGCG	180						
QY	181	GGCTCCGCGTGCCTCGTGTGTCGACGCTCCCGGCGCGTGGAGGCGCTTGAGATCCCA	240						
DB	181	GCTCTCGTGCCTCGTGTGTCGACGCTCCCGGCGCGTGGAGGCGCTTGAGATCCCA	240						
QY	241	AGGGGAGCAAAAAGCGCAGCTCCGGCAGAGGGAGGTGGACCTGTATATGGAATGT	300						
DB	241	AGGGGAGCAAAAAGCGCAGCTCCGGCAGAGGGAGGTGGACCTGTATATGGAATGT	300						
QY	301	GCATTACAAGGCCACGAGAGATGCCGTGCGAGACGGAGCCGCGGGGCCAATGTATTC	360						
DB	301	GCATTACAAGGCCACGAGAGATGCCGTGCGAGACGGAGCCGCGGGGCCAATGTATTC	360						
QY	361	CGGGTACACCTGGGATCCGAGGTCCGGATGATTCAAAAGAGAAAAGGGGAGTGTGGA	420						
DB	361	CGGGTACACCTGGGATCCGAGGTCCGGATGATTCAAAAGAGAAAAGGGGAGTGTGGA	420						
QY	421	GGGAAAGCTTTGAGAGATCTCTGGACACCACTAACAACAGTTCATGAGTTCATGGA	480						
DB	421	GGGAAAGCTTTGAGAGATCTCTGGACACCACTAACAACAGTTCATGAGTTCATGGA	480						
QY	481	ATTATGGCATAGATCTTGGGAAAATTTGCGAGTGTACATTTACAAGATGCGTCAATA	540						
DB	481	ATTATGGCATAGATCTTGGGAAAATTTGCGAGTGTACATTTACAAGATGCGTCAATA	540						
QY	541	GTCCTTAAGAGTTTGTTCAGTGGCTACCTCGGCTAAATGCGAATTCAGTGTGTC	600						
DB	541	GTCCTTAAGAGTTTGTTCAGTGGCTACCTCGGCTAAATGCGAATTCAGTGTGTC	600						
QY	601	AGGGTGGATTTTACATTCATGAGAGTGGATGTTGCGAGACCTTCCTCCATTAAGCTA	660						
DB	601	AGGGTGGATTTTACATTCATGAGAGTGGATGTTGCGAGACCTTCCTCCATTAAGCTA	660						
QY	661	TAAATTTATTTGGAACAAGAACCCCTGAATGAATTAATTAATTAATTCATGCACTT	720						
DB	661	TAAATTTATTTGGAACAAGAACCCCTGAATGAATTAATTAATTAATTCATGCACTT	720						
QY	721	CTTCTGTGGAAGACTTGTGTGAAGAAATTTGGTGTGATTTAGTGATTTGCTATCTGGG	780						
DB	721	CTTCTGTGGAAGACTTGTGTGAAGAAATTTGGTGTGATTTAGTGATTTGCTATCTGGG	780						
QY	781	TTGGCACTTTGTCAGATTAACCAAAAAGAGATGCTTACTAGATGGAATTCAGTTTCTC	840						
DB	781	TTGGCACTTTGTCAGATTAACCAAAAAGAGATGCTTACTAGATGGAATTCAGTTTCTC	840						
QY	841	GCATCATTTATGGAAGACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTTTT	900						
DB	841	GCATCATTTATGGAAGACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTTTT	900						
QY	901	TTATTTATGCTTGGAAATGTTTACATTTAAATGATTTTAAATTAATTAATTAATTAAT	960						
DB	901	TTATTTATGCTTGGAAATGTTTACATTTAAATGATTTTAAATTAATTAATTAATTAAT	960						

QY 961 GAATGAAAGCAAGCTAATATGTTACAGACCAAGTGTGATTTTCACACTGTTTAA 1020  
DB 961 GAATGAAAGCAAGCTAATATGTTACAGACCAAGTGTGATTTTCACACTGTTTAA 1020  
QY 1021 ACTTACATTAATCATTTGCTTCATCAACCAAGGTTGATTAATTTTGTAGTGGT 1080  
DB 1021 ACTTACATTAATCATTTGCTTCATCAACCAAGGTTGATTAATTTTGTAGTGGT 1080  
QY 1081 AGAATACCTTCTTCATAGTCACATTCCTCAACCTTAATTTGGAATATGTTGCTGT 1140  
DB 1081 AGAATACCTTCTTCATAGTCACATTCCTCAACCTTAATTTGGAATATGTTGCTGT 1140  
QY 1141 TTTGTTTTTCTCTAGTATAGCAATTTTAAATAAATAAAGCTACCAATCTTTGTAC 1200  
DB 1141 TTTGTTTTTCTCTAGTATAGCAATTTTAAATAAATAAAGCTACCAATCTTTGTAC 1200  
QY 1201 AATTTGTAATGTAGGAATTTTATATCTGTTAAATAAATAATTTTCCACA 1257  
DB 1201 AATTTGTAATGTAGGAATTTTATATCTGTTAAATAAATAATTTTCCACA 1257

RESULT 15  
US-10-007-194A-430  
Sequence 430, Application US/10007194A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830PIC6  
CURRENT APPLICATION NUMBER: US/10/007,194A  
CURRENT FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763

PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24



PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/105881  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/105882

PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106023  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 1257; DB 44; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 2,7e-220; Indels 0; Gaps 0;  
Matches 1257; Conservative 0; Mismatches 0;

1 GGAGAGAGCGCGCGGTGAAAGCGCATATGAGCGCTCGGCGGCTCGAGAGCGG 60  
1 GGAGAGAGCGCGCGGTGAAAGCGCATATGAGCGCTCGGCGGCTCGAGAGCGG 60  
61 CGAGCGAGAGCGCTGACCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
61 CGAGCGAGAGCGCTGACCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
121 CCGGCGAGCGCGGAGCGCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
121 CCGGCGAGCGCGGAGCGCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
181 GCGTCCTGCT 240  
181 GCGTCCTGCT 240  
241 AGGGAGACCAAAAGCGCGAGCTCGGCGAGAGGAGGTGTGACCTGTATATGAAAT 300  
241 AGGGAGACCAAAAGCGCGAGCTCGGCGAGAGGAGGTGTGACCTGTATATGAAAT 300  
301 GCTTACAGGGCGAGCGAGAGTGGCTGTGAGAGCGGAGCGCGCGCGCGCGCG 360  
301 GCTTACAGGGCGAGCGAGAGTGGCTGTGAGAGCGGAGCGCGCGCGCGCGCG 360  
361 CGGCTACACCTGGAGTCCAGGTGGATGATTCAAAGAGAAAGGGGAAATGTCTGA 420  
361 CGGCTACACCTGGAGTCCAGGTGGATGATTCAAAGAGAAAGGGGAAATGTCTGA 420  
421 GGGAAAGCTTTGAGAGAGCTGTGAGACCCAACTACAACTGTTCATGAGGATTCATGA 480  
421 GGGAAAGCTTTGAGAGAGCTGTGAGACCCAACTACAACTGTTCATGAGGATTCATGA 480  
481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTGATTCAAAGATGATGTTCAATA 540  
481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTGATTCAAAGATGATGTTCAATA 540  
541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTTAAATGAGAAATGCATGCTGTC 600  
541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTTAAATGAGAAATGCATGCTGTC 600  
601 AGCGTGTGATTTGACATTCATGATGAGTGTGATGAGGACCTTCCATTGAGCTA 660  
601 AGCGTGTGATTTGACATTCATGATGAGTGTGATGAGGACCTTCCATTGAGCTA 660  
661 TAAATTTATTTGACCAAGAGCCCTGAAATGAATTCAAATTAATTTATGCGACTT 720  
661 TAAATTTATTTGACCAAGAGCCCTGAAATGAATTCAAATTAATTTATGCGACTT 720  
721 CTCTGTGGAAGAGCTTTGTAAGAAATTTGCTGTGATTTGATGATGATTTGCTG 780  
721 CTCTGTGGAAGAGCTTTGTAAGAAATTTGCTGTGATTTGATGATGATTTGCTG 780  
781 TTGGCAGCTTTGAGATTAACCAAAAGAGATGTTCTACATGATGATGATGATGCTC 840  
781 TTGGCAGCTTTGAGATTAACCAAAAGAGATGTTCTACATGATGATGATGATGCTC 840  
841 GCATCATTTATGAGAACTACCAAAATTAATTTATTTTCAATTTGCTACCTTTT 900  
841 GCATCATTTATGAGAACTACCAAAATTAATTTATTTTCAATTTGCTACCTTTT 900  
901 TTATTTAGCTTTGGAATGCTTCACTTAATGACATTTTAAATTAATTTATGATACATCT 960  
901 TTATTTAGCTTTGGAATGCTTCACTTAATGACATTTTAAATTAATTTATGATACATCT 960



QY	961	GAATGAAGAAGAAAGCTAAATATGTTTCACACCAAAGTGGATTTCACATGTTTTAA	1020
Db	961	GAATGAAGAAGAAAGCTAAATATGTTTCACACCAAAGTGGATTTCACATGTTTTAA	1020
QY	1021	ATCTAGCATATATCAATTTTGGCTTCACATCAAAAGTGGTTCCAAATATTTTAAATGTTGGT	1080
Db	1021	ATCTAGCATATATCAATTTTGGCTTCACATCAAAAGTGGTTCCAAATATTTTAAATGTTGGT	1080
QY	1081	AGAAATACCTTCATAGTACCAATTCCTCAACCATATAAATTGGAAATATGTTGGTCT	1140
Db	1081	AGAAATACCTTCATAGTACCAATTCCTCAACCATATATTTGGAAATATGTTGGTCT	1140
QY	1141	TTTGGTTTTTCTCTAGTAGATAGCAATTTTAAAAAAATATTAAGCTACCAATCTTGTATC	1200
Db	1141	TTTGGTTTTTCTCTAGTAGATAGCAATTTTAAAAAAATATTAAGCTACCAATCTTGTATC	1200
QY	1201	AATTTGGTAAAGTTAAGAAATTTTATATATCTGTAAATAAAAATATTTCCACAA	1257
Db	1201	AATTTGGTAAAGTTAAGAAATTTTATATATCTGTAAATAAAAATATTTCCACAA	1257





246 AGGGAACCAAAAGCCGACGCTCCGCGACAGAGGAGGTGCTGACCTGTAATGGAATG 305  
OY GCTTACAAAGCCGACGAGAGTCCCTGCTGACAGACGGAGCCCTGGGCCAATGTTATTC 360  
DB GCTTACAAAGCCGACGAGAGTCCCTGCTGACAGACGGAGCCCTGGGCCAATGTTATTC 365  
OY CGGGACACCGGGGATCCGAGGTGCGGATGATTCGAAAGGAGGAGGAGGAGGAGTTCGA 420  
DB CGGGACACCGGGGATCCGAGGTGCGGATGATTCGAAAGGAGGAGGAGGAGGAGTTCGA 425  
OY GGGAAAGCTTTGAGAGAGTCTGACACCACTACAGACAGTGTTCATGAGTTTCATGGA 480  
DB GGGAAAGCTTTGAGAGAGTCTGACACCACTACAGACAGTGTTCATGAGTTTCATGGA 485  
OY ATATGACATAGATCTGGGAAATTTGCGGAGTGTATTCACAAAGATGGTTCAAATA 540  
DB ATATGACATAGATCTGGGAAATTTGCGGAGTGTATTCACAAAGATGGTTCAAATA 545  
OY GTGCTCTAGAGTTTGTTCAGTGTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB GTGCTCTAGAGTTTGTTCAGTGTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605  
OY AGCGTGTGATTTTACATTCATGAGAGTGTGATGTTTACAGACCTTCCCATGAGCTA 660  
DB AGCGTGTGATTTTACATTCATGAGAGTGTGATGTTTACAGACCTTCCCATGAGCTA 665  
OY TAAATTTATTTGAGACCAAGAGCCCTGAAATGATTCACAAATTAATATTCATGCACT 720  
DB TAAATTTATTTGAGACCAAGAGCCCTGAAATGATTCACAAATTAATATTCATGCACT 725  
OY CTTCCTGAGAGGACTTTGAGAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB CTTCCTGAGAGGACTTTGAGAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785  
OY TTGGCACTTTGTCAGATTCACCAAAAGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCT 840  
DB TTGGCACTTTGTCAGATTCACCAAAAGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCT 845  
OY GCATCATTTATGAGAGACTTACCAAAATTAATGCTTTAATTTTCACTGCTGCTGCT 900  
DB GCATCATTTATGAGAGACTTACCAAAATTAATGCTTTAATTTTCACTGCTGCTGCT 905  
OY TTATTTATGCTTGAATGCTTCACTTAAATGACATTTAAATTAATTAATTAATTAATTA 960  
DB TTATTTATGCTTGAATGCTTCACTTAAATGACATTTAAATTAATTAATTAATTAATTA 965  
OY GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTGACACTGTTTAA 1020  
DB GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTGACACTGTTTAA 1025  
OY ATCTAGCATTTATTCATTTGCTTCAATCAAAAGTGTGCTGCTGCTGCTGCTGCTGCT 1080  
DB ATCTAGCATTTATTCATTTGCTTCAATCAAAAGTGTGCTGCTGCTGCTGCTGCTGCT 1085  
OY AGAATACCTTTCTCATAGTCACTTCTCAACCTATTAATTTGGAATATTTGAGGCT 1140  
DB AGAATACCTTTCTCATAGTCACTTCTCAACCTATTAATTTGGAATATTTGAGGCT 1145  
OY TTTGTTTTTCTCTAGTATGAGATTTTAAAGGATTTAAAGCTTACCAATCTTTGAC 1200  
DB TTTGTTTTTCTCTAGTATGAGATTTTAAAGGATTTAAAGCTTACCAATCTTTGAC 1205  
OY AATTTGTAATGTTAAGAAATTTTAAATCTGTAATTAATTAATTAATTAATTAATTA 1257  
DB AATTTGTAATGTTAAGAAATTTTAAATCTGTAATTAATTAATTAATTAATTAATTA 1262

RESULT 2  
US-10-470-050-171/c  
; Sequence 171, Application US/10470050  
; GENERAL INFORMATION:  
; APPLICANT: Orr, Michael S.  
; APPLICANT: Nation, Michele

APPLICANT: Digans, James C.  
APPLICANT: Zeng, Wen  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Gene Expression Profiles in Breast Tissue  
FILE REFERENCE: 44921-5070-US  
CURRENT APPLICATION NUMBER: US/10/470.050  
CURRENT FILING DATE: 2003-07-25  
PRIOR APPLICATION NUMBER: US 60/263,757  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: US 60/286,090  
PRIOR FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: US 60/292,517  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: PCT/US02/02176  
PRIOR FILING DATE: 2002-01-25  
NUMBER OF SEQ ID NOS: 1246  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 171  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. AA584310  
US-10-470-050-171

Query Match 45.0%; Score 565.8; DB 6; Length 582;  
Best Local Similarity 98.8%; Pred. No. 3.5e-141;  
Matches 570; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

661 AGCCCTGAAATGATTCACAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 740  
DB AGCCCTGAAATGATTCACAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 745  
OY 741 GAAGAAATGCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 800  
DB GAAGAAATGCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 805  
OY 801 CCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 860  
DB CCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 865  
OY 861 CCAAAATTAATGCTTAAATTTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920  
DB CCAAAATTAATGCTTAAATTTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 925  
OY 921 TCATTAATGATATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 980  
DB TCATTAATGATATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 985  
OY 981 TATGTTTACAGACCAAGTGTGATTTGACACTGTTTAAATTAATTAATTAATTAATTA 1040  
DB TATGTTTACAGACCAAGTGTGATTTGACACTGTTTAAATTAATTAATTAATTAATTA 1045  
OY 1041 CTTCATCAAAAGGCTTCAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100  
DB CTTCATCAAAAGGCTTCAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105  
OY 1101 ACATTTCTCAACCTATTAATTTGGAATATTTGCTGCTGCTGCTGCTGCTGCTGCT 1160  
DB ACATTTCTCAACCTATTAATTTGGAATATTTGCTGCTGCTGCTGCTGCTGCTGCT 1165  
OY 1161 AGCATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1220  
DB AGCATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1225  
OY 1221 TTTTATATATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1257  
DB TTTTATATATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1262

RESULT 3  
US-10-085-783A-57095  
; Sequence 57095, Application US/10085783A



```
NAME/KEY: misc_feature
LOCATION: (27)..(28)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (75)..(75)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (147)..(147)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (150)..(150)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (210)..(210)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (222)..(222)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (251)..(251)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (262)..(262)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (305)..(305)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (351)..(351)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (382)..(382)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-10107
```

```
Query Match 25.3%; Score 318.4; DB 6; Length 396;
Best Local Similarity 96.7%; Pred. No. 3.7e-75;
Matches 319; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 597 TGTGAGCTTGTGATTTTACATTCATGAGCTGATTTTCCGACCTTCCCATTTAA 656
DB 67 TGTGAGCGTGTGATTTTACATTCATGAGCTGATTTTCCGACCTTCCCATTTAA 126
QY 657 GCTAATATTTTGGACCAAGAAAGCCCTGAAATGAATTCACAAATTAATTCATGCG 716
DB 127 GCTAATATTTTGGACCAAGAAAGCCCTGAAATGAATTCACAAATTAATTCATGCG 186
QY 717 ACTTCTCTGTGAGAGACTTTGGAAGAAATGCTGCTGATTAAGTGAATGCTGATC 776
DB 187 ACTTCTCTGTGAGAGACTTTGGAAGAAATGCTGCTGATTAAGTGAATGCTGATC 246
QY 777 TGGGTGGCACTTGTGATTTTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTT 836
DB 247 TGGGTGGCACTTGTGATTTTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTT 306
QY 837 TCTGCAATCATTTATGAAGAACTACCAAAATTAATGCTTAATTTTCTGCTACCTCT 896
DB 307 TCTGCAATCATTTATGAAGAACTACCAAAATTAATGCTTAATTTTCTGCTACCTCT 366
QY 897 TTTTATATATGCTTGAAGATGCTTCACTT 926
DB 367 TTTTATATATGCTTGAAGATGCTTCACTT 396
```

```
RESULT 6
US-10-085-783A-8707
; Sequence 8707, Application US/10085783A
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8707
; LENGTH: 316
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (53)..(53)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (196)..(196)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (259)..(259)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (268)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-8707
```

```
Query Match 22.5%; Score 282.4; DB 6; Length 316;
Best Local Similarity 95.8%; Pred. No. 1.3e-65;
Matches 298; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

QY 949 ATGTATACATCTGAATGAAAGCA--AAGCTAAATATGTTTACAGACCAAGTGTATTT 1006
DB 1 ATGTATACATCTGAATGAAAGCAAGCAAGCTGAATATGTTTACAGACCAAGTGTATTT 60
QY 1007 CACACGTGTTTAAATCAGCATATATATTTGCTTCAATCAAAAGTGTTCATATTT 1066
DB 61 CACACGTGTTTAAATCAGCATATATATTTGCTTCAATCAAAAGTGTTCATATTT 120
QY 1067 TTTTATAGTGTAGAAATCTTCTCATATGTCATATCTCAACCTATATTTGGA 1126
DB 121 TTTTATAGTGTAGAAATCTTCTCATATGTCATATCTCAACCTATATTTGGA 180
QY 1127 TATTTGTGTGCTTTGTTTCTTCTAGTATAGCAATTTTAAAAAATATTAAGCT 1186
DB 181 TATTTGTGTGCTTTGTTTCTTCTAGTATAGCAATTTTAAAAAATATTAAGCT 240
QY 1187 ACCAATCTTTTACAAATTTGTAATGTTAGCAATTTTATATCTGTTAAATTAAT 1246
DB 241 ACCAATCTTTTACAAATTTGTAATGTTAGCAATTTTATATCTGTTAAATTAAT 300
QY 1247 TATTTCAACA 1257
DB 301 TATTTCAACA 311
```



```
;; CURRENT APPLICATION NUMBER: US/10/085,783A
;; CURRENT FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: US 60/305,340
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/275,017
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: US 60/271,955
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 58994
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 11744
;; LENGTH: 251
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: (130)..(133)
;; OTHER INFORMATION: n is a, c, g, or t
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: (133)..(133)
;; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-11744
```

```
Query Match          19.8%; Score 249; DB 6; Length 251;
Best Local Similarity 99.2%; Pred. No. 9.6e-57;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1003 ATTTCACACGCTTTTAAATCTAGCATTTATTCATTTCCTCAATTCAGTGTTCNA 1062
    |||||||
DB 1 ATTTCACACGCTTTTAAATCTAGCATTTATTCATTTCCTCAATTCAGTGTTCNA 60
OY 1063 TATTTTGTAGTGTAGTGAATCTTCTTCATAGTACATTCCTCAACCTATATTT 1122
    |||||||
DB 61 TATTTTGTAGTGTAGTGAATCTTCTTCATAGTACATTCCTCAACCTATATTT 120
OY 1123 GGAATATGTGTGCTCTTTGTTTCTCTAGTATAGCATTTTAAAAATATATA 1182
    |||||||
DB 121 GGAATATGTGTGCTCTTTGTTTCTCTAGTATAGCATTTTAAAAATATATA 180
OY 1183 AGCTACCAATCTTTGTACAAATTTGTAATGTTAAGAAATTTTATATCTGTAAATTA 1242
    |||||||
DB 181 AGCTACCAATCTTTGTACAAATTTGTAATGTTAAGAAATTTTATATCTGTAAATTA 240
OY 1243 AAATTTATTTCC 1253
    |||||||
DB 241 AAATTTATTTCC 251
```

```
RESULT 10
US-10-357-930-30335/C
;; Sequence 30335, Application US/10357930
;; GENERAL INFORMATION:
;; APPLICANT: Schlegel, Robert
;; APPLICANT: Endegle, Wilson
;; APPLICANT: Monahan, John
;; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;; FILE REFERENCE: HUMAN PROSTATE CANCER
;; CURRENT APPLICATION NUMBER: US/10/357,930
;; PRIOR APPLICATION NUMBER: 09/785,276
;; PRIOR FILING DATE: 2003-02-16
;; PRIOR APPLICATION NUMBER: 60/183,319
;; PRIOR FILING DATE: 2000-02-17
;; PRIOR APPLICATION NUMBER: 60/189,862
;; PRIOR FILING DATE: 2000-03-16
;; PRIOR APPLICATION NUMBER: 60/207,454
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: 60/211,314
;; PRIOR FILING DATE: 2000-06-09
;; PRIOR APPLICATION NUMBER: 60/219,007
```

```
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 60/255,281
;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62232
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 30335
;; LENGTH: 1544
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: 1531..1544
;; OTHER INFORMATION: n - A,T,C or G
US-10-357-930-30335
```

```
Query Match          18.2%; Score 228.8; DB 6; Length 1544;
Best Local Similarity 96.5%; Pred. No. 8.6e-51;
Matches 245; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
```

```
OY 506 TCGGAGTGTACATTATACAAAGATGCTCAATAGTGTCTAAGAGTTTGTTCAGTGG 565
    |||
DB 497 TCAGAGATGTACATTATACAAAGATGCTCAATAGTGTCTAAGAGTTTGTTCAGTGG 438
OY 566 CTCACCTCGCTAAATGACAAATGCAATGCTGACGCTGTGATTTACATTCATATGG 625
    |||||||
DB 437 CTCACCTCGCTAAATGACAAATGCAATGCTGACGCTGTGATTTACATTCATATGG 378
OY 626 AGCTGAATGTTCAGAGACCTCTCCATTTGAAGCTATATTTTGGACCAAGAGCC 685
    |||||||
DB 377 AGCTGAATGTTCAGAGACCTCTCCATTTGAAGCTATATTTTGGACCAAGAGCC 318
OY 686 TGAATGATTTCAACATTAATATTCATGCACTTCTCTGGA--AGCACTTTGGA 743
    |||||||
DB 317 TGAATGATTTCAACATTAATATTCATGCACTTCTCTGGA--AGCACTTTGGA 258
OY 744 GGAATGTGTGCTGG 757
    |||||||
DB 257 GGAATGTGTGCTGG 244
```

```
RESULT 11
US-10-357-930-16054
;; Sequence 16054, Application US/10357930
;; GENERAL INFORMATION:
;; APPLICANT: Schlegel, Robert
;; APPLICANT: Endegle, Wilson
;; APPLICANT: Monahan, John
;; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;; FILE REFERENCE: HUMAN PROSTATE CANCER
;; CURRENT APPLICATION NUMBER: US/10/357,930
;; PRIOR APPLICATION NUMBER: 09/785,276
;; PRIOR FILING DATE: 2003-02-16
;; PRIOR APPLICATION NUMBER: 60/183,319
;; PRIOR FILING DATE: 2000-02-17
;; PRIOR APPLICATION NUMBER: 60/189,862
;; PRIOR FILING DATE: 2000-03-16
;; PRIOR APPLICATION NUMBER: 60/207,454
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: 60/211,314
;; PRIOR FILING DATE: 2000-06-09
;; PRIOR APPLICATION NUMBER: 60/219,007
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 60/255,281
;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62232
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16054
;; LENGTH: 474
;; TYPE: DNA
;; ORGANISM: Homo sapiens
```



```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 305..432
; OTHER INFORMATION: n - A,T,C or G
US-10-357-930-16054

```

```

Query Match      16.8%; Score 210.8; DB 6; Length 474;
Best Local Similarity 95.6%; Pred. No. 2.4e-46;
Matches 237; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

```

```

QY 506 TCGGAGTGTACATTTACAAAGATGCTCAATAGTGTCTCAAGAGCTTTGTCTGAG 565
DB 225 TCCAGATGTACATTTACAAAGATGCTCAATAGTGTCTCAAGAGCTTTGTCTGAG 284
QY 566 CTCACCTGCGCTAAATGAGAAATGATGCTGAGCTGTGTATTTACATTCATG 625
DB 285 CTCACCTTGGCTAAATGAGAAATGATGCTGAGCTGTGTATTTACATTCATG 344
QY 626 AGC-TGAAATGTCAGACCTCTCCCA-TTGAAGCTATAATTTATTTGAGCAAGAGAC 683
DB 345 ACCTTGAATGTCAGACCTCTCCCA-TTGAAGCTATAATTTATTTGAGCAAGAGAC 404
QY 684 CCGTGAATGATTCACAAATTAATTAATTCACAACTTCTGCTGAGAGACTTTGTGA 743
DB 405 CCGTGAATGATTCACAAATTAATTAATTCACAACTTCTGCTGAGAGACTTTGTGA 464
QY 744 GGAATTGG 751
DB 465 AGAATTTG 472

```

```

RESULT 12
US-10-085-783A-49278

```

```

; Sequence 49278, Application US/10085783A
; GENERAL INFORMATION:

```

```

; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49278

```

```

; LENGTH: 300
; TYPE: DNA
; ORGANISM: Human

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (53)..(53)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143)..(143)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (152)..(152)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (157)..(157)
; OTHER INFORMATION: n is a, c, g, or t

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (209)..(209)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (221)..(221)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (245)..(245)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (263)..(263)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (274)..(274)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-49278

```

```

Query Match      16.5%; Score 207.2; DB 6; Length 300;
Best Local Similarity 87.2%; Pred. No. 1.6e-45;
Matches 266; Conservative 0; Mismatches 34; Indels 5; Gaps 4;

```

```

QY 794 AGATTACCCAAAAGAGATGCTCTACGTGATGGAATTCAGTTCTCGCATCATTTTGA 853
DB 1 AGATTACCCAAAAGAGATGCTCTACGTGATGGAATTCAGTTCTCGCATCATTTTGA 60
QY 854 AGACTACCCAAAAGATGCTCTACGTGATGGAATTCAGTTCTCGCATCATTTTGA 913
DB 61 AGACTACCCAAAAGATGCTCTACGTGATGGAATTCAGTTCTCGCATCATTTTGA 120
QY 914 GATGCTCTACGTGATGGAATTCAGTTCTCGCATCATTTTGAATGATGGAATTCAG 973
DB 121 GATGCTCTACGTGATGGAATTCAGTTCTCGCATCATTTTGAATGATGGAATTCAG 178
QY 974 AGCTAAATATGTTACAGACCAAGTGTGATTTACAGCTGTTTAAATCTGACATTAT 1033
DB 179 AGCTAAATATGTTACAGACCAAGTGTGATTTACAGCTGTTTAAATCTGACATTAT 237
QY 1034 CATTTGCTTCATCAATCAAGTGTGATTTACAGCTGTTTAAATCTGACATTAT 1093
DB 238 CATTTGCTTCATCAATCAAGTGTGATTTACAGCTGTTTAAATCTGACATTAT 295
QY 1094 CATAG 1098
DB 296 CATAG 300

```

```

RESULT 13
US-10-085-783A-52384

```

```

; Sequence 52384, Application US/10085783A
; GENERAL INFORMATION:

```

```

; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2

```

```

1  SEQ ID NO 52384
2  LENGTH: 213
3  TYPE: DNA
4  ORGANISM: Human
5  FEATURE:
6  NAME/KEY: misc_feature
7  LOCATION: (30)..(30)
8  OTHER INFORMATION: n is a, c, g, or t
9  FEATURE:
10 NAME/KEY: misc_feature
11 LOCATION: (32)..(32)
12 OTHER INFORMATION: n is a, c, g, or t
13 FEATURE:
14 NAME/KEY: misc_feature
15 LOCATION: (37)..(37)
16 OTHER INFORMATION: n is a, c, g, or t
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: (41)..(41)
20 OTHER INFORMATION: n is a, c, g, or t
21 FEATURE:
22 NAME/KEY: misc_feature
23 LOCATION: (111)..(111)
24 OTHER INFORMATION: n is a, c, g, or t
25 FEATURE:
26 NAME/KEY: misc_feature
27 LOCATION: (119)..(119)
28 OTHER INFORMATION: n is a, c, g, or t
29 FEATURE:
30 NAME/KEY: misc_feature
31 LOCATION: (128)..(129)
32 OTHER INFORMATION: n is a, c, g, or t
33 FEATURE:
34 NAME/KEY: misc_feature
35 LOCATION: (138)..(138)
36 OTHER INFORMATION: n is a, c, g, or t
37 FEATURE:
38 NAME/KEY: misc_feature
39 LOCATION: (168)..(168)
40 OTHER INFORMATION: n is a, c, g, or t
41 FEATURE:
42 NAME/KEY: misc_feature
43 LOCATION: (175)..(175)
44 OTHER INFORMATION: n is a, c, g, or t
45 FEATURE:
46 NAME/KEY: misc_feature
47 LOCATION: (197)..(197)
48 OTHER INFORMATION: n is a, c, g, or t
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
```

Query Match	15.6%	Score 196.2	DB 6	Length 213
Best Local Similarity	93.0%	Pred. No. 1.1e-42		
Matches 198	Conservative 0	Mismatches 15	Indels 0	Gaps 0
QY 1040 GCTTCATCAAAAGTGGTTCCAAATATTTTTTATGTGGTAGAATACTTCTTCATAGT				
Db 1 GCTTCATCAAAAGTGGTTCCAAATATTTTTTATGTGGTAGAATACTTCTTCATAGT				
QY 1100 CACATTCCTCCACCTATTAATTTGGAATATGTGGTCTTTTGTCTTCTCTACTA				
Db 61 CACATTCCTCCACCTATTAATTTGGAATATGTGGTCTTTTGTCTTCTCTACTA				
QY 1160 TAGCAATTTTAAAAAATATATAAGCTACCAATCTTTGTACAAATTTGTAATGTTAAGAA				
Db 121 TAGCAATTTTAAAAAATATATAAGCTACCAATCTTTGTACAAATTTGTAATGTTAAGAA				
QY 1220 TTTTCTTTATATCTGTATAATATAATATATTC				
Db 181 TTTTCTTTATATCTGTATAATATAATATAATTC				

```

Sequence 9224, Application US/10085783A
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 431/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9224
LENGTH: 398
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (165)..(165)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (207)..(207)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (218)..(218)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (259)..(259)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (295)..(295)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (307)..(307)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (345)..(345)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (398)..(398)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-9224

```

Query Match	14.5%	Score 182.4	DB 6	Length 398
Best Local Similarity	85.9%	Pred. No. 8.5e-39		
Matches 281	Conservative 0	Mismatches 33	Indels 13	Gaps 7
QY	323	GCCCTGTCGAGACGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCT-GGGATCCAG	381	
Db	66	GCCTGGTCGAGACGGAGCCCTGGGGCCAAATGTCATTCGGGTACACCTGGGGATCCAG	125	
QY	382	GTCGGGATGCAATTTAAAGAGAAAAAGGGGGAATGTCGAGGAAAAAGCTTTGAGAGTCT	441	
Db	126	GTCGGGATGCAATTTAAAGAGAAAAAGGGGGAATTCGAGAGAAAAAGCTTTGAGAGTCT	185	
QY	442	GGACA-CCCAACTCAAGCAGTGTTCATGAGAGTCATGAAATTAAGCATAGATCTGGG	500	
Db	186	GGACAACCCCAACTCAAGCAGAGTGTCATGAGAGTCATGAAATTAAGCATAGATCTGGG	245	
QY	501	AAATTTGGGAGTGTCAATTTACAAAGATCCGTTCAAAATAGTCTTAAGA---GTTT	555	
Db	246	AAATTTGGGAGTGTCAATTTACAAAGATCCGTTCAAAATAGTCTTAAGAGATTTT	305	



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:15:11 ; Search time 84 Seconds  
(without alignments)  
459.173 Million cell updates/sec

Title: US-09-938-418-7  
Perfect score: 1301  
Sequence: 1 MRPGPASPORTLGLLL..GDASTGWSYSRIIIEELPK 243

Scoring table: BLOSUM62

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

A.Geneset\_19Jun03: \*

1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: *
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: *
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: *
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: *
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: *
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: *
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: *
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: *
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: *
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT: *
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: *
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: *
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: *
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: *
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: *
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: *
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: *
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: *
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: *
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: *
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: *
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: *
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: *

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1301	100.0	243	21	AAV99441	Human PRO1755 (UNG
2	1301	100.0	243	21	AAV99462	Human PRO1550 amid
3	1301	100.0	243	22	AAV23206	Human PRO1550 amid
4	1301	100.0	243	22	AAV87586	Human PRO1550. He
5	1301	100.0	243	22	AAV66190	Protein of the inv
6	1301	100.0	243	22	AAV66211	Protein of the inv
7	1301	100.0	243	23	ABP6836	Human pancreatic c
8	1301	100.0	243	23	ABG95911	Human secreted/tira
9	1301	100.0	243	23	ABG78938	Human breast tumou

10	1301	100.0	243	23	ABR35545	Human angiogenesis1
11	1301	100.0	243	23	AAE30462	Human tumorigen-assoc
12	1301	100.0	243	23	ABBB4939	Human PRO1550 prob
13	1301	100.0	243	23	ABU71294	Human PRO1550 prob
14	1301	100.0	243	24	ABU71566	Human secreted pol
15	1301	100.0	243	24	ABU72012	Human human secret
16	1301	100.0	243	24	ABU72169	Novel human secret
17	1301	100.0	243	24	ABU65751	Human pro polypept
18	1301	100.0	243	24	ABU66084	Human secreted/titra
19	1301	100.0	243	24	ABU67588	Novel human secret
20	1301	100.0	243	24	ABG75948	Human secreted/titra
21	1301	100.0	243	24	ABU65446	Human antigenic ta
22	1301	100.0	243	24	ABJ37761	Human PRO polypept
23	1301	100.0	243	24	ABJ37852	Human secreted/titra
24	1301	100.0	243	24	ABU56118	Human PRO polypept
25	1301	100.0	243	24	ABU57113	Human secreted/titra
26	1301	100.0	243	24	ABU10692	Human PRO polypept
27	1301	100.0	278	23	ABP68637	Human pancreatic c
28	1301	100.0	278	23	ABG78939	Human breast tumour
29	1301	100.0	278	24	ABJ37762	Human tumour-relat
30	1294	99.5	243	22	AAJ36667	Human secretory pro
31	1294	99.5	243	23	ABG36340	Human ovarian cano
32	1294	99.5	243	23	ABU05554	Breast cancer-asso
33	1294	99.5	243	23	ABBB80978	Human REMODELIN po
34	1294	99.5	243	24	ABBR48227	Human bladder cano
35	1294	99.5	243	24	ABG75758	Human REMODELIN pr
36	1294	99.5	243	24	ABU56607	Lung cancer-associ
37	1294	99.5	278	21	ABU08856	Amnio acid sequenc
38	1294	99.5	278	22	AAW25746	Human protein sequ
39	1294	99.5	278	23	ABG36338	Human ovarian cano
40	1294	99.5	278	24	ABBR47627	Breast cancer asso
41	1291	99.2	243	21	AAJ91529	Human secreted pro
42	1291	99.2	278	23	ABP68631	Human pancreatic c
43	1289	99.1	243	23	ABJ37031	Human breast cance
44	1216	93.5	245	24	ABBB80977	Rat REMODELIN poly
45	1216	93.5	245	24	ABG75716	Rat REMODELIN prot

## ALIGNMENTS

RESULT 1	
AAV99441	
ID AAV99441	standard; Protein; 243 AA

Human PRO1755 (UNQ828) amino acid sequence SEQ ID NO:352.

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening

OS Homo sapiens.

PN W0200012708-A2

PD 09-MAR-2000.

PF 01-SEP-1999; 99WO-US20111.

PR 01-SEP-1998; 98US-0098716.

PR 01-SEP-1998; 98US-0098750.

PR 02-SEP-1998; 98US-00988821.

PR 09-SEP-1998; 98US-0099536.

PR	09-SEP-1998;	98US-0099598.
----	--------------	---------------

PR 09-SEP-1998; 98US-0099642;



```
DB      61 GVPGDGSPGANVIGTPIPRDDFKGKGGCLKESEESTPNTYKOCSSSLNYGIDL 120
OY      121 GRIACFTFTKMSNALSALVLEFSGSLRLKCRNACCORWFTFTENGACSGPLPTIALITYLDO 180
DB      121 GRIACFTFTKMSNALSALVLEFSGSLRLKCRNACCORWFTFTENGACSGPLPTIALITYLDO 180
OY      181 GSPEKNSTINIHRTSSVEGLCEGIGAGLVDAIWMVGTCSDPKGDASTGMSVSRIITEE 240
DB      181 GSPEKNSTINIHRTSSVEGLCEGIGAGLVDAIWMVGTCSDPKGDASTGMSVSRIITEE 240
OY      241 LPK 243
DB      241 LPK 243

RESULT 2
AA99462
ID      AA99462 standard; Protein; 243 AA.
XX
AC      AA99462;
XX
DT      08-AUG-2000 (first entry)
XX
DE      Human PRO1550 amino acid sequence SEQ ID NO:431.
XX
KW      Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
        transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS      Homo sapiens.
XX
PN      WO200012708-A2.
XX
PD      09-MAR-2000.
XX
PE      01-SEP-1999; 99WO-US20111.
XX
PR      01-SEP-1998; 98US-0098716.
PR      01-SEP-1998; 98US-0098749.
PR      01-SEP-1998; 98US-0098750.
PR      02-SEP-1998; 98US-0098803.
PR      02-SEP-1998; 98US-0098821.
PR      02-SEP-1998; 98US-0098843.
PR      09-SEP-1998; 98US-0099536.
PR      09-SEP-1998; 98US-0099596.
PR      09-SEP-1998; 98US-0099598.
PR      09-SEP-1998; 98US-0099602.
PR      09-SEP-1998; 98US-0099642.
PR      10-SEP-1998; 98US-0099741.
PR      10-SEP-1998; 98US-0099754.
PR      10-SEP-1998; 98US-0099763.
PR      10-SEP-1998; 98US-0099792.
PR      10-SEP-1998; 98US-0099808.
PR      10-SEP-1998; 98US-0099812.
PR      10-SEP-1998; 98US-0099816.
PR      15-SEP-1998; 98US-0099815.
PR      15-SEP-1998; 98US-0100385.
PR      15-SEP-1998; 98US-0100388.
PR      15-SEP-1998; 98US-0100390.
PR      16-SEP-1998; 98US-0100584.
PR      16-SEP-1998; 98US-0100627.
PR      16-SEP-1998; 98US-0100661.
PR      16-SEP-1998; 98US-0100662.
PR      16-SEP-1998; 98US-0100664.
PR      17-SEP-1998; 98US-0100683.
PR      17-SEP-1998; 98US-0100684.
PR      17-SEP-1998; 98US-0100710.
PR      17-SEP-1998; 98US-0100711.
PR      17-SEP-1998; 98US-0100919.
PR      17-SEP-1998; 98US-0100930.
PR      18-SEP-1998; 98US-0100848.
PR      18-SEP-1998; 98US-0100849.
PR      18-SEP-1998; 98US-0101014.
```

```
PR      18-SEP-1998; 98US-0101068.
PR      18-SEP-1998; 98US-0101071.
PR      22-SEP-1998; 98US-0101279.
PR      23-SEP-1998; 98US-0101471.
PR      23-SEP-1998; 98US-0101472.
PR      23-SEP-1998; 98US-0101474.
PR      23-SEP-1998; 98US-0101475.
PR      23-SEP-1998; 98US-0101476.
PR      23-SEP-1998; 98US-0101477.
PR      23-SEP-1998; 98US-0101479.
PR      24-SEP-1998; 98US-0101738.
PR      24-SEP-1998; 98US-0101741.
PR      24-SEP-1998; 98US-0101743.
PR      24-SEP-1998; 98US-0101915.
PR      24-SEP-1998; 98US-0101916.
PR      29-SEP-1998; 98US-0102207.
PR      29-SEP-1998; 98US-0102240.
PR      29-SEP-1998; 98US-0102307.
PR      29-SEP-1998; 98US-0102330.
PR      29-SEP-1998; 98US-0102331.
PR      29-SEP-1998; 98US-0102484.
PR      30-SEP-1998; 98US-0102487.
PR      30-SEP-1998; 98US-0102570.
PR      30-SEP-1998; 98US-0102571.
PR      01-OCT-1998; 98US-0102684.
PR      01-OCT-1998; 98US-0102687.
PR      02-OCT-1998; 98US-0102965.
PR      06-OCT-1998; 98US-0103258.
PR      06-OCT-1998; 98US-0103449.
PR      07-OCT-1998; 98US-0103314.
PR      07-OCT-1998; 98US-0103315.
PR      07-OCT-1998; 98US-0103328.
PR      07-OCT-1998; 98US-0103395.
PR      07-OCT-1998; 98US-0103396.
PR      07-OCT-1998; 98US-0103401.
PR      08-OCT-1998; 98US-0103633.
PR      08-OCT-1998; 98US-0103678.
PR      08-OCT-1998; 98US-0103679.
PR      08-OCT-1998; 98US-0103711.
PR      14-OCT-1998; 98US-0104257.
PR      20-OCT-1998; 98US-0104987.
PR      20-OCT-1998; 98US-0105000.
PR      20-OCT-1998; 98US-0105002.
PR      21-OCT-1998; 98US-0105104.
PR      22-OCT-1998; 98US-0105169.
PR      22-OCT-1998; 98US-0105266.
PR      26-OCT-1998; 98US-0105693.
PR      26-OCT-1998; 98US-0105694.
PR      27-OCT-1998; 98US-0105807.
PR      27-OCT-1998; 98US-0105881.
PR      27-OCT-1998; 98US-0105882.
PR      27-OCT-1998; 98US-0106062.
PR      28-OCT-1998; 98US-0106023.
PR      28-OCT-1998; 98US-0106029.
PR      28-OCT-1998; 98US-0106030.
PR      28-OCT-1998; 98US-0106032.
PR      28-OCT-1998; 98US-0106033.
PR      28-OCT-1998; 98US-0106178.
PR      29-OCT-1998; 98US-0106248.
PR      29-OCT-1998; 98US-0106384.
PR      29-OCT-1998; 98US-0106500.
PR      30-OCT-1998; 98US-0106464.
PR      03-NOV-1998; 98US-0106856.
PR      03-NOV-1998; 98US-0106902.
PR      03-NOV-1998; 98US-0106905.
PR      03-NOV-1998; 98US-0106919.
PR      03-NOV-1998; 98US-0106932.
PR      03-NOV-1998; 98US-0106934.
PR      10-NOV-1998; 98US-0107783.
PR      17-NOV-1998; 98US-0108775.
PR      17-NOV-1998; 98US-0108779.
PR      17-NOV-1998; 98US-0108787.
PR      17-NOV-1998; 98US-0108788.
```

PR 17-NOV-1998; 98US-0108801.  
 PR 17-NOV-1998; 98US-0108802.  
 PR 17-NOV-1998; 98US-0108806.  
 PR 17-NOV-1998; 98US-0108807.  
 PR 17-NOV-1998; 98US-0108867.  
 PR 17-NOV-1998; 98US-0108925.  
 PR 18-NOV-1998; 98US-0108848.  
 PR 18-NOV-1998; 98US-0108849.  
 PR 18-NOV-1998; 98US-0108850.  
 PR 18-NOV-1998; 98US-0108851.  
 PR 18-NOV-1998; 98US-0108852.  
 PR 18-NOV-1998; 98US-0108858.  
 PR 18-NOV-1998; 98US-0108904.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2000-237871/20.  
 DR N-PSDB; AAA37144.  
 XX  
 PT New mammalian DNA sequences encoding transmembrane, receptor or  
 PT secreted PRO polypeptides, useful for screening of potential peptide or  
 PT small molecule inhibitors of the relevant receptor/ligand interactions  
 XX  
 PS Claim 12; Fig 246; 773pp; English.  
 XX  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent  
 CC PCR primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention.  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 1301; DB 21; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-122;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPGPAPSPQRLRGLLLLLLLLPAPSSASEIPKQKQKQRLRQREVYDLYNGMCLGPA 60  
 Db 1 MRQGPAPSPQRLRGLLLLLLLLPAPSSASEIPKQKQKQRLRQREVYDLYNGMCLGPA 60  
 QY 61 GVPGRDGPSPGANYPGTPIGIPGRDGFKEGKECELRSEFSESWTPNPKQCSWSSLNIGIDL 120  
 Db 61 GVPGRDGPSPGANYPGTPIGIPGRDGFKEGKECELRSEFSESWTPNPKQCSWSSLNIGIDL 120  
 QY 121 GKIAECTFTKMRNSALRYLFSGLRLKCNACCORRYFTFNAGECGPIPIEAIITLDQ 180  
 Db 121 GKIAECTFTKMRNSALRYLFSGLRLKCNACCORRYFTFNAGECGPIPIEAIITLDQ 180  
 QY 181 GSPENSTINIHRTSSVEGLCEGIGAGLVVAIVWGCSPYPRGDASTGNNVSRIITIE 240  
 Db 181 GSPENSTINIHRTSSVEGLCEGIGAGLVVAIVWGCSPYPRGDASTGNNVSRIITIE 240  
 QY 241 LPR 243  
 Db 241 LPR 243  
 Db 241 LPR 243  
 RESULT 3  
 AA029206  
 ID AAU29206 standard; Protein; 243 AA.  
 AC  
 XX AAU29206;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human PRO polypeptide sequence #183.

XX  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 XX 28-FEB-2001; 2001WO-US06520.  
 PE  
 XX  
 XX 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-193314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 29-MAR-2000; 2000US-193053P.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194449P.  
 PR 04-APR-2000; 2000US-194647P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196820P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-10644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 XX WPI: 2001-602746/68.  
 DR N-PSDB; AAS46107.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 PS Claim 11; Fig 366; 774pp; English.  
 XX  
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of







XX DE Human pancreatic cancer expressed protein SEQ ID NO 4559.  
 XX KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
 KW cytostatic; tumour.  
 XX OS Homo sapiens.  
 XX PN WO200260317-A2.  
 XX PD 08-AUG-2002.  
 XX PF 30-JAN-2002; 2002MO-US02781.  
 XX PR 30-JAN-2001; 2001US-265305P.  
 XX PR 31-JAN-2001; 2001US-265682P.  
 XX PR 09-FEB-2001; 2001US-267568P.  
 XX PR 21-MAR-2001; 2001US-278651P.  
 XX PR 28-APR-2001; 2001US-287112P.  
 XX PR 16-MAY-2001; 2001US-291631P.  
 XX PR 12-JUL-2001; 2001US-305484P.  
 XX PR 20-AUG-2001; 2001US-313999P.  
 XX PR 27-NOV-2001; 2001US-333626P.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
 XX DR WPI: 2002-627435/67.  
 XX DR N-PSDB; ABV99144.  
 XX PT New isolated polynucleotide and pancreatic tumor polypeptides, useful  
 XX PT for diagnosing, preventing and/or treating cancer, particularly  
 XX PT pancreatic cancer.  
 XX PS Claim 2; SEQ ID NO 4559; 300bp + Sequence Listing: English.  
 XX CC The invention relates to an isolated polynucleotide (1) comprising: (a)  
 XX CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);  
 XX CC (b) complements of (a); (c) sequences consisting of at least 20  
 XX CC contiguous residues of (a); (d) sequences that hybridize to (a), under  
 XX CC moderately stringent conditions; (e) sequences having at least 75% or 90%  
 XX CC identity to (a); or (f) degenerate variants of (a). Polypeptides  
 XX CC (ABP68596-ABP68637) encoded by (1) and oligonucleotide can be used to  
 XX CC detect cancer in a patient and compositions comprising polypeptides,  
 XX CC polynucleotides, antibodies, fusion proteins, T cell populations and  
 XX CC antigen presenting cells expressing the polypeptide are useful in  
 XX CC treating pancreatic cancer and stimulating an immune response. The  
 XX CC polynucleotides can be used as probes or primers for nucleic acid  
 XX CC hybridization, in the design and preparation of ribozyme molecules for  
 XX CC inhibiting expression of the tumour polypeptides and proteins in the  
 XX CC tumour cells, in vaccines and for gene therapy.  
 XX CC Note: The sequence data for this patent did not form part of the printed  
 XX CC specification, but was obtained in electronic format directly from WIPO  
 XX CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 243 AA:  
 XX  
 XX Query Match 100.0%; Score 1301; DB 23; Length 243;  
 XX Best Local Similarity 100.0%; Pred. No. 8.3e-122;  
 XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GSEPMNSTINHRTSSVEGICGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240  
 DB 181 GSEPMNSTINHRTSSVEGICGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIEE 240  
 QY 241 LPR 243  
 DB 241 LPR 243  
 DB 241 LPR 243  
 RESULT 8  
 ABG95911  
 ID ABG95911 standard; Protein; 243 AA.  
 XX AC ABG95911;  
 XX XX  
 DT 10-DEC-2002 (first entry)  
 XX XX  
 DE Human secreted/transmembrane protein PRO1550.  
 XX XX  
 KW Human; secreted protein; transmembrane protein; anti-rheumatic;  
 KW antiarthritic; osteopathic; sports-related joint problem;  
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.  
 XX OS Homo sapiens.  
 XX PN US2002119130-A1.  
 XX PD 29-AUG-2002.  
 XX PF 06-DEC-2001; 2001US-0006867.  
 XX PR 29-OCT-1997; 97US-063435P.  
 XX PR 22-APR-1998; 98US-064215P.  
 XX PR 29-APR-1998; 98US-082797P.  
 XX PR 15-MAY-1998; 98US-083435P.  
 XX PR 10-JUN-1998; 98US-085579P.  
 XX PR 10-JUN-1998; 98US-088811P.  
 XX PR 10-JUN-1998; 98US-088824P.  
 XX PR 11-JUN-1998; 98US-088825P.  
 XX PR 12-JUN-1998; 98US-089105P.  
 XX PR 16-JUN-1998; 98US-089514P.  
 XX PR 16-SEP-1998; 98WO-US19330.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 XX PR 14-MAY-1999; 99WO-US10733.  
 XX PR 02-JUN-1999; 99WO-US12252.  
 XX PR 01-SEP-1999; 99WO-US20111.  
 XX PR 15-SEP-1999; 99WO-US21090.  
 XX PR 22-DEC-1999; 99WO-US21194.  
 XX PR 18-FEB-2000; 2000WO-US04341.  
 XX PR 18-FEB-2000; 2000WO-US04342.  
 XX PR 30-MAR-2000; 2000WO-US08439.  
 XX PR 02-MAY-2000; 2000WO-US14042.  
 XX PR 02-JUN-2000; 2000WO-US15264.  
 XX PR 23-AUG-2000; 2000WO-US23322.  
 XX PR 24-AUG-2000; 2000WO-US23328.  
 XX PR 10-NOV-2000; 2000WO-US30873.  
 XX PR 01-DEC-2000; 2000WO-US32378.  
 XX PR 20-DEC-2000; 2000WO-US34956.  
 XX PR 28-FEB-2001; 2001WO-US06520.  
 XX PR 20-JUN-2001; 2001WO-US19692.  
 XX PR 29-JUL-2001; 2001WO-US21065.  
 XX PR 09-JUL-2001; 2001WO-US21735.  
 XX PA (GETH) GENENTECH INC.  
 XX PI Baton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX DR WPI: 2002-731348/79.  
 XX DR N-PSDB; AB574438.



```

QY      121 GKIAECTFKMRNSALRVLFSGSLRLKCRNACCOQWYFTFNAGECSGPLPIAIIYLDO 180
DB      121 GKIAECTFKMRNSALRVLFSGSLRLKCRNACCOQWYFTFNAGECSGPLPIAIIYLDO 180
QY      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIWTGCTSDPYPGDASTGMNSVSRIITIEE 240
DB      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIWTGCTSDPYPGDASTGMNSVSRIITIEE 240
QY      241 LPK 243
DB      241 LPK 243

RESULT 10
ABB95545
ID      ABB95545 standard; Protein: 243 AA.
XX
AC      ABB95545;
XX
DE      19-JUL-2002 (first entry)
XX
DE      Human angiogenesis related protein PRO1550 SEQ ID NO: 246.
XX
KW      Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW      cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnery;
KW      antiarteriosclerotic.
XX
OS      Homo sapiens.
XX
PN      W0200208284-A2.
XX
PD      31-JAN-2002.
XX
PF      09-JUL-2001; 2001MO-US21735.
XX
XX      20-JUL-2000; 2000US-219556P.
XX      25-JUL-2000; 2000US-220624P.
XX      25-JUL-2000; 2000US-220664P.
XX      28-JUL-2000; 2000MO-US20710.
XX      02-AUG-2000; 2000US-222695P.
XX      17-AUG-2000; 2000US-0643657.
XX      23-AUG-2000; 2000MO-US23522.
XX      24-AUG-2000; 2000MO-US23328.
XX      07-SEP-2000; 2000US-230978P.
XX      15-SEP-2000; 2000US-000000P.
XX      18-SEP-2000; 2000US-0664610.
XX      18-SEP-2000; 2000US-0665350.
XX      24-OCT-2000; 2000US-242922P.
XX      08-NOV-2000; 2000US-0709238.
XX      08-NOV-2000; 2000MO-US30952.
XX      10-NOV-2000; 2000MO-US30873.
XX      01-DEC-2000; 2000MO-US32678.
XX      20-DEC-2000; 2000US-0747259.
XX      20-DEC-2000; 2000MO-US34956.
XX      22-JAN-2001; 2001US-0767609.
XX      28-FEB-2001; 2001US-0796498.
XX      28-FEB-2001; 2001MO-US06520.
XX      01-MAR-2001; 2001MO-US06666.
XX      09-MAR-2001; 2001US-0802706.
XX      14-MAR-2001; 2001US-0808689.
XX      22-MAR-2001; 2001US-0816744.
XX      05-APR-2001; 2001US-0828368.
XX      10-MAY-2001; 2001US-0854280.
XX      10-MAY-2001; 2001US-0854280.
XX      25-MAY-2001; 2001US-0866028.
XX      25-MAY-2001; 2001US-0866034.
XX      25-MAY-2001; 2001MO-US17092.
XX      30-MAY-2001; 2001US-0870574.
XX      30-MAY-2001; 2001MO-US17443.
XX      01-JUN-2001; 2001MO-US17800.
XX      20-JUN-2001; 2001MO-US19692.

```

```

PR      28-JUN-2001; 2001MO-US00000.
XX
XX      (GETH ) GENENTECH INC.
PA      (BAKE/) BAKER K P.
PA      (FERR/) FERRARA N.
PA      (GERB/) GERBER H.
PA      (GERR/) GERRTSEN M E.
PA      (GODD/) GODDARD A.
PA      (GODO/) GODOMSKI P J.
PA      (GURN/) GURNEY A L.
PA      (HILL/) HILLAN K J.
PA      (MARS/) MARSTERS S A.
PA      (PANJ/) PAN J.
PA      (PAON/) PAONI N F.
PA      (STEP/) STEPHAN J F.
PA      (WATA/) WATANABE C K.
PA      (WILL/) WILLIAMS P M.
PA      (WOOD/) WOOD W I.
XX
XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX      WPI, 2002-171999/22.
DR      N-PSDB; ABL95683.
XX
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT      infarction), endothelial or angiogenic disorders in a mammal -
XX
XX      Claim 11; Fig 246; 567P; English.
XX
XX      The present invention provides the protein and coding sequences of human
CC      PRO proteins. These are useful for treating or diagnosing a
CC      cardiovascular, endothelial or angiogenic disorder, including cardiac
CC      hypertrophy, trauma, cancer, age-related macular degeneration,
CC      atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
CC      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC      healing. The present sequence is a PRO protein of the invention.
XX
SQ      Sequence 243 AA;
XX
XX      Query Match 100.0%; Score 1301; DB 23; Length 243;
XX      Best Local Similarity 100.0%; Pred. No. 8.3e-122;
XX      Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MRPGPAASFORLRLGILLLLLLLPAPSSASEIPKGRKQAKLRQREYVDLYNMCIOGPA 60
DB      1 MRPGPAASFORLRLGILLLLLLLPAPSSASEIPKGRKQAKLRQREYVDLYNMCIOGPA 60
QY      61 GVPGRDGPANVYIPGTGPIGRDGRKGEGLRESFESWTPNPKQCSWSSLYNGIDL 120
DB      61 GVPGRDGPANVYIPGTGPIGRDGRKGEGLRESFESWTPNPKQCSWSSLYNGIDL 120
QY      121 GKIAECTFKMRNSALRVLFSGSLRLKCRNACCOQWYFTFNAGECSGPLPIAIIYLDO 180
DB      121 GKIAECTFKMRNSALRVLFSGSLRLKCRNACCOQWYFTFNAGECSGPLPIAIIYLDO 180
QY      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIWTGCTSDPYPGDASTGMNSVSRIITIEE 240
DB      181 GSPENSTINIHRTSSVEGLCEGIGAGLVDAIWTGCTSDPYPGDASTGMNSVSRIITIEE 240
QY      241 LPK 243
DB      241 LPK 243

RESULT 11
AAE20462
ID      AAE20462 standard; Protein: 243 AA.
XX
AC      AAE20462;

```

```

XX 01-JUL-2002 (first entry)
DE Human tumour-associated antigenic target-170 (TA170) protein.
XX
XX Human: tumour-associated antigenic target-170; TA170; cytosolic;
KM gene therapy; tumour; breast; lung; liver; stomach; cancer; ADPPI;
KM antibody-dependent enzyme mediated produg therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..30
XX Protein /label= Signal_peptide
XX /label= Mature_TA170_protein
XX Modified-site 67..72
XX /note= "N-myristoylation site"
XX Modified-site 117..122
XX /note= "N-myristoylation site"
XX Modified-site 163..168
XX /note= "N-myristoylation site"
XX Modified-site 186..189
XX /note= "N-myristoylation site"
XX Modified-site 199..204
XX /note= "Asn is N-glycosylated"
XX Modified-site 203..208
XX /note= "N-myristoylation site"
XX
XX WO200216602-A2.
XX
XX 28-FEB-2002.
XX
XX 23-AUG-2001; 2001WO-US26626.
XX
XX 24-AUG-2000; 2000WO-US23328.
XX 01-DEC-2000; 2000WO-US3678.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US1800.
XX 20-JUN-2001; 2001WO-US19692.
XX 29-JUN-2001; 2001WO-US21066.
XX 09-JUL-2001; 2001WO-US21735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Polakis P;
XX Williams PM, Wood WL, Wu TD, Zhang Z;
XX
XX WPI: 2002-292065/33.
XX N-PSDB: AAD32717.
XX
XX New antibodies that bind tumor-associated antigenic target (TA170)
XX polypeptides, useful for treating and diagnosing tumor (e.g. breast,
XX lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle,
XX pigs, goats, rabbits or humans
XX
XX Claim 1; Fig 7; 124pp; English.
XX
XX The present invention relates to an isolated antibody that binds to
XX tumor-associated antigenic target (TA170) polypeptide. The antibody is
XX used for treating and diagnosing tumors (e.g. breast, lung, liver or
XX stomach tumors) in mammals, e.g. dogs, cats, cattle, horses, sheep,
XX pigs, goats, rabbits, or preferably humans. The antibody may also be
XX used in antibody-dependent enzyme mediated produg therapy (ADPPI).
XX The antibody is also useful for the therapeutic treatment or for the
XX diagnostic detection of cancer. TA170 cDNA is useful in gene therapy.
XX The present sequence is human TA170 protein. TA170 cDNA is designated
XX as DNA76393-1664.
XX
XX Sequence 243 AA:
XX
XX Query Match 100.0%; Score 1301; DB 23; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 8.3e-122;

```

```

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MRPGPAAPORLRLLILLQLPAPSSASEIPKQKQALRQREVVDLYNGMCIQSPA 60
DB 1 MRPGPAAPORLRLLILLQLPAPSSASEIPKQKQALRQREVVDLYNGMCIQSPA 60
OY 61 GYPGDSBPGANVIGTPIGRDGFKEBKGECLRESEESWTPNYKQCSWSLNYGIDL 120
DB 61 GYPGDSBPGANVIGTPIGRDGFKEBKGECLRESEESWTPNYKQCSWSLNYGIDL 120
OY 121 GKIACTFFKMSNSALRYLPSGSLRLCRNACCORWYFTFGARCSPPLPEATITVYDO 180
DB 121 GKIACTFFKMSNSALRYLPSGSLRLCRNACCORWYFTFGARCSPPLPEATITVYDO 180
OY 181 GSPENNSTINIHRTSSVSGLCGIGAGLVDAIHWGTCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENNSTINIHRTSSVSGLCGIGAGLVDAIHWGTCSDPYKGDASTGMSVSRITIEE 240
OY 241 LPK 243
DB 241 LPK 243
RESULT 12
ABB84939
ID ABB84939 standard; Protein; 243 AA.
AC ABB84939;
DE 16-MAY-2002 (first entry)
XX
XX Human PRO1550 protein sequence SEQ ID NO:246.
XX
XX Human; angiogenesis; cardiant; cytosolic; antitumorogenic; hypotensive;
XX vulnereary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
XX
XX Homo sapiens.
XX
XX WO200200690-A2.
XX
XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US4956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 01-MAR-2001; 2001WO-US06520.
XX

```

PR 09-MAR-2001: 2001US-0802706.  
 PR 14-MAR-2001: 2001US-0808689.  
 PR 22-MAR-2001: 2001US-0816744.  
 PR 05-APR-2001: 2001US-0828366.  
 PR 10-MAY-2001: 2001US-0854208.  
 PR 10-MAY-2001: 2001US-0854280.  
 PR 25-MAY-2001: 2001US-0866028.  
 PR 25-MAY-2001: 2001US-0866034.  
 PR 25-MAY-2001: 2001US-0866034.  
 PR 30-MAY-2001: 2001US-0870574.  
 PR 30-MAY-2001: 2001US-0870574.  
 PR 01-JUN-2001: 2001US-0871443.  
 PR 01-JUN-2001: 2001US-0871443.  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gerltsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Peoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 DR MPI; 2002-090516/12.  
 DR N-PSDB; ABL88194.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 PS  
 PS Claim 11; Fig 246; 565bp; English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABL88194 to  
 CC ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 XX  
 SQ Sequence 243 AA:  
 Query Match 100.0%; Score 1301; DB 23; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-122;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPGPASPQRRLGILLLLQLPAPSSASEIPKQKQAKLRQREVVDLYNMCLOGPA 60  
 DB 1 MRPGPASPQRRLGILLLLQLPAPSSASEIPKQKQAKLRQREVVDLYNMCLOGPA 60  
 QY 61 GVPGRGSGPQANVYIPPTGPIPGRDGFKGKGECLRSFEESWTPNPKQCSWSILNYGIDL 120  
 DB 61 GVPGRGSGPQANVYIPPTGPIPGRDGFKGKGECLRSFEESWTPNPKQCSWSILNYGIDL 120  
 QY 121 GRTAECTFTKMSNSALRYLFSGLRLKCNACCOWYEFNAGCSGPIPAITYLDQ 180  
 DB 121 GRTAECTFTKMSNSALRYLFSGLRLKCNACCOWYEFNAGCSGPIPAITYLDQ 180  
 QY 181 GSPEMNSTINIRHTSSVEGICGAGLVDAIWTGSDPYKGDASTGNSVSRIITEE 240  
 DB 181 GSPEMNSTINIRHTSSVEGICGAGLVDAIWTGSDPYKGDASTGNSVSRIITEE 240  
 QY 241 LPK 243  
 DB 241 LPK 243

XX  
 AC ABL88194;  
 XX  
 DT 10-JUN-2003 (first entry)  
 XX  
 DE Human PRO1550 protein.  
 XX  
 KW Human; PRO; secreted; transmembrane; cytosolic; TNF-alpha; blood;  
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;  
 KW differentiation; tumour; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036143-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 02-JUL-2002; 2002US-0187600.  
 XX  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28351.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 29-AUG-2001; 2001WO-US27099.  
 PR 18-SEP-1997; 97US-059263P.  
 PR 18-SEP-1997; 97US-059266P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-063120P.  
 PR 28-OCT-1997; 97US-063121P.  
 PR 28-OCT-1997; 97US-063540P.  
 PR 28-OCT-1997; 97US-063541P.  
 PR 28-OCT-1997; 97US-063544P.  
 PR 28-OCT-1997; 97US-063564P.  
 PR 29-OCT-1997; 97US-063734P.  
 PR 31-OCT-1997; 97US-063870P.  
 PR 13-NOV-1997; 97US-064103P.  
 PR 21-NOV-1997; 97US-065120P.  
 PR 24-NOV-1997; 97US-064466P.  
 PR 24-NOV-1997; 97US-066772P.  
 PR 11-DEC-1997; 97US-069335P.  
 PR 12-DEC-1997; 97US-069425P.

RESULT 13  
 AB071294  
 ID AB071294 standard; Protein; 243 AA.

PR 17-DEC-1997; 97US-069870P.  
PR 18-DEC-1997; 97US-068017P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077649P.  
PR 20-MAR-1998; 98US-078886P.  
PR 20-MAR-1998; 98US-079399P.  
PR 27-MAR-1998; 98US-079664P.  
PR 27-MAR-1998; 98US-079786P.  
PR 31-MAR-1998; 98US-080107P.  
PR 31-MAR-1998; 98US-080194P.  
PR 01-APR-1998; 98US-080327P.  
PR 01-APR-1998; 98US-080333P.  
PR 08-APR-1998; 98US-081049P.  
PR 08-APR-1998; 98US-081070P.  
PR 09-APR-1998; 98US-081198P.  
PR 15-APR-1998; 98US-081838P.  
PR 21-APR-1998; 98US-082568P.  
PR 21-APR-1998; 98US-082569P.  
PR 22-APR-1998; 98US-082704P.  
PR 22-APR-1998; 98US-082797P.  
PR 28-APR-1998; 98US-083322P.  
PR 29-APR-1998; 98US-083495P.  
PR 29-APR-1998; 98US-083496P.  
PR 29-APR-1998; 98US-083499P.  
PR 29-APR-1998; 98US-083559P.  
PR 05-MAY-1998; 98US-084366P.  
PR 06-MAY-1998; 98US-084414P.  
PR 07-MAY-1998; 98US-084639P.  
PR 07-MAY-1998; 98US-084640P.  
PR 15-MAY-1998; 98US-084643P.  
PR 15-MAY-1998; 98US-085579P.  
PR 15-MAY-1998; 98US-085580P.  
PR 15-MAY-1998; 98US-085582P.  
PR 18-MAY-1998; 98US-085700P.  
PR 22-MAY-1998; 98US-086023P.  
PR 22-MAY-1998; 98US-086392P.  
PR 28-MAY-1998; 98US-086486P.  
PR 28-MAY-1998; 98US-087098P.  
PR 28-MAY-1998; 98US-087208P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088033P.  
PR 05-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088722P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088740P.  
PR 10-JUN-1998; 98US-088811P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088825P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088863P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089090P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.

PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090461P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090688P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 26-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091010P.  
PR 01-JUL-1998; 98US-091359P.  
PR 01-JUL-1998; 98US-091548P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091486P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091632P.  
PR 04-JUL-1998; 98US-094006P.  
PR 04-AUG-1998; 98US-095282P.  
PR 10-AUG-1998; 98US-095998P.  
PR 17-AUG-1998; 98US-096012P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096959P.  
PR 26-AUG-1998; 98US-097022P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-098014P.  
PR 01-SEP-1998; 98US-098716P.  
PR 01-SEP-1998; 98US-098723P.  
PR 02-SEP-1998; 98US-098803P.  
PR 02-SEP-1998; 98US-098821P.  
PR 02-SEP-1998; 98US-098843P.  
PR 09-SEP-1998; 98US-099602P.  
PR 10-SEP-1998; 98US-099741P.  
PR 10-SEP-1998; 98US-099754P.  
PR 10-SEP-1998; 98US-099763P.  
PR 10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 1301; DB 24; Length 243;  
Best Local Similarity 100.0%; Pred. No. 8.3e-122; Indels 0; Gaps 0;  
Matches 243; Conservative 0; Mismatches 0;

QY 1 MRPOGPASPORIRKILLILLILLQLPAPSSASEIPGKOKAOLROREVDLYNGKIOGPA 60  
|||||  
DB 1 MRPOGPASPORIRKILLILLILLQLPAPSSASEIPGKOKAOLROREVDLYNGKIOGPA 60  
|||||  
QY 61 GVPGRDGGPGANVIGTPIGPIGRDGFKEGKECECLRESFEESWTPNYKOCSSSINTYIDL 120  
|||||  
DB 61 GVPGRDGGPGANVIGTPIGPIGRDGFKEGKECECLRESFEESWTPNYKOCSSSINTYIDL 120  
|||||  
QY 121 GKIAECTFTKMRNSALAVLFFSGSLRLKCRNACCORWYFTFTNGACRCSPLPIEATIIYDQ 180  
|||||  
DB 121 GKIAECTFTKMRNSALAVLFFSGSLRLKCRNACCORWYFTFTNGACRCSPLPIEATIIYDQ 180  
|||||  
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDPKPKDASTGMNSVSRITIEE 240  
|||||  
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIVWGTCSDPKPKDASTGMNSVSRITIEE 240  
|||||



QY 241 LPK 243  
DB 241 LPK 243

RESULT 14  
AB071566  
ID AB071566 standard; Protein; 243 AA.  
XX  
AC AB071566;  
XX  
DF 10-JUN-2003 (first entry)  
XX  
DE Human secreted polypeptide PRO1550.  
XX  
KM Human; gene therapy; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003013855-A1.  
PD  
XX 16-JAN-2003.  
PF 03-MAY-2002; 2002US-0063616.  
XX  
XX 30-DEC-1998; 98KR-0062142.  
PR 08-MAR-1999; 99MO-US05028.  
PR 14-MAY-1999; 99MO-US10733.  
PR 30-DEC-1999; 99MO-US31274.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 21-MAR-2000; 2000MO-US07532.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 10-NOV-2000; 2000MO-US30873.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 20-DEC-2000; 2000MO-US34956.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 14-MAY-1999; 99US-0311832.  
PR 25-AUG-1999; 99US-0380137.  
PR 25-AUG-1999; 99US-0380138.  
PR 25-AUG-1999; 99US-0380139.  
PR 25-AUG-1999; 99US-0380142.  
PR 15-SEP-1999; 99US-0397342.  
PR 18-OCT-1999; 99US-0403297.  
PR 12-NOV-1999; 99US-0423844.  
PR 22-AUG-2000; 2000US-0644848.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 08-NOV-2000; 2000US-0709238.  
PR 20-DEC-2000; 2000US-0747259.  
PR 22-MAR-2001; 2001US-0816744.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 30-MAY-2001; 2001US-0870574.  
PR 05-JUN-2001; 2001US-0874503.  
PR 29-JUN-2001; 2001US-0869599.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-DEC-2001; 2001US-0006867.  
XX  
XX (GETH ) GENENTECH INC.  
PI Eaton DL., Fliviaroff E., Gerritsen ME., Goddard A., Godowski PJ;  
PI Grimaldi JC., Gurney AL., Watanabe CK., Wood WI;  
XX WPI: 2003-330485/31.  
DR N-PSDB; ACA58870.  
XX  
PT New isolated antibody specifically binding a PRO polypeptide, useful

PT for the preparation of a medicament for treating disorders with the  
PT aberrant expression or activity of the PRO polypeptide, such as tumor  
PT conditions and cancer  
XX  
XX  
PS Disclosure; Page 194-195; 406pp; English.  
XX  
XX The invention relates to an antibody that binds to a polypeptide with a  
CC fully defined sequence given in the specification. The methods and  
CC compositions (containing antibodies that specifically bind a PRO  
CC polypeptide) of the present invention are useful for the preparation of a  
CC medicament for the treatment of disorders associated with the aberrant  
CC expression or activity of the PRO polypeptide, such as tumor conditions  
CC and cancer. They can also be used to generate transgenic or knockout  
CC animals useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
CC molecular weight markers for protein electrophoresis, chromosome  
CC identification and tissue typing. The PRO polypeptides are useful to  
CC induce angiogenesis e.g wound healing; in the treatment of sports-related  
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
CC antibodies may be used in various diagnostic, competitive binding and/or  
CC immunoprecipitation assays. The present sequence represents the amino  
CC acid sequence of a PRO polypeptide of the invention.  
XX  
XX  
SQ Sequence 243 AA;  
Query Match 100.0%; Score 1301; DB 24; Length 243;  
Best Local Similarity 100.0%; Pred. No. 8 3e-122;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRPGPAPSPQRRLGLLLILLLLLPAPSSASEIPKQKAKLOREVVLDYNGMCLGPA 60  
DB 1 MRPGPAPSPQRRLGLLLILLLLLPAPSSASEIPKQKAKLOREVVLDYNGMCLGPA 60  
QY 61 GVPGRGSSPANYIPGPGIPGRDGFGEGLREFEESWPNKQCSWLNTGIDL 120  
DB 61 GVPGRGSSPANYIPGPGIPGRDGFGEGLREFEESWPNKQCSWLNTGIDL 120  
QY 121 GKIAECTFTMRNSALRVFSGSLRKCNNACQRYFFFNAGECSGPIPIAITYLDQ 180  
DB 121 GKIAECTFTMRNSALRVFSGSLRKCNNACQRYFFFNAGECSGPIPIAITYLDQ 180  
QY 181 GSPENNSTINIHRTSSVEGLCEGIGALVDVAIVGTCSDPKGDASTGNSVSRITIEE 240  
DB 181 GSPENNSTINIHRTSSVEGLCEGIGALVDVAIVGTCSDPKGDASTGNSVSRITIEE 240  
QY 241 LPK 243  
DB 241 LPK 243

RESULT 15  
AB072012  
ID AB072012 standard; Protein; 243 AA.  
XX  
XX AB072012;  
AC  
XX  
XX 11-JUN-2003 (first entry)  
DT  
XX  
DE Novel human secreted and transmembrane protein PRO1550.  
XX  
XX  
XX Human; secreted and transmembrane polypeptide;  
KM chromosome mapping; gene mapping; transgenic animal; knockout animal;  
KM therapeutic agent screening; chromosome identification; tissue typing;  
KM gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003018183-A1.  
PN  
XX  
XX 23-JAN-2003.  
PD  
XX  
XX 01-MAY-2002; 2002US-0063512.  
PF

